Based on this analysis, it was predicted that this GAS-specific protein and its epitopes, could be useful antigens for vaccines or diagnostics.

Example 2984

A DNA sequence <SEQ ID 9013> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9014>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 3
McG: Discrim Score:     10.50
GvH: Signal Score (-7.5): -5.2
     Possible site: 40
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 4 value: -12.26 threshold:  0.0
   INTEGRAL    Likelihood =-12.26   Transmembrane   98 - 114 (  94 - 116)
   INTEGRAL    Likelihood = -8.17   Transmembrane    5 -  21 (   1 -  27)
   INTEGRAL    Likelihood = -6.95   Transmembrane   62 -  78 (  57 -  80)
   INTEGRAL    Likelihood = -5.84   Transmembrane   37 -  53 (  30 -  55)
   PERIPHERAL  Likelihood = 17.35      81
 modified ALOM score:   2.95

*** Reasoning Step: 3

----- Final Results -----
              bacterial membrane --- Certainty=0.5904(Affirmative) < succ>
               bacterial outside --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
ORF01345(292 - 636 of 951)
PIR|G64646|G64646(56 - 168 of 205) hypothetical protein HP1015 - Helicobacter pylori
(strain 26695)
%Match = 4.4
%Identity = 30.6  %Similarity = 54.1
Matches = 34  Mismatches = 46  Conservative Sub.s = 26

87       117       147       177       207       237       267       297
LSGMGATFVPQTLIHRYLDKECNVYHFHKNKLFSEYIMIYKKDVELSGIALLLYKAFLTK*FR*FY*KSVYFLPKSV*NR
                                                                           |
                          RYFLQNIIHIHQNKELQFIKKCLLGYFFAPLCGAILLVLFIVSSGAKSFQISNLFNN
                                  10        20        30        40        50

327       357       381       411       441       471       501
PMIYKIIASLFLVLIPIFSQVL--VKIFKLKKFNIMFPDVAFPIFVFLIPLISSSLLKQNLLPYYLILISLLAIGITI--
 : | :: |||| :   :  :   :: |: :    | : ||  :  ::  | | |:     |     :||:  |::|
QLAYIVLLSLFLCALGFIAGAIGFYRLSKITRHLSFFENFAFSFLAVILCAILSYLV-----PNASNALSLIGNGVSIFY
           70        80        90        100       110           120       130

549       579       606       636       666       696       726       756
--KLLRTKTLFSYKRFLKLFWRSGF-ILTFLFYLGLLVIIFIKVQ*KELDKLNCTPKVRQKI*RLGCFSDEIKL*R*TRN
  || |  :|:: :||    : ||| :| | | | || |:
LHKLYRELSLYTQERF----FLSGFRLLLFSFMLALLGILVQALVIIFLTTAVVLMCVALGFLARAFLNFSQVFLKA
                   150       160       170       180       190       200
```

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2985

A DNA sequence <SEQ ID 9015> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9016>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 10
```

```
McG: Discrim Score:     13.20
GvH: Signal Score (-7.5): -2.08
     Possible site: 34
>>> Seems to have a cleavable N-term signal seq.
ALOM program   count: 0 value:  10.45 threshold:  0.0
   PERIPHERAL  Likelihood = 10.45      36
 modified ALOM score:  -2.59

*** Reasoning Step: 3

----- Final Results -----
                bacterial outside --- Certainty=0.3000(Affirmative) < succ>
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
43.9/72.0% over 56aa
                                                                    Streptococcus
pneumoniae
  EGAD|7626| epua protein Insert characterized
  SP|Q03159|EPUA_STRPN EPUA PROTEIN. Insert characterized
  GP|47373|emb|CAA38133.1||X54225 7 kDa protein Insert characterized
  PIR|S10640|S10640 epuA protein - Insert characterized

ORF01809(331 - 501 of 801)
EGAD|7626|7426(8 - 64 of 64) epua protein {Streptococcus pneumoniae}SP|Q03159|EPUA_STRPN
EPUA     PROTEIN.GP|47373|emb|CAA38133.1||X54225     7     kDa     protein     {Streptococcus
pneumoniae}PIR|S10640|S10640 epuA protein - Streptococcus pneumoniae
%Match = 10.0
%Identity = 43.9  %Similarity = 71.9
Matches = 25  Mismatches = 16  Conservative Sub.s = 16

171       201       231       261       291       321       351       381
RSCLLTYELVQL*SWQEWLRKGKQ*LAN*PI*TVVIINSMKN*RLLVLILNV*VRRNMASSGWKYVLKQIGLIVLVILLA
                                                        :    ||:|:: |:::|::|
                                                    MKMNKKSSYVVKRLLLVIIVLILG
                                                            10        20

411       441       471       501       531       561       591       621
LLFLAVGLMLGYSVFGDGEHAYSILSLDKWQNIIGKFLGK*KEPL*VI*CL*WFPLRVNFSSRIIQ*QKNKNK*QLRL*L
 | | :|||:|| ::| |:  ::|||  ||| :| || |
TLALGIGLMVGYGILGKGQDPWAILSPAKWQELIHKFTGN
              40        50        60
```

A related DNA sequence <SEQ ID 10507> was identified in GBS which encodes amino acid sequence <SEQ ID 10508>.

SEQ ID 9016 (GBS168) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 33 (lane 9; MW 7.6kDa) and in Figure 34 (lane 5; MW 7.6kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 42 (lane 2; MW 32.6kDa).

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vacc

Example 2986

A DNA sequence <SEQ ID 9017> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9018>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 8
McG: Discrim Score:     -2.85
```

```
GvH: Signal Score (-7.5): -5.7
     Possible site: 21
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 0 value:   5.25 threshold:  0.0
   PERIPHERAL  Likelihood =  5.25     103
 modified ALOM score:  -1.55

*** Reasoning Step: 3

----- Final Results -----
              bacterial cytoplasm --- Certainty=0.1210(Affirmative) < succ>
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
56.1/72.0% over 131aa
                                        Escherichia coli
  EGAD|40237| arsenate reductase Insert characterized
  SP|P52147|ARC2_ECOLI ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER). Edit characterized
  GP|1061418|gb|AAB09628.1||U38947 ArsC {Plasmid R46} Insert characterized

ORF00095(304 - 699 of 1008)
EGAD|40237|42398(1 - 132 of 141) arsenate reductase {Escherichia coli} SP|P52147|ARC2_ECOLI
ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER). GP|1061418|gb|AAB09628.1||U38947 ArsC
{Plasmid R46}
%Match = 22.0
%Identity = 56.1  %Similarity = 72.0
Matches = 74  Mismatches = 37  Conservative Sub.s = 21

129       159       189       219       249       279       309       339
RIHSSLSL*PIFHRKRPYPSRAFRRYFSNSCG*LWC*YCDDWRELLAGLGINFYFLKTLVALKIERKMMEKIRIYHNPNC
                                                                 |  | |||||:|
                                                                MSNITIYHNPHC
                                                                        10

369       399       429       459       489       519       549       579
GTSRNVLAIIRHCGIEPEIIYYLKTPPSRMELVELLLEMKLSARELLRTDVPAYEKFNLESSSVTDEEMIDAMIQDPILI
||||| | :||: |||| :| ||:||||| ||::|: :| :| | ||| :|  ||:: |     ||:::|| |:| ||||
GTSRNTLEMIRNSGIEPTVILYLETPPSRDELLKLIADMGISVRALLRKNVEPYEELGLAEDKFTDDQLIDFMLQHPILI
                30        40        50        60        70        80        90

609       639       669       699       729       759       789       819
NRPIVVTSKGAKLCRPCEAILTILPVKMEKDFVKEDGQIIQSL*HIV**IMV*EVSK*HY*KKLMRLETFCKQKASQHQN
|||||||  | ||||| | :| |||   :  | ||||: :
NRPIVVTPLGTKLCRPSEVVLDILPDAQKAAFTKEDGEKVVDDSGKRLK
               110       120       130       140
```

SEQ ID 9018 (GBS45) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 8 (lane 4; MW 18.6kDa).

The GBS45-His fusion product was purified (Figure 97A; see also Figure 191, lane 5) and used to immunise mice (lane 1 product; 20µg/mouse). The resulting antiserum was used for Western blot (Figure 97B), FACS (Figure 97C), and in the *in vivo* passive protection assay (Table III). These tests confirm that the protein is immunoaccessible on GBS bacteria and that it is an effective protective immunogen.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2987

A DNA sequence <SEQ ID 9019> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9020>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 3
McG: Discrim Score:      6.84
GvH: Signal Score (-7.5): 2.98
     Possible site: 25
>>> Seems to have a cleavable N-term signal seq.
ALOM program   count: 0 value:  13.69 threshold:  0.0
   PERIPHERAL  Likelihood = 13.69      77
 modified ALOM score:  -3.24

*** Reasoning Step: 3

----- Final Results -----
               bacterial outside --- Certainty=0.3000(Affirmative) < succ>
             bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
            bacterial cytoplasm --- Certainty=0.0000(Not Clear)
```

A DNA sequence <SEQ ID 10337> was identified in GBS which encodes amino acid sequence <SEQ ID 10338>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

SEQ ID 9020 (GBS55) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 17 (lane 7; MW 11.3kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 33 (lane 5; MW 36.3kDa).

GBS55-GST was purified as shown in Figure 197, lane 5.

GBS671 was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 161 (lane 2-4; MW 12kDa) and in Figure 188 (lane 2; MW 12kDa). Purified protein is shown in Figure 242, lane 3.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2988

A DNA sequence <SEQ ID 9021> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9022>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 3
McG: Discrim Score:    -14.35
GvH: Signal Score (-7.5): -2.12
     Possible site: 44
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 4 value: -13.90 threshold:  0.0
   INTEGRAL    Likelihood =-13.90   Transmembrane  101 - 117 (  92 - 126)
   INTEGRAL    Likelihood = -7.64   Transmembrane  130 - 146 ( 125 - 148)
   INTEGRAL    Likelihood = -6.64   Transmembrane   24 -  40 (  20 -  45)
   INTEGRAL    Likelihood = -2.44   Transmembrane   55 -  71 (  55 -  75)
   PERIPHERAL  Likelihood = 17.40       2
 modified ALOM score:   3.28

*** Reasoning Step: 3

----- Final Results -----
             bacterial membrane --- Certainty=0.6562(Affirmative) < succ>
              bacterial outside --- Certainty=0.0000(Not Clear) < succ>
            bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

SEQ ID 9022 (GBS215) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 175 (lane 10; MW 45kDa).

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2989

A DNA sequence <SEQ ID 9023> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9024>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 0
McG: Discrim Score:     11.66
GvH: Signal Score (-7.5): -5.3
     Possible site: 61
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 2 value: -14.12 threshold:  0.0
   INTEGRAL    Likelihood =-14.12   Transmembrane   13 -  29 (   5 -  35)
   INTEGRAL    Likelihood = -8.17   Transmembrane   44 -  60 (  39 -  65)
   PERIPHERAL  Likelihood = 39.00       29
 modified ALOM score:   3.32

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.6647(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

SEQ ID 9024 (GBS217) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 85 (lane 2; MW 36.1kDa) and in Figure 156 (lane 1 & 3; MW 36kDa).

GBS217-GST was purified as shown in Figure 224, lane 5-6.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2990

A DNA sequence <SEQ ID 9025> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9026>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 10
McG: Discrim Score:      8.20
GvH: Signal Score (-7.5): -3.7
     Possible site: 33
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 4 value:  -9.98 threshold:  0.0
   INTEGRAL    Likelihood = -9.98   Transmembrane   22 -  38 (  12 -  43)
   INTEGRAL    Likelihood = -7.80   Transmembrane   61 -  77 (  56 -  85)
   INTEGRAL    Likelihood = -5.20   Transmembrane  121 - 137 ( 117 - 148)
   INTEGRAL    Likelihood = -2.97   Transmembrane   99 - 115 (  98 - 119)
   PERIPHERAL  Likelihood = 10.77       5
 modified ALOM score:   2.50

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.4991(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

A related DNA sequence <SEQ ID 10701> was identified in GBS which encodes amino acid sequence <SEQ ID 10702>.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2991

A DNA sequence <SEQ ID 9027> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9028>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 7
McG: Discrim Score:     10.61
GvH: Signal Score (-7.5): -4.21
     Possible site: 51
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 3 value: -10.99 threshold:  0.0
   INTEGRAL    Likelihood =-10.99   Transmembrane   38 -  54 (  33 -  61)
   INTEGRAL    Likelihood = -8.01   Transmembrane    5 -  21 (   1 -  26)
   INTEGRAL    Likelihood = -7.01   Transmembrane   65 -  81 (  60 -  87)
   PERIPHERAL  Likelihood = 13.85      99
 modified ALOM score:   2.70

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.5394(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2992

A DNA sequence <SEQ ID 9029> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9030>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 10
McG: Discrim Score:    -21.39
GvH: Signal Score (-7.5): -1.85
     Possible site: 57
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 1 value:  -8.44 threshold:  0.0
   INTEGRAL    Likelihood = -8.44   Transmembrane   38 -  54 (  36 -  59)
   PERIPHERAL  Likelihood = 19.10      18
 modified ALOM score:   2.19

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.4376(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2993

A DNA sequence <SEQ ID 9031> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9032>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 5
McG: Discrim Score:     12.87
GvH: Signal Score (-7.5): -3.57
     Possible site: 41
```

```
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 4 value: -10.30 threshold:  0.0
   INTEGRAL    Likelihood =-10.30   Transmembrane   69 -  85 (  63 -  98)
   INTEGRAL    Likelihood = -8.65   Transmembrane    4 -  20 (   1 -  29)
   INTEGRAL    Likelihood = -2.07   Transmembrane   96 - 112 (  95 - 118)
   PERIPHERAL  Likelihood =  9.71     113
 modified ALOM score:   2.56

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.5118(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
20.1/50.5% over 114aa
                                                                  Streptococcus pneumoniae
  GP|9798572| BlpX protein Insert characterized

ORF02100(316 - 660 of 999)
GP|9798572|emb|CAC03527.1||AJ276410(9 - 123 of 132) BlpX protein {Streptococcus pneumoniae}
%Match = 5.0
%Identity = 20.0  %Similarity = 50.4
Matches = 23  Mismatches = 57  Conservative Sub.s = 35

90        120       150       180       210       240       270       300
LMSLF*DPQVSGEELDKFTVRLDSHRKSNSRG*NQLVIILRLYSQIN*REPNMLVGPFLNKGEHMTQDYICYL*SRGGED

                                                                        MEV

330       360       390       420       450       480       510       540
MHNILRFLGIVIISAVILFSIGSFYDLTLMKNILLICWSFLFDLLVFVFKQRQTTEVLTWYQVVKQFWLFIKCTILIPIL
 :   |:: :: :|:|:   :|:|  ::::    |: :| ||:  ||::  :     :    :  :| :    |:   ||
FNMKYRLFFVIFLSSVLDILLGTFLQISIVSIGWLVLYSGLFEAGVFLLANKGVAVKIKEVDIRNRFKFIFGKTLWFQIL
               20        30        40        50        60        70        80

570       600       630       660       690       720       750       780
VAFIIMKGCLTSISDILIYFYLHLVVVYYTIGMILSLGRIISPEHSMFNKLRK*NELYLKFVFNRADLTICCLPCLS*FF
:   ::      :   || || |: :|:  :  :||  ::   :: : :
LLIFLIIKLYLGLDARLILFYGHIFIVFNALMYLLSSSQVSLKKNKLSS
              100       110       120       130
```

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2994

A DNA sequence <SEQ ID 9033> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9034>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 9
McG: Discrim Score:      3.25
GvH: Signal Score (-7.5): -3.39
     Possible site: 59
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 4 value:  -6.64 threshold:  0.0
   INTEGRAL    Likelihood = -6.64   Transmembrane   46 -  62 (  43 -  64)
   INTEGRAL    Likelihood = -5.15   Transmembrane   17 -  33 (  15 -  34)
   PERIPHERAL  Likelihood = 11.03     100
 modified ALOM score:   1.83

*** Reasoning Step: 3

----- Final Results -----
```

```
                bacterial membrane --- Certainty=0.3654(Affirmative) < succ>
                 bacterial outside --- Certainty=0.0000(Not Clear) < succ>
               bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
35.5/63.8% over 127aa

  OMNI|NT01BS4455| wall teichoic acid glycosylation protein GtcA Insert characterized

ORF01715(343 - 750 of 1053)
OMNI|NT01BS4455(58 - 185 of 187) wall teichoic acid glycosylation protein GtcA
%Match = 8.0
%Identity = 35.5  %Similarity = 63.7
Matches = 44  Mismatches = 39  Conservative Sub.s = 35

210       240       270       300       330       360       390       411
GN*ASRVV*NNLLSISQTKSKAKLMGDFLITLKHP*YNKNMVKLKSLLKKSIQNEVSLYLLFGLLTSLLYLV---IRQGI
     : :     :        : :| |    :          ::         |: :|:: |::|::: :    |   |
PRRNHQTIICIGPASHLPQLFRRTLGIFYFRQRAREAKNFEKFFRKRGTSVKYREIIMYIIMGVFTTIVNIASFYILVEI
                20        30        40        50        60        70        80

441       471       501       531       549       579       609       639
FNFSQDAPFSAIVANIIAILFAFFTNDRFVFKQTKIEQLQRL----QTFVIARLGTLGLDLILAVIFVDQFPSIIGQFVQ
 |    |  : : | |:::|||: ||  :||:| |   || |      |   |: :||:|| : :|:| ||
MNVDYKA--ATVAAWILSVLFAYITNKLYVFQQ-KTHDLQSLLKELTAFFSVRVLSLGIDLGMMIILVGQF---------
                100       110       120       130       140       150

669       690       720       750       780       810       840       870
HNLNKINTIESL---VSQILIILLNYILSKFVIFKDKKRQL*QELSFLIFLLWIFG*ET*YLHALIQFFLSQFLERWHSV
      || |:|   :   :|:::||: ||:::||  | :
------NTNETLAKILDNAVIVVVNYVASKWLVFKKTKEEGV
            160       170       180
```

SEQ ID 9034 (GBS283) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 63 (lane 8; MW 67.6kDa).

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2995

A DNA sequence <SEQ ID 9035> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9036>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 2
SRCFLG: 0
McG: Length of UR:   22
     Peak Value of UR:   3.86
     Net Charge of CR: 2
McG: Discrim Score:     16.84
GvH: Signal Score (-7.5): -4.38
     Possible site: 21
>>> Seems to have an uncleavable N-term signal seq
Amino Acid Composition: calculated from 1
ALOM program   count: 1 value: -12.37 threshold:  0.0
   INTEGRAL    Likelihood =-12.37   Transmembrane    7 -  23 (   1 -  26)
   PERIPHERAL  Likelihood = 12.84       64
 modified ALOM score:   2.97
icm1 HYPID: 7  CFP: 0.595

*** Reasoning Step: 3

----- Final Results -----
                bacterial membrane --- Certainty=0.5946(Affirmative) < succ>
```

```
bacterial outside --- Certainty=0.0000(Not Clear) < succ>
bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

SEQ ID 9036 (GBS286) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 52 (lane 11; MW 16.4kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 59 (lane 2; MW 41.3kDa) and in Figure 63 (lane 9; MW 41.4kDa).

The GBS286-GST fusion product was purified (Figure 210, lane 9; Figure 225, lane 9) and used to immunise mice. The resulting antiserum was used for FACS (Figure 274), which confirmed that the protein is immunoaccessible on GBS bacteria.

GBS668 was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 139 (lane 2-4; MW 43.5kDa) and in Figure 187 (lane 6; MW 43kDa). It was also expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 139 (lane 6 & 7; MW 18.6kDa) and in Figure 179 (lane 12; MW 19kDa).

GBS668-GST was purified as shown in Figure 237 (lane 10). GBS668-His was purified as shown in Figure 231 (lanes 5 & 6).

GBS673 was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 161 (lane 8-10; MW 17kDa) and in Figure 188 (lane 4; MW 17kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 162 (lane 8; MW 41.5kDa) and in Figure 239 (lane 7; MW 41kDa). Purified GBS673-His is shown in Figure 242, lane 5. Purified GBS673-GST is shown in Figure 246, lane 2.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2996

A DNA sequence <SEQ ID 9037> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9038>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 6
McG: Discrim Score:    -18.42
GvH: Signal Score (-7.5): -6.16
     Possible site: 57
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 2 value:  -8.49 threshold:  0.0
   INTEGRAL    Likelihood = -8.49   Transmembrane   51 -  67 (  44 -  95)
   INTEGRAL    Likelihood = -3.08   Transmembrane   70 -  86 (  68 -  95)
   PERIPHERAL  Likelihood = 12.89       32
 modified ALOM score:   2.20

*** Reasoning Step: 3

----- Final Results -----
              bacterial membrane --- Certainty=0.4397(Affirmative) < succ>
               bacterial outside --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

SEQ ID 9038 (GBS386) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 70 (lane 2; MW 14kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 72 (lane 8; MW 39.5kDa).

GBS386-GST was purified as shown in Figure 213, lane 8.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2997

A DNA sequence <SEQ ID 9039> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9040>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 8
McG: Discrim Score:    -15.47
GvH: Signal Score (-7.5): -6.21
     Possible site: 14
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 2 value:  -3.61 threshold:  0.0
   INTEGRAL    Likelihood = -3.61   Transmembrane   94 - 110 (  94 - 111)
   INTEGRAL    Likelihood = -1.70   Transmembrane   75 -  91 (  75 -  91)
   PERIPHERAL  Likelihood =  5.94     139
 modified ALOM score:   1.22

*** Reasoning Step: 3

----- Final Results -----
              bacterial membrane --- Certainty=0.2444(Affirmative) < succ>
               bacterial outside --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
ORF01481(394 - 720 of 1065)
GP|9657521|gb|AAF96047.1||AE004354(16 - 121 of 243) uridine phosphorylase {Vibrio cholerae}
%Match = 5.3
%Identity = 28.0  %Similarity = 48.6
Matches = 30  Mismatches = 54  Conservative Sub.s = 22

150       180       210       240       270       300       330       360
V*KHMV*AI*YGNLP*KW*IVPLSIFIFANLTLPFKFH*VKIEKIFLTR**NIVN*GLKEMLMIINSFDNSRKAIINPED

                                                                        MSIQ

390       420       450       480       510       540       570       600
INSPIKGFPKTVITCFARETFNRILEELPHREIARTSVANLEIPIYELEFKGQKIGFFNAYVGASACVAILEDIIVFGME
           |: |      |||   | : |       | |  ::  ||: | |   :  :|| : :  :|::   | :
PHIHVAQVAPRVVVCGEPNRANRIASLLNNAE---LVAENREYRLFSGEFEEQPITVCSTGIGAPSMIIAVEELARSGAK
               20        30           40        50        60        70        80

630       660       690       720       750       780       810       840
SLIVFGTCGVLDSSIEETSIIIPRSAIRDEGTSFHYSEASSEIAVNTNSIFLLCG*FRCRSMGSKIFRK*RGFRKER*NC
:::  |: | : | |    :|:   |:|||| |  |  |:
AIVRVGSAGAMQSEIGLGELILVEGAVRDEGGSKAYIGAAYPAYSSFELVVEMQRFLAEQSVPIHRGIVRSHDSFYTDEE
                100       110       120       130       140       150       160
```

SEQ ID 9040 (GBS388) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 70 (lane 3; MW 21kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 72 (lane 9; MW 45.6kDa).

The GBS388-GST fusion product was purified (Figure 213, lane 10) and used to immunise mice. The resulting antiserum was used for FACS (Figure 311), which confirmed that the protein is immunoaccessible on GBS bacteria.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2998

A DNA sequence <SEQ ID 9041> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9042>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 9
McG: Discrim Score:    -11.81
GvH: Signal Score (-7.5): -7.49
     Possible site: 25
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 1 value:  -5.68 threshold:  0.0
   INTEGRAL    Likelihood = -5.68   Transmembrane   78 -  94 (  77 -  95)
   PERIPHERAL  Likelihood =  4.61     134
 modified ALOM score:   1.64

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.3272(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
ORF01912(307 - 720 of 1056)
GP|3845252|gb|AAC71927.1||AE001412(81 - 242 of 244) hypothetical protein {Plasmodium
falciparum} PIR|D71608|D71608 hypothetical protein PFB0690w - malaria parasite (Plasmodium
falciparum)
%Match = 4.0
%Identity = 31.2  %Similarity = 53.5
Matches = 45  Mismatches = 58  Conservative Sub.s = 32

231       261       291                 348       378       405
KKGRFLIDLYCNVMNFKNSKIA*NQCFDV**RVVNHLLN-LSKENIAKIDFDFLNEALNA-NIRLKELVDELKISK----
                                        || | : | :: : |: |  |  :    :|| | |  || |
KYNELQSLLSKEEEKYDFVKNELGDLQKQKDLLKWHLCNNIKKLSMKRSDYKFKTETKSKLESKLKSLKDMNKIHKFEHD
             60        70        80        90       100       110       120

450       480       501       531       558       588       618
----------ELDSKGWSKKDSRTIKILYDGLINK---HIVSLDRADYNII-QVIPFANVHVLLFLIPERENSKNYRIY
           ||::| : | |   |: :::  |||   ::  : :   ::  :     |    |:|| ::||:||| |
TLEELVHKMEQELETKMYIKND---IENIFNECINKKDEYLKDITQERISVFKERKKRQNQLQKLLLIMKQENNKNYNIN
             140          150       160       170       180       190       200

648       672       693       720       750       780       810       840
NYSDYEMELINE--DRQQFSKYET---VDL-DQLILVDIFNIDDYISSYLTI*DIENLDLGLLKLINYADNKSDRHILQT
    ||  |:||    : :  :||   :|| |   | |::
YLKKYESNLMNEINSYKNYKDFETKIAMDLIDDHSLNDLYVT
               220       230       240
```

A related DNA sequence <SEQ ID 10589> was identified in GBS which encodes amino acid sequence <SEQ ID 10590>.

SEQ ID 9042 (GBS408) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 76 (lane 6; MW 20.4kDa). It was also expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 171 (lane 5; MW 45.3kDa).

GBS408-GST was purified as shown in Figure 218, lane 9.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 2999

A DNA sequence <SEQ ID 9043> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9044>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 9
McG: Discrim Score:     -9.62
GvH: Signal Score (-7.5): -4.84
     Possible site: 61
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 2 value: -11.09 threshold:  0.0
   INTEGRAL    Likelihood =-11.09   Transmembrane   45 -  61 (  37 -  72)
   INTEGRAL    Likelihood = -8.60   Transmembrane   76 -  92 (  70 -  97)
   PERIPHERAL  Likelihood = 11.62       95
 modified ALOM score:   2.72

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.5437(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
ORF01977(442 - 627 of 948)
EGAD|88220|96064(204 - 583 of 751) hypothetical 848 kDa protein f23f125 in chromosome iii
{Caenorhabditis elegans} SP|P46501|YLX5_CAEEL HYPOTHETICAL 84.8 KDA PROTEIN F23F12.5 IN
CHROMOSOME III. GP|529214|gb|AAA20607.1||U12965 F23F12.5 gene product {Caenorhabditis
elegans}
%Match = 4.6
%Identity = 35.9  %Similarity = 59.4
Matches = 23  Mismatches = 24  Conservative Sub.s = 15

192       222       252       282       312       342       372       402
DFVSSFFIS*SQTNYNRISFLLKLAKHQLECLNNVAQGLSV**YSSMKDYINRILHFIKEHMTYHVNFIDDFLDIKWEKV

VTLSAYFPFTITVERYYAMNKSEKYEKMPIILGPLFVLFIVKLELKIKDKVTLFQVIVNFGVIFQIYKNETFSHGDVAFS
       120       130       140       150       160       170       180       190

432       462       492       522       552
SNIHLRFWTTIIAYLVIFILSISTVILNLVLLFQGFLTQNPIIYLLFFITLVCAFY----------------------~~~~
             |:|:|::::  |::|||||   ||  |   :| ||:     |:
LYPPGTAEKVFTFYVVLFLINLLDVMFNLVLLQMSFLNTNRFHWLCFFLWQFALFFCCQQIFSIFYNFSPGLSCDD~~~~
       200       210       220       230       240       250       260

600       627       657       687       717       747
--------------------FAYKFITYTPTIVKNAL-QYIKKLKNV*NNKVICTLTLYQLCFRVFFHTKITKKDSYLTI
                     | : : || |:  :  | ||
AGNFYLSQFVSGAVIAFAKIFVFLLDTYVPSFDRRRLHQYPQIAMILCYCVIMVLMILPESDCGSQGSRDLAIIIINIIG
               560       570       580       590       600       610       620
```

SEQ ID 9044 (GBS411) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 78 (lane 2; MW 16kDa).

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3000

A DNA sequence <SEQ ID 9045> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9046>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 6
McG: Discrim Score:    -17.94
GvH: Signal Score (-7.5): -4.63
     Possible site: 45
>>> Seems to have no N-terminal signal sequence
ALOM program   count: 1 value:  -6.10 threshold:  0.0
   INTEGRAL    Likelihood = -6.10   Transmembrane   31 -  47 (  26 -  49)
   PERIPHERAL  Likelihood = 15.33       3
 modified ALOM score:   1.72

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.3442(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
ORF01982(313 - 501 of 801)
GP|2444082|gb|AAC79518.1||U88974(93  -  156  of  156)  ORF2  {Streptococcus  thermophilus
temperate bacteriophage O1205} PIR|T13290|T13290 hypothetical protein 2 - Streptococcus
phage phi-O1205
%Match = 11.5
%Identity = 48.4  %Similarity = 59.4
Matches = 31  Mismatches = 25  Conservative Sub.s = 7

174       204       234       264       294       324       354       384
DVDQNIESHKLFKRHFV*RAILPQSKRK*EN**LCVISEPR*KLKSKLGELKMGFFAQRCPYCQSTKVQFMNQDRKGFNG
                                                          | :||||:|| |:|| | || |:
LLMFVGVALLFARLFWEIKHPMTKEQKEQLKIERAKAKEEFRKSRNEFKKAMAEARAVKCPYCKSTDVEFMVQQRKSFSI
            50        60        70        80        90       100       110

414       441       471       501       531       561       591       621
CVGCIGFLIAWPF-LLLGLVGKKGKNNWHCTNCGRTFKTK*KSPTLKFCPRRA*GKF*YSKNLLFGRGFYHTYFNRK*GI
     | ::      | |: |||||  ||| |||  | ||
GKAAAGTIMTGGVGALAGFAGKKGKKEWHCKNCGAVFTTK
           130       140       150
```

SEQ ID 9046 (GBS412) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 171 (lane 6; MW 36kDa). Purified GBS412-GST is shown in Figure 218, lane 10-11.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3001

A DNA sequence <SEQ ID 9047> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9048>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 0
McG: Discrim Score:      3.67
GvH: Signal Score (-7.5): -3.62
     Possible site: 41
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 5 value:  -7.27 threshold:  0.0
   INTEGRAL    Likelihood = -7.27   Transmembrane   48 -  64 (  32 -  68)
   INTEGRAL    Likelihood = -6.26   Transmembrane   87 - 103 (  85 - 105)
```

```
   INTEGRAL    Likelihood = -6.21   Transmembrane   29 -  45 (  26 -  46)
   INTEGRAL    Likelihood = -3.29   Transmembrane  110 - 126 ( 109 - 130)
   INTEGRAL    Likelihood = -2.87   Transmembrane    2 -  18 (   1 -  18)
   PERIPHERAL  Likelihood =  4.24      66
modified ALOM score:   1.95

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.3909(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
ORF01286(304 - 672 of 993)
GP|8272442|dbj|BAA96471.1||AB036428(90 - 212 of 218) type IV prepilin peptidase homologue
{Streptococcus mutans}
%Match = 16.8
%Identity = 46.3  %Similarity = 72.4
Matches = 57  Mismatches = 34  Conservative Sub.s = 32

102       132       162       192       222       252       282       312
*RRLPI*T*IPNFFKRFCTSNKTFIYEF*QKTIQFSRKSATAC*LSL*R*TDYL**KS*SLFYHFSNININYKKDFMIMS
                                                                          :::
LGSFFGLVVDRYPQKSIIFPRSHCNKCYNCLTMRDLIPIFSRIINKNSCRFCGYPIPLRYSLVELLCGLISTGFALDLLT
                 30        40        50        60        70        80        90

342       372       402       432       462       492       522       552
TIYFISLCMSFILSYYDIKYQEYPIFLWILFTISTIILTPITKVSIVLCLFGILAEVVDINIGSGDFLYLATIGLSLPLH
|     | |  :|| ||:: | ||: ||| ||   : : |:  :|::| ||||:|  : :||||||||:||||: ||| |:
TSQVCLLFMGVLLSLYDLQDQSYPLTLWIGFTFLLMFIYPLNLISLILFLFGIFAALKNINIGSGDFFYLATLALSLNLQ
                 110       120       130       140       150       160       170

582       612       642       672       702       732       762       792
QMLFIIQIGAWLGIIYCLVMRKMKKTIAFLPFLSIAYIIVTSYSLLF*SL*IIRKVIKLWVLVAFWIFRMTNCTTKINHG
|:::|||| : |||:| |: :| |:  ||:||| : ::|:
QIIWIIQIASLLGILYSLLFQKHKEPFAFVPFLFLGHLIIIFSHLI
                 190       200       210
```

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3002

A DNA sequence <SEQ ID 9049> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9050>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 2
McG: Discrim Score:     10.43
GvH: Signal Score (-7.5): -4.39
     Possible site: 54
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 4 value: -10.30 threshold:  0.0
   INTEGRAL    Likelihood =-10.30   Transmembrane   62 -  78 (  59 -  84)
   INTEGRAL    Likelihood = -6.10   Transmembrane    4 -  20 (   1 -  22)
   INTEGRAL    Likelihood = -4.25   Transmembrane  128 - 144 ( 123 - 145)
   INTEGRAL    Likelihood = -3.13   Transmembrane   88 - 104 (  87 - 104)
   PERIPHERAL  Likelihood =  2.01     109
modified ALOM score:   2.56

*** Reasoning Step: 3

----- Final Results -----
               bacterial membrane --- Certainty=0.5118(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
```

```
bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has homology with the following sequences in the databases:

```
SP|Q48729|LSPA_LACLC(1 - 149 of 150) LIPOPROTEIN SIGNAL PEPTIDASE (EC 3.4.23.36)
(PROLIPOPROTEIN SIGNAL PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II).
%Match = 16.3
%Identity = 40.7  %Similarity = 66.0
Matches = 61  Mismatches = 50  Conservative Sub.s = 38

180       210       240       270       300       330       360       390
EWYHCYSIRRSSR*PNDLYQTKRS*FISDGFKICCCYGRVF*GI*FIGEVMRKIIIPIITILLIALDQLSKLWIVKHIEL
                                                  |:|::  :| :: |  ||: | |:| :|:|
                                                  MKKLLSLVIIVVGIIADQVFKNWVVANIQL
                                                          10        20        30

420       450       480       510       540       570       600       630
NQIKEFIPNIVSLTYLRNYGAAFSILQNQQWLFTLITIFVVGVAIIYLMKHINGSYWLLISLTLIISGGLGNFIDRLRLG
   |:  |:::||||::| |||:| :  |||:| ::|  |: ||: :| |   | | :  |||||:| |||:: |:| |
GDTKKIWPDVLSLTYIKNDGAAWSSFSGQQWFFLVLTPIVLIVALWFLWKK-MGQNWYFAGLTLIIAGALGNLLTRVRQG
        40        50        60        70        80        90        100

660       690       720       750       780       810       840       870
YVVDMVHLDFINFAIFNVADSYLTIGIICLMIALWKEESNGNHN*NSRS*AR*SFSG*F*TVA*SS**RN*KRDCVSKWT
:||||      :| |||:||  |::| : | ||:  ::
FVVDMFXNRIYDFPIFNIADILLSVGFVVLFIAILTDKETK
        120       130       140       150
```

There is also homology to SEQ ID 7750.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vacc

Example 3003

A DNA sequence <SEQ ID 9051> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9052>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 7
McG: Discrim Score:     13.24
GvH: Signal Score (-7.5): -2.18
     Possible site: 19
>>> Seems to have a cleavable N-term signal seq.
ALOM program   count: 0 value:   2.01 threshold:  0.0
   PERIPHERAL  Likelihood =  2.01      21
 modified ALOM score:  -0.90

*** Reasoning Step: 3

----- Final Results -----
               bacterial outside --- Certainty=0.3000(Affirmative) < succ>
              bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

The protein has no homology with any sequences in the databases.

SEQ ID 9052 (GBS138) was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 19 (lane 2; MW 15kDa)

GBS672 was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 161 (lane 5-7; MW 15kDa) and in Figure 188 (lane 3; MW 15kDa). Purified protein is shown in Figure 242, lane 4.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3004

A DNA sequence <SEQ ID 9053> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9054>. Analysis of the amino acid sequence reveals the following:

```
Lipop: Possible site: -1   Crend: 8
McG: Discrim Score:     18.01
GvH: Signal Score (-7.5): -2.35
     Possible site: 26
>>> Seems to have a cleavable N-term signal seq.
ALOM program   count: 0 value:  14.80 threshold:  0.0
   PERIPHERAL  Likelihood = 14.80      51
 modified ALOM score:  -3.46

*** Reasoning Step: 3

----- Final Results -----
               bacterial outside --- Certainty=0.3000(Affirmative) < succ>
              bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

SEQ ID 9054 (GBS143) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 23 (lane 2; MW 33.5kDa).

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3005

A DNA sequence <SEQ ID 9055> was identified in *S.agalactiae* which encodes amino acid sequence <SEQ ID 9056>. Analysis of the amino acid sequence reveals the following:

```
Lipop Possible site: -1   Crend: 0
McG: Discrim Score:      7.43
GvH: Signal Score (-7.5): -6.25
     Possible site: 41
>>> Seems to have an uncleavable N-term signal seq
ALOM program   count: 1 value: -10.77 threshold:  0.0
   INTEGRAL    Likelihood =-10.77   Transmembrane    2 -  18 (   1 -  20)
   PERIPHERAL  Likelihood =  5.14      29
 modified ALOM score:   2.65

*** Reasoning Step: 3

----- Final Results -----
              bacterial membrane --- Certainty=0.5310(Affirmative) < succ>
               bacterial outside --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

SEQ ID 9056 (GBS229) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 55 (lane 3; MW 35.9kDa).

GBS229-GST was purified as shown in Figure 206, lane 5.

Based on this analysis, it is predicted that this protein from *S.agalactiae*, and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3006

A DNA sequence <SEQ ID 9183> was identified in GAS which encodes amino acid sequence <SEQ ID 9184>. Analysis of the amino acid sequence reveals the following:

```
Possible site: 29

>>> Seems to have a cleavable N-term signal seq.

----- Final Results -----
               bacterial outside --- Certainty=0.3000(Affirmative) < succ>
              bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3007

A DNA sequence <SEQ ID 9185> was identified in GAS which encodes amino acid sequence <SEQ ID 9186>. Analysis of the amino acid sequence reveals the following:

```
Possible site: 28

>>> Seems to have a cleavable N-term signal seq.

----- Final Results -----
               bacterial outside --- Certainty=0.3000(Affirmative) < succ>
              bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3008

A DNA sequence <SEQ ID 9187> was identified in GAS which encodes amino acid sequence <SEQ ID 9188>. Analysis of the amino acid sequence reveals the following:

```
Possible site: 36

>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.70   Transmembrane  850 - 866 ( 850 - 866)
   INTEGRAL    Likelihood = -1.22   Transmembrane   15 -  31 (  15 -  31)

----- Final Results -----
              bacterial membrane --- Certainty=0.1680(Affirmative) < succ>
               bacterial outside --- Certainty=0.0000(Not Clear) < succ>
             bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3009

A DNA sequence <SEQ ID 9189> was identified in GAS which encodes amino acid sequence <SEQ ID 9190>. Analysis of the amino acid sequence reveals the following:

```
LPXTG motif: 259-263

Possible site: 13
```

```
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -3.93   Transmembrane  270 - 286 ( 268 - 288)

----- Final Results -----
               bacterial membrane --- Certainty=0.2572(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3010

A DNA sequence <SEQ ID 9191> was identified in GAS which encodes amino acid sequence <SEQ ID 9192>. Analysis of the amino acid sequence reveals the following:

```
Possible site: 21

>>> May be a lipoprotein

----- Final Results -----
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3011

A DNA sequence <SEQ ID 9193> was identified in GAS which encodes amino acid sequence <SEQ ID 9194>. Analysis of the amino acid sequence reveals the following:

```
Possible site: 29

>>> May be a lipoprotein

----- Final Results -----
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3012

A DNA sequence <SEQ ID 9195> was identified in GAS which encodes amino acid sequence <SEQ ID 9196>. Analysis of the amino acid sequence reveals the following:

```
Possible site: 34

>>> Seems to have a cleavable N-term signal seq.

----- Final Results -----
                bacterial outside --- Certainty=0.3000(Affirmative) < succ>
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3013

A DNA sequence <SEQ ID 9197> was identified in GAS which encodes amino acid sequence <SEQ ID 9198>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 13
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -3.50   Transmembrane  346 - 362 ( 343 - 366)
   INTEGRAL    Likelihood = -2.97   Transmembrane  177 - 193 ( 176 - 195)

----- Final Results -----
               bacterial membrane --- Certainty=0.2402(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3014

A DNA sequence <SEQ ID 9199> was identified in GAS which encodes amino acid sequence <SEQ ID 9200>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 19
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.33   Transmembrane   24 -  40 (  24 -  40)

----- Final Results -----
               bacterial membrane --- Certainty=0.1532(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3015

A DNA sequence <SEQ ID 9201> was identified in GAS which encodes amino acid sequence <SEQ ID 9202>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 33
>>> Seems to have a cleavable N-term signal seq.
   INTEGRAL    Likelihood = -6.00   Transmembrane  194 - 210 ( 192 - 214)

----- Final Results -----
               bacterial membrane --- Certainty=0.3399(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>

LPXTG motif: 183-187
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3016

A DNA sequence <SEQ ID 9203> was identified in GAS which encodes amino acid sequence <SEQ ID 9204>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 32
>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood =-11.25   Transmembrane    9 -  25 (   4 -  28)
```

```
----- Final Results -----
               bacterial membrane --- Certainty=0.5501(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3017

A DNA sequence <SEQ ID 9205> was identified in GAS which encodes amino acid sequence <SEQ ID 9206>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 37
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -3.03   Transmembrane  462 - 478 ( 460 - 479)
   INTEGRAL    Likelihood = -0.90   Transmembrane   18 -  34 (  18 -  34)

----- Final Results -----
               bacterial membrane --- Certainty=0.2211(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>

LPXTG motif: 450-454
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3018

A DNA sequence <SEQ ID 9207> was identified in GAS which encodes amino acid sequence <SEQ ID 9208>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 26
>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood = -2.60   Transmembrane   15 -  31 (  12 -  32)

----- Final Results -----
               bacterial membrane --- Certainty=0.2041(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3019

A DNA sequence <SEQ ID 9209> was identified in GAS which encodes amino acid sequence <SEQ ID 9210>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 28
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.38   Transmembrane   16 -  32 (  16 -  32)

----- Final Results -----
               bacterial membrane --- Certainty=0.1553(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3020

A DNA sequence <SEQ ID 9211> was identified in GAS which encodes amino acid sequence <SEQ ID 9212>. Analysis of the amino acid sequence reveals the following:

```
      Possible cleavage site: 24
>>> Seems to have a cleavable N-term signal seq.

----- Final Results -----
               bacterial outside --- Certainty= 0.300(Affirmative) < succ>
             bacterial membrane --- Certainty= 0.000(Not Clear) < succ>
            bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3021

A DNA sequence <SEQ ID 9213> was identified in GAS which encodes amino acid sequence <SEQ ID 9214>. Analysis of the amino acid sequence reveals the following:

```
      Possible cleavage site: 23
>>> May be a lipoprotein

----- Final Results -----
             bacterial membrane --- Certainty= 0.000(Not Clear) < succ>
              bacterial outside --- Certainty= 0.000(Not Clear) < succ>
            bacterial cytoplasm --- Certainty= 0.000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3022

A DNA sequence <SEQ ID 9215> was identified in GAS which encodes amino acid sequence <SEQ ID 9216>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 19

>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood = -2.76   Transmembrane    3 -  19 (   2 -  20)

----- Final Results -----
             bacterial membrane --- Certainty=0.2105(Affirmative) < succ>
              bacterial outside --- Certainty=0.0000(Not Clear) < succ>
            bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>

RGD motif: 396-398
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3023

A DNA sequence <SEQ ID 9217> was identified in GAS which encodes amino acid sequence <SEQ ID 9218>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 18

>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -0.80   Transmembrane  251 - 267 ( 251 - 267)
   INTEGRAL    Likelihood = -0.75   Transmembrane  179 - 195 ( 179 - 195)

----- Final Results -----
               bacterial membrane --- Certainty=0.1319(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3024

A DNA sequence <SEQ ID 9219> was identified in GAS which encodes amino acid sequence <SEQ ID 9220>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 39

>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.22   Transmembrane   52 -  68 (  51 -  68)

----- Final Results -----
               bacterial membrane --- Certainty=0.1489(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3025

A DNA sequence <SEQ ID 9221> was identified in GAS which encodes amino acid sequence <SEQ ID 9222>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 52

>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood =-12.58   Transmembrane   39 -  55 (  32 -  86)
   INTEGRAL    Likelihood = -9.55   Transmembrane   60 -  76 (  56 -  86)

----- Final Results -----
               bacterial membrane --- Certainty=0.6031(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3026

A DNA sequence <SEQ ID 9223> was identified in GAS which encodes amino acid sequence <SEQ ID 9224>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 18
>>> Seems to have an uncleavable N-term signal seq

----- Final Results -----
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
```

```
bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3027

A DNA sequence <SEQ ID 9225> was identified in GAS which encodes amino acid sequence <SEQ ID 9226>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 26
>>> Seems to have an uncleavable N-term signal seq

----- Final Results -----
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3028

A DNA sequence <SEQ ID 9227> was identified in GAS which encodes amino acid sequence <SEQ ID 9228>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 33
>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood = -8.44   Transmembrane   18 -  34 (  13 -  40)
   INTEGRAL    Likelihood = -7.86   Transmembrane   59 -  75 (  54 -  79)

----- Final Results -----
               bacterial membrane --- Certainty=0.4376(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3029

A DNA sequence <SEQ ID 9229> was identified in GAS which encodes amino acid sequence <SEQ ID 9230>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 27
>>> Seems to have a cleavable N-term signal seq.

----- Final Results -----
                bacterial outside --- Certainty=0.3000(Affirmative) < succ>
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3030

A DNA sequence <SEQ ID 9231> was identified in GAS which encodes amino acid sequence <SEQ ID 9232>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 24
>>> Seems to have an uncleavable N-term signal seq

----- Final Results -----
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3031

A DNA sequence <SEQ ID 9233> was identified in GAS which encodes amino acid sequence <SEQ ID 9234>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 49
>>> Seems to have a cleavable N-term signal seq.
   INTEGRAL    Likelihood = -9.87   Transmembrane   58 -  74 (  53 -  81)

----- Final Results -----
               bacterial membrane --- Certainty=0.4949(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3032

A DNA sequence <SEQ ID 9235> was identified in GAS which encodes amino acid sequence <SEQ ID 9236>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 16
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -0.06   Transmembrane   92 - 108 (  92 - 108)

----- Final Results -----
               bacterial membrane --- Certainty=0.1022(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3033

A DNA sequence <SEQ ID 9237> was identified in GAS which encodes amino acid sequence <SEQ ID 9238>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 40
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.38   Transmembrane   18 -  34 (  18 -  34)

----- Final Results -----
               bacterial membrane --- Certainty=0.1553(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3034

A DNA sequence <SEQ ID 9239> was identified in GAS which encodes amino acid sequence <SEQ ID 9240>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 19
>>> Seems to have an uncleavable N-term signal seq

----- Final Results -----
               bacterial membrane --- Certainty=0.0000(Not Clear) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3035

A DNA sequence <SEQ ID 9241> was identified in GAS which encodes amino acid sequence <SEQ ID 9242>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 57
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.01   Transmembrane  155 - 171 ( 154 - 171)

----- Final Results -----
               bacterial membrane --- Certainty=0.1404(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3036

A DNA sequence <SEQ ID 9243> was identified in GAS which encodes amino acid sequence <SEQ ID 9244>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 28
>>> Seems to have a cleavable N-term signal seq.
   INTEGRAL    Likelihood = -4.25   Transmembrane  113 - 129 ( 111 - 131)

----- Final Results -----
               bacterial membrane --- Certainty=0.2699(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3037

A DNA sequence <SEQ ID 9245> was identified in GAS which encodes amino acid sequence <SEQ ID 9246>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 56
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -0.69   Transmembrane  110 - 126 ( 110 - 126)

----- Final Results -----
               bacterial membrane --- Certainty=0.1277(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
```

```
bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3038

A DNA sequence <SEQ ID 9247> was identified in GAS which encodes amino acid sequence <SEQ ID 9248>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 58
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -1.28   Transmembrane  130 - 146 ( 128 - 146)

----- Final Results -----
               bacterial membrane --- Certainty=0.1510(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3039

A DNA sequence <SEQ ID 9249> was identified in GAS which encodes amino acid sequence <SEQ ID 9250>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 39
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -4.57   Transmembrane   74 -  90 (  72 -  92)
   INTEGRAL    Likelihood = -3.13   Transmembrane  169 - 185 ( 166 - 185)
   INTEGRAL    Likelihood = -3.13   Transmembrane   28 -  44 (  27 -  44)

----- Final Results -----
               bacterial membrane --- Certainty=0.2826(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3040

A DNA sequence <SEQ ID 9251> was identified in GAS which encodes amino acid sequence <SEQ ID 9252>. Analysis of the amino acid sequence reveals the following:

```
      Possible cleavage site: 56
>>> Seems to have a cleavable N-term signal seq.
   INTEGRAL    Likelihood =-12.21   Transmembrane    93 - 109 (  87 - 114)
   INTEGRAL    Likelihood = -8.65   Transmembrane   227 - 243 ( 226 - 243)

----- Final Results -----
               bacterial membrane --- Certainty=0.588(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3041

A DNA sequence <SEQ ID 9253> was identified in GAS which encodes amino acid sequence <SEQ ID 9254>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 45
>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood = -6.53   Transmembrane   73 -  89 (  70 -  94)
   INTEGRAL    Likelihood = -4.41   Transmembrane   32 -  48 (  30 -  51)
   INTEGRAL    Likelihood = -2.55   Transmembrane   10 -  26 (  10 -  26)
   INTEGRAL    Likelihood = -2.39   Transmembrane  106 - 122 ( 104 - 123)
   INTEGRAL    Likelihood = -1.75   Transmembrane  153 - 169 ( 152 - 169)

----- Final Results -----
               bacterial membrane --- Certainty=0.3612(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3042

A DNA sequence <SEQ ID 9255> was identified in GAS which encodes amino acid sequence <SEQ ID 9256>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 44
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood =-11.68   Transmembrane   25 -  41 (  15 -  46)
   INTEGRAL    Likelihood = -9.24   Transmembrane  255 - 271 ( 248 - 276)
   INTEGRAL    Likelihood = -7.59   Transmembrane   82 -  98 (  79 - 100)
   INTEGRAL    Likelihood = -4.30   Transmembrane  115 - 131 ( 113 - 135)
   INTEGRAL    Likelihood = -0.11   Transmembrane  148 - 164 ( 148 - 164)

----- Final Results -----
               bacterial membrane --- Certainty=0.5670(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3043

A DNA sequence <SEQ ID 9257> was identified in GAS which encodes amino acid sequence <SEQ ID 9258>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 51
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood =-11.04   Transmembrane  137 - 153 ( 126 - 160)
   INTEGRAL    Likelihood =-10.56   Transmembrane   36 -  52 (  29 -  58)
   INTEGRAL    Likelihood =-10.08   Transmembrane  407 - 423 ( 399 - 426)
   INTEGRAL    Likelihood = -4.94   Transmembrane  230 - 246 ( 228 - 250)
   INTEGRAL    Likelihood = -4.83   Transmembrane   79 -  95 (  77 -  98)
   INTEGRAL    Likelihood = -4.35   Transmembrane  202 - 218 ( 201 - 220)
   INTEGRAL    Likelihood = -1.12   Transmembrane  293 - 309 ( 293 - 309)

----- Final Results -----
               bacterial membrane --- Certainty=0.5416(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3044

A DNA sequence <SEQ ID 9259> was identified in GAS which encodes amino acid sequence <SEQ ID 9260>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 31
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -2.76   Transmembrane  137 - 153 ( 137 - 154)

----- Final Results -----
               bacterial membrane --- Certainty=0.2105(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3045

A DNA sequence <SEQ ID 9261> was identified in GAS which encodes amino acid sequence <SEQ ID 9262>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 36
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -7.91   Transmembrane  238 - 254 ( 236 - 264)
   INTEGRAL    Likelihood = -6.16   Transmembrane   69 -  85 (  65 -  89)
   INTEGRAL    Likelihood = -6.00   Transmembrane  136 - 152 ( 134 - 155)
   INTEGRAL    Likelihood = -4.73   Transmembrane   29 -  45 (  21 -  48)
   INTEGRAL    Likelihood = -2.97   Transmembrane  194 - 210 ( 193 - 220)

----- Final Results -----
               bacterial membrane --- Certainty=0.4163(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3046

A DNA sequence <SEQ ID 9263> was identified in GAS which encodes amino acid sequence <SEQ ID 9264>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 39
>>> Seems to have a cleavable N-term signal seq.
   INTEGRAL    Likelihood = -9.87   Transmembrane  574 - 590 ( 568 - 601)
   INTEGRAL    Likelihood = -9.18   Transmembrane  243 - 259 ( 238 - 262)
   INTEGRAL    Likelihood = -7.11   Transmembrane   66 -  82 (  65 -  87)
   INTEGRAL    Likelihood = -1.28   Transmembrane  270 - 286 ( 270 - 287)

----- Final Results -----
               bacterial membrane --- Certainty=0.4949(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3047

A DNA sequence <SEQ ID 9265> was identified in GAS which encodes amino acid sequence <SEQ ID 9266>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 33
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood = -7.91   Transmembrane   98 - 114 (  92 - 124)
   INTEGRAL    Likelihood = -6.21   Transmembrane   19 -  35 (  14 -  37)
   INTEGRAL    Likelihood = -5.36   Transmembrane  170 - 186 ( 169 - 189)
   INTEGRAL    Likelihood = -5.15   Transmembrane  147 - 163 ( 136 - 167)
   INTEGRAL    Likelihood = -1.12   Transmembrane   77 -  93 (  77 -  93)

----- Final Results -----
               bacterial membrane --- Certainty=0.4163(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3048

A DNA sequence <SEQ ID 9267> was identified in GAS which encodes amino acid sequence <SEQ ID 9268>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 47
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood =-11.94   Transmembrane   27 -  43 (  19 -  51)
   INTEGRAL    Likelihood = -4.83   Transmembrane  152 - 168 ( 151 - 171)
   INTEGRAL    Likelihood = -4.09   Transmembrane  277 - 293 ( 276 - 294)
   INTEGRAL    Likelihood = -3.82   Transmembrane  195 - 211 ( 193 - 217)
   INTEGRAL    Likelihood = -2.50   Transmembrane  120 - 136 ( 120 - 137)
   INTEGRAL    Likelihood = -0.64   Transmembrane   81 -  97 (  81 -  98)

----- Final Results -----
               bacterial membrane --- Certainty=0.5776(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3049

A DNA sequence <SEQ ID 9269> was identified in GAS which encodes amino acid sequence <SEQ ID 9270>. Analysis of the amino acid sequence reveals the following:

```
     Possible site: 36
>>> Seems to have no N-terminal signal sequence
     INTEGRAL    Likelihood = -8.49   Transmembrane   27 -  43 (  14 -  50)
     INTEGRAL    Likelihood = -8.17   Transmembrane   58 -  74 (  52 -  79)
     INTEGRAL    Likelihood = -7.38   Transmembrane  165 - 181 ( 161 - 193)
     INTEGRAL    Likelihood = -3.66   Transmembrane  247 - 263 ( 246 - 270)
     INTEGRAL    Likelihood = -1.54   Transmembrane  134 - 150 ( 134 - 150)

----- Final Results -----
               bacterial membrane --- Certainty=0.440(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3050

A DNA sequence <SEQ ID 9271> was identified in GAS which encodes amino acid sequence <SEQ ID 9272>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 55
>>> Seems to have no N-terminal signal sequence
   INTEGRAL    Likelihood =-14.75   Transmembrane  389 - 405 ( 377 - 413)
   INTEGRAL    Likelihood = -8.44   Transmembrane   31 -  47 (  29 -  54)
   INTEGRAL    Likelihood = -7.17   Transmembrane  181 - 197 ( 179 - 205)
   INTEGRAL    Likelihood = -7.01   Transmembrane  339 - 355 ( 326 - 360)
   INTEGRAL    Likelihood = -6.58   Transmembrane  105 - 121 ( 102 - 124)
   INTEGRAL    Likelihood = -5.36   Transmembrane  225 - 241 ( 222 - 244)
   INTEGRAL    Likelihood = -0.43   Transmembrane  139 - 155 ( 139 - 155)
   INTEGRAL    Likelihood = -0.16   Transmembrane  283 - 299 ( 282 - 300)

----- Final Results -----
               bacterial membrane --- Certainty=0.6901(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3051

A DNA sequence <SEQ ID 9273> was identified in GAS which encodes amino acid sequence <SEQ ID 9274>. Analysis of the amino acid sequence reveals the following:

```
      Possible cleavage site: 25
>>> Seems to have a cleavable N-term signal seq.
   INTEGRAL    Likelihood = -5.31   Transmembrane  155 - 171 ( 154 - 174)
   INTEGRAL    Likelihood = -3.50   Transmembrane  111 - 127 ( 110 - 128)
   INTEGRAL    Likelihood = -2.07   Transmembrane   80 -  96 (  78 -  96)
   INTEGRAL    Likelihood = -0.90   Transmembrane   57 -  73 (  57 -  74)

----- Final Results -----
               bacterial membrane --- Certainty=0.312(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3052

A DNA sequence <SEQ ID 9275> was identified in GAS which encodes amino acid sequence <SEQ ID 9276>. Analysis of the amino acid sequence reveals the following:

```
      Possible site: 27
>>> Seems to have an uncleavable N-term signal seq
   INTEGRAL    Likelihood = -3.93   Transmembrane  463 - 479 ( 461 - 480)

----- Final Results -----
               bacterial membrane --- Certainty=0.2572(Affirmative) < succ>
                bacterial outside --- Certainty=0.0000(Not Clear) < succ>
              bacterial cytoplasm --- Certainty=0.0000(Not Clear) < succ>
```

Based on this analysis, it is predicted that this GAS protein , and its epitopes, could be useful antigens for vaccines and/or diagnostics.

Example 3053

A DNA sequence <SEQ ID 8741> was identified in GBS which encodes amino acid sequence <SEQ ID 8742>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3054

A DNA sequence <SEQ ID 8685> was identified in GBS which encodes amino acid sequence <SEQ ID 8686>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3055

A DNA sequence <SEQ ID 10303> was identified in GBS which encodes amino acid sequence <SEQ ID 10304>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3056

A DNA sequence <SEQ ID 10305> was identified in GBS which encodes amino acid sequence <SEQ ID 10306>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3057

A DNA sequence <SEQ ID 10307> was identified in GBS which encodes amino acid sequence <SEQ ID 10308>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3058

A DNA sequence <SEQ ID 10309> was identified in GBS which encodes amino acid sequence <SEQ ID 10310>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3059

A DNA sequence <SEQ ID 10311> was identified in GBS which encodes amino acid sequence <SEQ ID 10312>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3060

A DNA sequence <SEQ ID 10313> was identified in GBS which encodes amino acid sequence <SEQ ID 10314>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3061

A DNA sequence <SEQ ID 10315> was identified in GBS which encodes amino acid sequence <SEQ ID 10316>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3062

A DNA sequence <SEQ ID 10317> was identified in GBS which encodes amino acid sequence <SEQ ID 10318>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3063

A repeated DNA sequence <SEQ ID 10319> was identified in GBS which encodes amino acid sequence <SEQ ID 10320>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3064

A DNA sequence <SEQ ID 10321> was identified in GBS which encodes amino acid sequence <SEQ ID 10322>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3065

A DNA sequence <SEQ ID 10323> was identified in GBS which encodes amino acid sequence <SEQ ID 10324>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3066

A DNA sequence <SEQ ID 10325> was identified in GBS which encodes amino acid sequence <SEQ ID 10326>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3067

A DNA sequence <SEQ ID 10327> was identified in GBS which encodes amino acid sequence <SEQ ID 10328>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3068

A DNA sequence <SEQ ID 10329> was identified in GBS which encodes amino acid sequence <SEQ ID 10330>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3069

A DNA sequence <SEQ ID 10331> was identified in GBS which encodes amino acid sequence <SEQ ID 10332>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3070

A DNA sequence <SEQ ID 10333> was identified in GBS which encodes amino acid sequence <SEQ ID 10334>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3071

A DNA sequence <SEQ ID 10335> was identified in GBS which encodes amino acid sequence <SEQ ID 10336>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3072

A DNA sequence <SEQ ID 10339> was identified in GBS which encodes amino acid sequence <SEQ ID 10340>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3073

A DNA sequence <SEQ ID 10341> was identified in GBS which encodes amino acid sequence <SEQ ID 10342>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3074

A DNA sequence <SEQ ID 10343> was identified in GBS which encodes amino acid sequence <SEQ ID 10344>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3075

A DNA sequence <SEQ ID 10345> was identified in GBS which encodes amino acid sequence <SEQ ID 10346>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3076

A DNA sequence <SEQ ID 10347> was identified in GBS which encodes amino acid sequence <SEQ ID 10348>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3077

A DNA sequence <SEQ ID 10349> was identified in GBS which encodes amino acid sequence <SEQ ID 10350>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3078

A DNA sequence <SEQ ID 10351> was identified in GBS which encodes amino acid sequence <SEQ ID 10352>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3079

A DNA sequence <SEQ ID 10353> was identified in GBS which encodes amino acid sequence <SEQ ID 10354>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3080

A DNA sequence <SEQ ID 10355> was identified in GBS which encodes amino acid sequence <SEQ ID 10356>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3081

A DNA sequence <SEQ ID 10357> was identified in GBS which encodes amino acid sequence <SEQ ID 10358>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3082

A DNA sequence <SEQ ID 10359> was identified in GBS which encodes amino acid sequence <SEQ ID 10360>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3083

A DNA sequence <SEQ ID 10361> was identified in GBS which encodes amino acid sequence <SEQ ID 10362>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3084

A DNA sequence <SEQ ID 10363> was identified in GBS which encodes amino acid sequence <SEQ ID 10364>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3085

A DNA sequence <SEQ ID 10365> was identified in GBS which encodes amino acid sequence <SEQ ID 10366>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3086

A DNA sequence <SEQ ID 10367> was identified in GBS which encodes amino acid sequence <SEQ ID 10368>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3087

A DNA sequence <SEQ ID 10369> was identified in GBS which encodes amino acid sequence <SEQ ID 10370>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3088

A DNA sequence <SEQ ID 10371> was identified in GBS which encodes amino acid sequence <SEQ ID 10372>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3089

A DNA sequence <SEQ ID 10373> was identified in GBS which encodes amino acid sequence <SEQ ID 10374>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3090

A DNA sequence <SEQ ID 10375> was identified in GBS which encodes amino acid sequence <SEQ ID 10376>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3091

A DNA sequence <SEQ ID 10377> was identified in GBS which encodes amino acid sequence <SEQ ID 10378>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3092

A DNA sequence <SEQ ID 10379> was identified in GBS which encodes amino acid sequence <SEQ ID 10380>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3093

A DNA sequence <SEQ ID 10381> was identified in GBS which encodes amino acid sequence <SEQ ID 10382>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3094

A DNA sequence <SEQ ID 10383> was identified in GBS which encodes amino acid sequence <SEQ ID 10384>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3095

A DNA sequence <SEQ ID 10385> was identified in GBS which encodes amino acid sequence <SEQ ID 10386>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3096

A DNA sequence <SEQ ID 10387> was identified in GBS which encodes amino acid sequence <SEQ ID 10388>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3097

A DNA sequence <SEQ ID 10389> was identified in GBS which encodes amino acid sequence <SEQ ID 10390>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3098

A DNA sequence <SEQ ID 10391> was identified in GBS which encodes amino acid sequence <SEQ ID 10392>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3099

A DNA sequence <SEQ ID 10393> was identified in GBS which encodes amino acid sequence <SEQ ID 10394>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3100

A DNA sequence <SEQ ID 10395> was identified in GBS which encodes amino acid sequence <SEQ ID 10396>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3101

A DNA sequence <SEQ ID 10397> was identified in GBS which encodes amino acid sequence <SEQ ID 10398>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3102

A DNA sequence <SEQ ID 10399> was identified in GBS which encodes amino acid sequence <SEQ ID 10400>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3103

A DNA sequence <SEQ ID 10401> was identified in GBS which encodes amino acid sequence <SEQ ID 10402>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3104

A DNA sequence <SEQ ID 10403> was identified in GBS which encodes amino acid sequence <SEQ ID 10404>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3105

A DNA sequence <SEQ ID 10405> was identified in GBS which encodes amino acid sequence <SEQ ID 10406>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3106

A DNA sequence <SEQ ID 10407> was identified in GBS which encodes amino acid sequence <SEQ ID 10408>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3107

A DNA sequence <SEQ ID 10409> was identified in GBS which encodes amino acid sequence <SEQ ID 10410>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3108

A DNA sequence <SEQ ID 10411> was identified in GBS which encodes amino acid sequence <SEQ ID 10412>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3109

A DNA sequence <SEQ ID 10413> was identified in GBS which encodes amino acid sequence <SEQ ID 10414>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3110

A DNA sequence <SEQ ID 10415> was identified in GBS which encodes amino acid sequence <SEQ ID 10416>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3111

A DNA sequence <SEQ ID 10417> was identified in GBS which encodes amino acid sequence <SEQ ID 10418>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3112

A DNA sequence <SEQ ID 10419> was identified in GBS which encodes amino acid sequence <SEQ ID 10420>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3113

A DNA sequence <SEQ ID 10421> was identified in GBS which encodes amino acid sequence <SEQ ID 10422>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3114

A DNA sequence <SEQ ID 10423> was identified in GBS which encodes amino acid sequence <SEQ ID 10424>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3115

A DNA sequence <SEQ ID 10425> was identified in GBS which encodes amino acid sequence <SEQ ID 10426>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3116

A DNA sequence <SEQ ID 10427> was identified in GBS which encodes amino acid sequence <SEQ ID 10428>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3117

A DNA sequence <SEQ ID 10429> was identified in GBS which encodes amino acid sequence <SEQ ID 10430>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3118

A DNA sequence <SEQ ID 10431> was identified in GBS which encodes amino acid sequence <SEQ ID 10432>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3119

A DNA sequence <SEQ ID 10433> was identified in GBS which encodes amino acid sequence <SEQ ID 10434>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3120

A DNA sequence <SEQ ID 10435> was identified in GBS which encodes amino acid sequence <SEQ ID 10436>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3121

A DNA sequence <SEQ ID 10437> was identified in GBS which encodes amino acid sequence <SEQ ID 10438>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3122

A DNA sequence <SEQ ID 10441> was identified in GBS which encodes amino acid sequence <SEQ ID 10442>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3123

A DNA sequence <SEQ ID 10443> was identified in GBS which encodes amino acid sequence <SEQ ID 10444>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3124

A DNA sequence <SEQ ID 10445> was identified in GBS which encodes amino acid sequence <SEQ ID 10446>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3125

A DNA sequence <SEQ ID 10447> was identified in GBS which encodes amino acid sequence <SEQ ID 10448>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3126

A DNA sequence <SEQ ID 10449> was identified in GBS which encodes amino acid sequence <SEQ ID 10450>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3127

A DNA sequence <SEQ ID 10451> was identified in GBS which encodes amino acid sequence <SEQ ID 10452>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3128

A DNA sequence <SEQ ID 10453> was identified in GBS which encodes amino acid sequence <SEQ ID 10454>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3129

A DNA sequence <SEQ ID 10455> was identified in GBS which encodes amino acid sequence <SEQ ID 10456>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3130

A DNA sequence <SEQ ID 10457> was identified in GBS which encodes amino acid sequence <SEQ ID 10458>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10907> which encodes amino acid sequence <SEQ ID 10908> was also identified.

Example 3131

A DNA sequence <SEQ ID 10459> was identified in GBS which encodes amino acid sequence <SEQ ID 10460>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3132

A DNA sequence <SEQ ID 10461> was identified in GBS which encodes amino acid sequence <SEQ ID 10462>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3133

A DNA sequence <SEQ ID 10463> was identified in GBS which encodes amino acid sequence <SEQ ID 10464>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3134

A DNA sequence <SEQ ID 10465> was identified in GBS which encodes amino acid sequence <SEQ ID 10466>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3135

A DNA sequence <SEQ ID 10467> was identified in GBS which encodes amino acid sequence <SEQ ID 10468>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3136

A DNA sequence <SEQ ID 10469> was identified in GBS which encodes amino acid sequence <SEQ ID 10470>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3137

A DNA sequence <SEQ ID 10471> was identified in GBS which encodes amino acid sequence <SEQ ID 10472>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3138

A DNA sequence <SEQ ID 10473> was identified in GBS which encodes amino acid sequence <SEQ ID 10474>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3139

A DNA sequence <SEQ ID 10475> was identified in GBS which encodes amino acid sequence <SEQ ID 10476>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3140

A DNA sequence <SEQ ID 10477> was identified in GBS which encodes amino acid sequence <SEQ ID 10478>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3141

A DNA sequence <SEQ ID 10479> was identified in GBS which encodes amino acid sequence <SEQ ID 10480>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3142

A DNA sequence <SEQ ID 10481> was identified in GBS which encodes amino acid sequence <SEQ ID 10482>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3143

A DNA sequence <SEQ ID 10483> was identified in GBS which encodes amino acid sequence <SEQ ID 10484>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3144

A DNA sequence <SEQ ID 10485> was identified in GBS which encodes amino acid sequence <SEQ ID 10486>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3145

A DNA sequence <SEQ ID 10487> was identified in GBS which encodes amino acid sequence <SEQ ID 10488>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3146

A DNA sequence <SEQ ID 10489> was identified in GBS which encodes amino acid sequence <SEQ ID 10490>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3147

A DNA sequence <SEQ ID 10491> was identified in GBS which encodes amino acid sequence <SEQ ID 10492>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3148

A DNA sequence <SEQ ID 10493> was identified in GBS which encodes amino acid sequence <SEQ ID 10494>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3149

A DNA sequence <SEQ ID 10495> was identified in GBS which encodes amino acid sequence <SEQ ID 10496>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3150

A DNA sequence <SEQ ID 10497> was identified in GBS which encodes amino acid sequence <SEQ ID 10498>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3151

A DNA sequence <SEQ ID 10499> was identified in GBS which encodes amino acid sequence <SEQ ID 10500>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3152

A DNA sequence <SEQ ID 10501> was identified in GBS which encodes amino acid sequence <SEQ ID 10502>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3153

A DNA sequence <SEQ ID 10503> was identified in GBS which encodes amino acid sequence <SEQ ID 10504>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3154

A DNA sequence <SEQ ID 10505> was identified in GBS which encodes amino acid sequence <SEQ ID 10506>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3155

A DNA sequence <SEQ ID 10509> was identified in GBS which encodes amino acid sequence <SEQ ID 10510>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3156

A DNA sequence <SEQ ID 10511> was identified in GBS which encodes amino acid sequence <SEQ ID 10512>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3157

A DNA sequence <SEQ ID 10513> was identified in GBS which encodes amino acid sequence <SEQ ID 10514>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3158

A DNA sequence <SEQ ID 10515> was identified in GBS which encodes amino acid sequence <SEQ ID 10516>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3159

A DNA sequence <SEQ ID 10517> was identified in GBS which encodes amino acid sequence <SEQ ID 10518>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3160

A DNA sequence <SEQ ID 10519> was identified in GBS which encodes amino acid sequence <SEQ ID 10520>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3161

A DNA sequence <SEQ ID 10521> was identified in GBS which encodes amino acid sequence <SEQ ID 10522>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3162

A DNA sequence <SEQ ID 10523> was identified in GBS which encodes amino acid sequence <SEQ ID 10524>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3163

A DNA sequence <SEQ ID 10525> was identified in GBS which encodes amino acid sequence <SEQ ID 10526>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3164

A DNA sequence <SEQ ID 10527> was identified in GBS which encodes amino acid sequence <SEQ ID 10528>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3165

A DNA sequence <SEQ ID 10529> was identified in GBS which encodes amino acid sequence <SEQ ID 10530>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3166

A DNA sequence <SEQ ID 10531> was identified in GBS which encodes amino acid sequence <SEQ ID 10532>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3167

A DNA sequence <SEQ ID 10533> was identified in GBS which encodes amino acid sequence <SEQ ID 10534>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3168

A DNA sequence <SEQ ID 10535> was identified in GBS which encodes amino acid sequence <SEQ ID 10536>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3169

A DNA sequence <SEQ ID 10537> was identified in GBS which encodes amino acid sequence <SEQ ID 10538>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3170

A DNA sequence <SEQ ID 10539> was identified in GBS which encodes amino acid sequence <SEQ ID 10540>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3171

A DNA sequence <SEQ ID 10541> was identified in GBS which encodes amino acid sequence <SEQ ID 10542>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3172

A DNA sequence <SEQ ID 10543> was identified in GBS which encodes amino acid sequence <SEQ ID 10544>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3173

A DNA sequence <SEQ ID 10545> was identified in GBS which encodes amino acid sequence <SEQ ID 10546>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

SEQ ID 10546 (GBS665) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 137 (lane 8-10; MW 41kDa) and in Figure 187 (lane 5; MW 41kDa). It was also was expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 137 (lane 11 & 12; MW 16.1kDa), in Figure 141 (lane 4; MW 16kDa) and in Figure 179 (lane 6; MW 16kDa). Purified GBS665-GST is shown in Figure 243, lane 4.

GBS665-His was purified as shown in Figure 230, lane 7-8.

Example 3174

A DNA sequence <SEQ ID 10547> was identified in GBS which encodes amino acid sequence <SEQ ID 10548>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10909> which encodes amino acid sequence <SEQ ID 10910> was also identified.

Example 3175

A DNA sequence <SEQ ID 10549> was identified in GBS which encodes amino acid sequence <SEQ ID 10550>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3176

A DNA sequence <SEQ ID 10551> was identified in GBS which encodes amino acid sequence <SEQ ID 10552>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3177

A DNA sequence <SEQ ID 10553> was identified in GBS which encodes amino acid sequence <SEQ ID 10554>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3178

A DNA sequence <SEQ ID 10555> was identified in GBS which encodes amino acid sequence <SEQ ID 10556>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3179

A DNA sequence <SEQ ID 10557> was identified in GBS which encodes amino acid sequence <SEQ ID 10558>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3180

A DNA sequence <SEQ ID 10559> was identified in GBS which encodes amino acid sequence <SEQ ID 10560>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3181

A DNA sequence <SEQ ID 10561> was identified in GBS which encodes amino acid sequence <SEQ ID 10562>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3182

A DNA sequence <SEQ ID 10563> was identified in GBS which encodes amino acid sequence <SEQ ID 10564>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3183

A DNA sequence <SEQ ID 10565> was identified in GBS which encodes amino acid sequence <SEQ ID 10566>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3184

A DNA sequence <SEQ ID 10567> was identified in GBS which encodes amino acid sequence <SEQ ID 10568>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3185

A DNA sequence <SEQ ID 10569> was identified in GBS which encodes amino acid sequence <SEQ ID 10570>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3186

A DNA sequence <SEQ ID 10571> was identified in GBS which encodes amino acid sequence <SEQ ID 10572>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3187

A DNA sequence <SEQ ID 10573> was identified in GBS which encodes amino acid sequence <SEQ ID 10574>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3188

A DNA sequence <SEQ ID 10575> was identified in GBS which encodes amino acid sequence <SEQ ID 10576>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3189

A DNA sequence <SEQ ID 10577> was identified in GBS which encodes amino acid sequence <SEQ ID 10578>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3190

A DNA sequence <SEQ ID 10579> was identified in GBS which encodes amino acid sequence <SEQ ID 10580>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3191

A DNA sequence <SEQ ID 10581> was identified in GBS which encodes amino acid sequence <SEQ ID 10582>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3192

A DNA sequence <SEQ ID 10583> was identified in GBS which encodes amino acid sequence <SEQ ID 10584>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3193

A DNA sequence <SEQ ID 10585> was identified in GBS which encodes amino acid sequence <SEQ ID 10586>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3194

A DNA sequence <SEQ ID 10587> was identified in GBS which encodes amino acid sequence <SEQ ID 10588>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3195

A DNA sequence <SEQ ID 10591> was identified in GBS which encodes amino acid sequence <SEQ ID 10592>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3196

A DNA sequence <SEQ ID 10593> was identified in GBS which encodes amino acid sequence <SEQ ID 10594>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3197

A DNA sequence <SEQ ID 10595> was identified in GBS which encodes amino acid sequence <SEQ ID 10596>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3198

A DNA sequence <SEQ ID 10597> was identified in GBS which encodes amino acid sequence <SEQ ID 10598>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10797> which encodes amino acid sequence <SEQ ID 10798> was also identified.

Example 3199

A DNA sequence <SEQ ID 10599> was identified in GBS which encodes amino acid sequence <SEQ ID 10600>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3200

A DNA sequence <SEQ ID 10601> was identified in GBS which encodes amino acid sequence <SEQ ID 10602>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3201

A DNA sequence <SEQ ID 10603> was identified in GBS which encodes amino acid sequence <SEQ ID 10604>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3202

A DNA sequence <SEQ ID 10605> was identified in GBS which encodes amino acid sequence <SEQ ID 10606>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3203

A DNA sequence <SEQ ID 10607> was identified in GBS which encodes amino acid sequence <SEQ ID 10608>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3204

A DNA sequence <SEQ ID 10609> was identified in GBS which encodes amino acid sequence <SEQ ID 10610>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3205

A DNA sequence <SEQ ID 10611> was identified in GBS which encodes amino acid sequence <SEQ ID 10612>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3206

A DNA sequence <SEQ ID 10613> was identified in GBS which encodes amino acid sequence <SEQ ID 10614>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3207

A DNA sequence <SEQ ID 10615> was identified in GBS which encodes amino acid sequence <SEQ ID 10616>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3208

A DNA sequence <SEQ ID 10617> was identified in GBS which encodes amino acid sequence <SEQ ID 10618>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3209

A DNA sequence <SEQ ID 10619> was identified in GBS which encodes amino acid sequence <SEQ ID 10620>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3210

A DNA sequence <SEQ ID 10621> was identified in GBS which encodes amino acid sequence <SEQ ID 10622>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3211

A DNA sequence <SEQ ID 10623> was identified in GBS which encodes amino acid sequence <SEQ ID 10624>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3212

A DNA sequence <SEQ ID 10625> was identified in GBS which encodes amino acid sequence <SEQ ID 10626>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3213

A DNA sequence <SEQ ID 10627> was identified in GBS which encodes amino acid sequence <SEQ ID 10628>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3214

A DNA sequence <SEQ ID 10629> was identified in GBS which encodes amino acid sequence <SEQ ID 10630>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3215

A DNA sequence <SEQ ID 10631> was identified in GBS which encodes amino acid sequence <SEQ ID 10632>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3216

A DNA sequence <SEQ ID 10633> was identified in GBS which encodes amino acid sequence <SEQ ID 10634>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10939> which encodes amino acid sequence <SEQ ID 10940> was also identified.

SEQ ID 10634 (GBS675) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 162 (lane 14 & 15; MW 56kDa). It was also expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 163 (lane 2; MW 31kDa) and in Figure 188 (lane 5; MW 31kDa).

Purified GBS675-His is shown in Figure 240, lane 7-8.

Example 3217

A DNA sequence <SEQ ID 10635> was identified in GBS which encodes amino acid sequence <SEQ ID 10636>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3218

A DNA sequence <SEQ ID 10637> was identified in GBS which encodes amino acid sequence <SEQ ID 10638>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3219

A DNA sequence <SEQ ID 10639> was identified in GBS which encodes amino acid sequence <SEQ ID 10640>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3220

A DNA sequence <SEQ ID 10641> was identified in GBS which encodes amino acid sequence <SEQ ID 10642>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3221

A DNA sequence <SEQ ID 10643> was identified in GBS which encodes amino acid sequence <SEQ ID 10644>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3222

A DNA sequence <SEQ ID 10645> was identified in GBS which encodes amino acid sequence <SEQ ID 10646>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3223

A DNA sequence <SEQ ID 10647> was identified in GBS which encodes amino acid sequence <SEQ ID 10648>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3224

A DNA sequence <SEQ ID 10649> was identified in GBS which encodes amino acid sequence <SEQ ID 10650>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3225

A DNA sequence <SEQ ID 10651> was identified in GBS which encodes amino acid sequence <SEQ ID 10652>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3226

A DNA sequence <SEQ ID 10653> was identified in GBS which encodes amino acid sequence <SEQ ID 10654>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3227

A DNA sequence <SEQ ID 10655> was identified in GBS which encodes amino acid sequence <SEQ ID 10656>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3228

A DNA sequence <SEQ ID 10657> was identified in GBS which encodes amino acid sequence <SEQ ID 10658>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3229

A DNA sequence <SEQ ID 10659> was identified in GBS which encodes amino acid sequence <SEQ ID 10660>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3230

A DNA sequence <SEQ ID 10661> was identified in GBS which encodes amino acid sequence <SEQ ID 10662>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3231

A DNA sequence <SEQ ID 10663> was identified in GBS which encodes amino acid sequence <SEQ ID 10664>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3232

A DNA sequence <SEQ ID 10665> was identified in GBS which encodes amino acid sequence <SEQ ID 10666>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10917> which encodes amino acid sequence <SEQ ID 10918> was also identified.

A DNA sequence <SEQ ID 10667> was identified in GBS which encodes amino acid sequence <SEQ ID 10668>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3233

A DNA sequence <SEQ ID 10669> was identified in GBS which encodes amino acid sequence <SEQ ID 10670>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3234

A DNA sequence <SEQ ID 10671> was identified in GBS which encodes amino acid sequence <SEQ ID 10672>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3235

A DNA sequence <SEQ ID 10673> was identified in GBS which encodes amino acid sequence <SEQ ID 10674>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3236

A DNA sequence <SEQ ID 10675> was identified in GBS which encodes amino acid sequence <SEQ ID 10676>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3237

A DNA sequence <SEQ ID 10677> was identified in GBS which encodes amino acid sequence <SEQ ID 10678>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3238

A DNA sequence <SEQ ID 10679> was identified in GBS which encodes amino acid sequence <SEQ ID 10680>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3239

A DNA sequence <SEQ ID 10681> was identified in GBS which encodes amino acid sequence <SEQ ID 10682>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3240

A DNA sequence <SEQ ID 10683> was identified in GBS which encodes amino acid sequence <SEQ ID 10684>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3241

A DNA sequence <SEQ ID 10685> was identified in GBS which encodes amino acid sequence <SEQ ID 10686>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3242

A DNA sequence <SEQ ID 10687> was identified in GBS which encodes amino acid sequence <SEQ ID 10688>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3243

A DNA sequence <SEQ ID 10689> was identified in GBS which encodes amino acid sequence <SEQ ID 10690>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3244

A DNA sequence <SEQ ID 10691> was identified in GBS which encodes amino acid sequence <SEQ ID 10692>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

SEQ ID 10692 (GBS676) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 163 (lane 3-5; MW 66kDa) and in Figure 239 (lane 8; MW 66kDa). It was also expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 163 (lane 7 & 8; MW 41kDa) and in Figure 188 (lane 6; MW 41kDa). Purified GBS676-His is shown in Figure 240, lane 4-5. Purified GBS676-GST is shown in Figure 246, lanes 10 & 11.

Example 3245

A DNA sequence <SEQ ID 10693> was identified in GBS which encodes amino acid sequence <SEQ ID 10694>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3246

A DNA sequence <SEQ ID 10695> was identified in GBS which encodes amino acid sequence <SEQ ID 10696>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3247

A DNA sequence <SEQ ID 10697> was identified in GBS which encodes amino acid sequence <SEQ ID 10698>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3248

A DNA sequence <SEQ ID 10699> was identified in GBS which encodes amino acid sequence <SEQ ID 10700>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3249

A DNA sequence <SEQ ID 10703> was identified in GBS which encodes amino acid sequence <SEQ ID 10704>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3250

A DNA sequence <SEQ ID 10705> was identified in GBS which encodes amino acid sequence <SEQ ID 10706>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3251

A DNA sequence <SEQ ID 10707> was identified in GBS which encodes amino acid sequence <SEQ ID 10708>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3252

A DNA sequence <SEQ ID 10709> was identified in GBS which encodes amino acid sequence <SEQ ID 10710>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10803> which encodes amino acid sequence <SEQ ID 10804> was also identified.

Example 3253

A DNA sequence <SEQ ID 10711> was identified in GBS which encodes amino acid sequence <SEQ ID 10712>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics. A related GBS nucleic acid sequence <SEQ ID 10913> which encodes amino acid sequence <SEQ ID 10914> was also identified.

Example 3254

A DNA sequence <SEQ ID 10713> was identified in GBS which encodes amino acid sequence <SEQ ID 10714>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3255

A DNA sequence <SEQ ID 10715> was identified in GBS which encodes amino acid sequence <SEQ ID 10716>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3256

A DNA sequence <SEQ ID 10717> was identified in GBS which encodes amino acid sequence <SEQ ID 10718>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3257

A DNA sequence <SEQ ID 10719> was identified in GBS which encodes amino acid sequence <SEQ ID 10720>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3258

A DNA sequence <SEQ ID 10721> was identified in GBS which encodes amino acid sequence <SEQ ID 10722>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3259

A DNA sequence <SEQ ID 10723> was identified in GBS which encodes amino acid sequence <SEQ ID 10724>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3260

A DNA sequence <SEQ ID 10725> was identified in GBS which encodes amino acid sequence <SEQ ID 10726>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3261

A DNA sequence <SEQ ID 10727> was identified in GBS which encodes amino acid sequence <SEQ ID 10728>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3262

A DNA sequence <SEQ ID 10729> was identified in GBS which encodes amino acid sequence <SEQ ID 10730>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

SEQ ID 10730 (GBS670) was expressed in *E.coli* as a GST-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 140 (lane 2-4; MW 45.3kDa). It was also expressed in *E.coli* as a His-fusion product. SDS-PAGE analysis of total cell extract is shown in Figure 140 (lane 5-7; MW 20.4kDa) and in Figure 179 (lane 10; MW 20kDa).

GBS670-His was purified as shown in Figure 230, lane 9-10.

Example 3263

A DNA sequence <SEQ ID 10731> was identified in GBS which encodes amino acid sequence <SEQ ID 10732>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3264

A DNA sequence <SEQ ID 10733> was identified in GBS which encodes amino acid sequence <SEQ ID 10734>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3265

A DNA sequence <SEQ ID 10735> was identified in GBS which encodes amino acid sequence <SEQ ID 10736>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3266

A DNA sequence <SEQ ID 10737> was identified in GBS which encodes amino acid sequence <SEQ ID 10738>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3267

A DNA sequence <SEQ ID 10739> was identified in GBS which encodes amino acid sequence <SEQ ID 10740>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3268

A DNA sequence <SEQ ID 10741> was identified in GBS which encodes amino acid sequence <SEQ ID 10742>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3269

A DNA sequence <SEQ ID 10743> was identified in GBS which encodes amino acid sequence <SEQ ID 10744>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3270

A DNA sequence <SEQ ID 10745> was identified in GBS which encodes amino acid sequence <SEQ ID 10746>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3271

A DNA sequence <SEQ ID 10747> was identified in GBS which encodes amino acid sequence <SEQ ID 10748>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3272

A DNA sequence <SEQ ID 10749> was identified in GBS which encodes amino acid sequence <SEQ ID 10750>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3273

A DNA sequence <SEQ ID 10751> was identified in GBS which encodes amino acid sequence <SEQ ID 10752>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3274

A DNA sequence <SEQ ID 10753> was identified in GBS which encodes amino acid sequence <SEQ ID 10754>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3275

A DNA sequence <SEQ ID 10755> was identified in GBS which encodes amino acid sequence <SEQ ID 10756>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3276

A DNA sequence <SEQ ID 10757> was identified in GBS which encodes amino acid sequence <SEQ ID 10758>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3277

A DNA sequence <SEQ ID 10759> was identified in GBS which encodes amino acid sequence <SEQ ID 10760>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3278

A DNA sequence <SEQ ID 10761> was identified in GBS which encodes amino acid sequence <SEQ ID 10762>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3279

A DNA sequence <SEQ ID 10763> was identified in GBS which encodes amino acid sequence <SEQ ID 10764>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3280

A DNA sequence <SEQ ID 10765> was identified in GBS which encodes amino acid sequence <SEQ ID 10766>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3281

A DNA sequence <SEQ ID 10767> was identified in GBS which encodes amino acid sequence <SEQ ID 10768>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3282

A DNA sequence <SEQ ID 10769> was identified in GBS which encodes amino acid sequence <SEQ ID 10770>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3283

A DNA sequence <SEQ ID 10771> was identified in GBS which encodes amino acid sequence <SEQ ID 10772>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3284

A repeated DNA sequence <SEQ ID 10791> was identified in GBS which encodes amino acid sequence <SEQ ID 10792>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3285

A DNA sequence <SEQ ID 10805> was identified in GBS which encodes amino acid sequence <SEQ ID 10806>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3286

A DNA sequence <SEQ ID 10807> was identified in GBS which encodes amino acid sequence <SEQ ID 10808>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3287

A DNA sequence <SEQ ID 10809> was identified in GBS which encodes amino acid sequence <SEQ ID 10810>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3288

A DNA sequence <SEQ ID 10811> was identified in GBS which encodes amino acid sequence <SEQ ID 10812>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3289

A DNA sequence <SEQ ID 10813> was identified in GBS which encodes amino acid sequence <SEQ ID 10814>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3290

A DNA sequence <SEQ ID 10815> was identified in GBS which encodes amino acid sequence <SEQ ID 10816>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3291

A DNA sequence <SEQ ID 10817> was identified in GBS which encodes amino acid sequence <SEQ ID 10818>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3292

A DNA sequence <SEQ ID 10819> was identified in GBS which encodes amino acid sequence <SEQ ID 10820>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3293

A DNA sequence <SEQ ID 10821> was identified in GBS which encodes amino acid sequence <SEQ ID 10822>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3294

A DNA sequence <SEQ ID 10823> was identified in GBS which encodes amino acid sequence <SEQ ID 10824>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3295

A DNA sequence <SEQ ID 10825> was identified in GBS which encodes amino acid sequence <SEQ ID 10826>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3296

A DNA sequence <SEQ ID 10827> was identified in GBS which encodes amino acid sequence <SEQ ID 10828>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3297

A DNA sequence <SEQ ID 10829> was identified in GBS which encodes amino acid sequence <SEQ ID 10830>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3298

A DNA sequence <SEQ ID 10831> was identified in GBS which encodes amino acid sequence <SEQ ID 10832>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3299

A DNA sequence <SEQ ID 10833> was identified in GBS which encodes amino acid sequence <SEQ ID 10834>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3300

A DNA sequence <SEQ ID 10835> was identified in GBS which encodes amino acid sequence <SEQ ID 10836>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3301

A DNA sequence <SEQ ID 10837> was identified in GBS which encodes amino acid sequence <SEQ ID 10838>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3302

A DNA sequence <SEQ ID 10839> was identified in GBS which encodes amino acid sequence <SEQ ID 10840>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3303

A DNA sequence <SEQ ID 10841> was identified in GBS which encodes amino acid sequence <SEQ ID 10842>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3304

A DNA sequence <SEQ ID 10843> was identified in GBS which encodes amino acid sequence <SEQ ID 10844>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3305

A DNA sequence <SEQ ID 10845> was identified in GBS which encodes amino acid sequence <SEQ ID 10846>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3306

A DNA sequence <SEQ ID 10847> was identified in GBS which encodes amino acid sequence <SEQ ID 10848>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3307

A DNA sequence <SEQ ID 10849> was identified in GBS which encodes amino acid sequence <SEQ ID 10850>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3308

A DNA sequence <SEQ ID 10851> was identified in GBS which encodes amino acid sequence <SEQ ID 10852>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3309

A DNA sequence <SEQ ID 10853> was identified in GBS which encodes amino acid sequence <SEQ ID 10854>. Related sequences are <SEQ ID 10855>, <SEQ ID 10856>, <SEQ ID 10857>, <SEQ ID 10858>, <SEQ ID 10859>, <SEQ ID 10860>, <SEQ ID 10861>, <SEQ ID 10862>, <SEQ ID 10863>, <SEQ ID 10864>, <SEQ ID 10865> and <SEQ ID 10866>. These proteins and their epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3310

A DNA sequence <SEQ ID 10867> was identified in GBS which encodes amino acid sequence <SEQ ID 10868>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3311

A DNA sequence <SEQ ID 10869> was identified in GBS which encodes amino acid sequence <SEQ ID 10870>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3312

A DNA sequence <SEQ ID 10871> was identified in GBS which encodes amino acid sequence <SEQ ID 10872>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3313

A DNA sequence <SEQ ID 10873> was identified in GBS which encodes amino acid sequence <SEQ ID 10874>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3314

A DNA sequence <SEQ ID 10875> was identified in GBS which encodes amino acid sequence <SEQ ID 10876>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3315

A DNA sequence <SEQ ID 10877> was identified in GBS which encodes amino acid sequence <SEQ ID 10878>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3316

A DNA sequence <SEQ ID 10879> was identified in GBS which encodes amino acid sequence <SEQ ID 10880>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3317

A DNA sequence <SEQ ID 10881> was identified in GBS which encodes amino acid sequence <SEQ ID 10882>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3318

A DNA sequence <SEQ ID 10883> was identified in GBS which encodes amino acid sequence <SEQ ID 10884>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3319

A DNA sequence <SEQ ID 10885> was identified in GBS which encodes amino acid sequence <SEQ ID 10886>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3320

A DNA sequence <SEQ ID 10887> was identified in GBS which encodes amino acid sequence <SEQ ID 10888>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3321

A DNA sequence <SEQ ID 10889> was identified in GBS which encodes amino acid sequence <SEQ ID 10890>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3322

A DNA sequence <SEQ ID 10891> was identified in GBS which encodes amino acid sequence <SEQ ID 10892>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3323

A DNA sequence <SEQ ID 10893> was identified in GBS which encodes amino acid sequence <SEQ ID 10894>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3324

A DNA sequence <SEQ ID 10895> was identified in GBS which encodes amino acid sequence <SEQ ID 10896>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3325

A DNA sequence <SEQ ID 10897> was identified in GBS which encodes amino acid sequence <SEQ ID 10898>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3326

A DNA sequence <SEQ ID 10899> was identified in GBS which encodes amino acid sequence <SEQ ID 10900>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3327

A DNA sequence <SEQ ID 10901> was identified in GBS which encodes amino acid sequence <SEQ ID 10902>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3328

A DNA sequence <SEQ ID 10903> was identified in GBS which encodes amino acid sequence <SEQ ID 10904>. This protein and its epitopes could be useful antigens for vaccines and/or diagnostics.

Example 3329

Seven rRNA genes were identified in *S.agalactiae*. These are SEQ IDs 12018 to 12024. These rRNA genes are particularly useful for diagnostic purposes and for phlyogenetic studies. An alignment of the rRNA sequences is shown below:

```
12023  ----------------------------------TTTCGAGTCAAAGTCATCAGCGTT
12024  ------------------------------------------------------------
12019  -----TCCAATCATACTTAATTTCACTAATATCTGGATTTTGACATATTCAGTTAATTCT
12021  ...ATCGAATTGAACGGACTCAATTTGGTTGTTATGTAATTTT--ACATAATCTATGATTTCT
12020  ------------------------------------------------------------
12018  ------------------------------------------------------------
12022  ----------------------------CTTCTTTGTTTTCTTTAGAGATATTAACTGTA

12023  TACTGTTACGGCAGCAGTTCCAAGAGTTACTCCACTCACAAGGACTGCTGATAATATTCT
12024  ------------------------------------------------------------
12019  TTTTCATGCTTTTTGAGATAAGCTACTTGTTCTTTTTTTATTACTTTTTTACCTTTCTTT
12021  TGCTCATGCTCTTTGAGATAGGCTAATTGTTCTTTTTTTGTCATTTTTTTATCTTTCTTC
12020  ------------------------------------------------------------
12018  ------------------------------------------------------------
12022  CCCACTTTGGGCGTTAAAATACCTAAAGTAGCCTTTATTAAAGTTGATTTAGCAGCCCCA

12023  TTTTTTCATTTTTATTAAACTACTCCTTTAC--GATAAGACATTAAATATTTTACCAAAA
12024  ------------------------------------------------------------
12019  ACTGCTGACTGTTTGCTATTTTTTACTTCGTTTGACTGACTTTTAGATTCACTATTCATT
12021  ACTTCTGATTGCTTGCTATTTTTTACTTCGTTTGACTGAATTTTATGTTCACTATTCATT
12020  ------------------------------------------------------------
12018  ----------------------------CTTT-GATACAATATTATCAAAATTATATTAA
12022  TTTTCACCTGTTAAGGTAACAAACTCCCCACT-GTCTAAATGGTAATTAACCCCTTCCAG

12023  AATTCACGAAATTATATTACGTCATTGTTACATTTATATTTGAAATCAACTATTTCTAAA
12024  ------------------------------------------------------------
12019  TGACAGCCTGCTAGTAACATCCCAATAATAGATATGGGAATTAACCATTTTACATATTTT
12021  TGACAGCCTCCAAGTATCATCCCAAAAATTGATATGGGAATTAACCATTTTATATATTTT
12020  ------------------------------------------------------------
12018  CGGTAAAGATATTGTTAAAGACCAAACTTGGATTATCAATCGT----TATCAAGAAATTA
12022  CA-CAGGATCGCTATCGTACTGAAAAGTAAGACCACTAACTGTAATATATCGCATGATTA

12023  TGAACCATAATCAAATCTAGAAAACGATAACCTTCTTCTATTCACTCT---ATCAATATA
12024  ------------------------------------------------------------
12019  TTCAACATGCTCTCTTTTCTTAGAAAATAAACTTCCCATGTCAAGTATCTAATAAAAATA
12021  CTCATCATGTTCTCTTTTCTTAGAATATAAATTTTATATATCAAGTATATAATGAAATTA
12020  ------------------------------------------------------------
12018  TTAGTG---ATTTGTCTTTAGGAAGCACTA--------TTGCAGAAGA---AATTACTCG
12022  CCCTTCT--AATTCTCTAGAGAAAAGATCAAGAAAACGTTCTAAAACG---ACCTTTTCG

12023  ATTACTCCATAGTGAAACTAAAAGAGAAATAAAAAAAGAGTATAATTACTCTTAAAATTA
12024  ------------------------------------------------------------
12019  ATTATTATTTACCAGTATGTTAAAACTAATATTAGTATAACAAA-TTTTCACGAGTTTAA
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12021  ACTATTATTCACCAACATTATAAAATTAATTTTAGTATAACAAAATTTTCACGTATTTTT
12020  ----------ATCAAAAAAACATGACCAGTATGAATTAAAGCAACGTATAATCAATGCCT
12018  CTCTAT--AGAGCAGCTAGCTTCACTTCCCATAGAAAATAATCAGTTTTTAT-ATGAT--
12022  TCCTTTGAAAAATGATTTACTAATCTTCCGTAAACCCCTAACGTATTGTCATGATGATGT

12023  TAATATTTACGGAGAATAAGGGATTCGAACCCTTGCGCCAGTTACCCGACCTAACGATTT
12024  ------------------------------------------------------------
12019  TT--TTTTAGTCGTAACATATACACTGAAAAATCTTATTATTTTATACTACCTATCTATC
12021  ATAGTTTTAGTCTTAACATGTAAACAGAAA------A----------------------TC
12020  TAATGCGTAAAGGATACCAGTACGAAGATA-------------------------------TC
12018  ---TGTTTTTTAGCAGCCGGTGAAGATA-------------------ACAACGCAAAGTT
12022  GTGTGTTCATCTGCAATGGGTTTAGCAAGT----TCA---------GATAACTCAAAATA

12023  AGCAAACCGTCCTCTTCAGCCTCTTGAG--TAATTCTCCAAATTAATATTAATGGGCACG
12024  ------------------------------------------------------------
12019  ATTCACAAACACTTTTATTACTTCAGAACCTATGACATTTAGGAGTCCTCTTTGAATTTC
12021  ATTTGTATA-----T----------------------TTTAAATGCCCTAATTAAATT--
12020  AAAAGTGC------T----------------------TTAAGAGAATATTTATAAGAT--
12018  AGTTGCA-ACGTTTTTTAATCAAAATGA--CATTCCTGCAAGATATGTTCATCCAAACGA
12022  AGTAATACGAGCATCTTTAGAATCTTTA--TTCGCTTTCAACATATCCTGAGA-AATTAA

12023  AGTGGACTCGAACCACCGACCTCACGCTTATCAGGCGTGCGCTCTAACCACCTGAGCTAC
12024  ------------------------------------------------------------
12019  ATTTAAATGTTGAGTCTCCACTAACTCTTGAAAAATTTCCTTATTATTTCTGCTTGTTTT
12021  ------------------------------AATAATT-----AATATTTATTATTATATA
12020  ------------------------------AATAACTCTCAGACGATGTATT-TTACAGA
12018  AGCAGGAATTATTGTAACTAAAGAACCATG--TAATGCACGAATTATT--CCAG----GA
12022  ACTTTTTACTGCTTTAGTTACAGCTGCCTGACTAATATTTAACTTCTTAGCTAAATCAGA

12023  GCGCCCAAGCAAATGCTTGGTTTTACTTTTATGTAAAGTAAGCGGGTGACGAGAATCGA-
12024  ------------------------------------------------------------
12019  AAACCTTCTATAACGATTGCAATAATGAAAAACAAATATAAGTAATTTTCAGTAACTTTT
12021  AATTCTTCTACAATGA----------AAAAAATAAATATAT--A-TTACAAGTAACATT-
12020  AAAT----TATGATAA-----A----CTATAACAGACGTAT--AAATTGTAGAAAGTTG-
12018  AGTTATGATAAGATTGA------GAACTTATGTCTATACAATGAGGTTCTTGTTATCCCT
12022  ATTTGTCAACTGCTCTT------GTGATAAAAGCATCAGAATGTGTTCTTGCGTATTAGT

12023  -ACTCGCGACAACAGCTTGGAAGGCTGTAGTTTTACCACTAAACTACACCCGCTAAAAAC
12024  ------------------------------------------------------------
12019  TCTCAAAATTACCAGCACAATACAAAAAAGACAAGGCTTCTAAACCTTGTCTTTATAAAT
12021  --TCACAATAAATTATCTAGTAGAAAAAAGACAAGGTTTAGAAACCTTGTCTTTATAAGT
12020  ----GTAGGCTATGAGATTACCTAAAGAAGGCGACTTTATTACAATTCAAAGTTACAAAC
12018  GGATTT---------TTTGG--AGTCACAGAAGATAAC-CAAATTTGTACCTTTTCAAGA
12022  CAATTTAA-CATCACTTTGACAAGTACCAAACAATAATTCATGTTGATTTTCTGCTTTAA

12023  TTATATAATAAATGGCGCGAGACGGAATCGAACCGCCGACACATGGAGCTTCAATCCATT
12024  ------------------------------------------------------------
12019  ATACCGGCGGCCGGGGTCGAACCGGCACGTCCGTGAGGACACTGGATTTTGAGTCCAGCG
12021  ATACCGGCGGCCGGGGTCGAACCGGCACGTCCGTGAGGACACTGGATTTTGAGTCCAGCG
12020  ATGATGGTAGTTTACACCGAACTTG-----GCGTGACACCA-TGGTATTAAAAACAACCG
12018  GGGGGATCTGACATTACTGGATC--------CCTAATTGC---------AGCAGGCATAAA
12022  GCAAGATTTGAC-TCACTAAATGG-------TCTAATTTTTGTTCTAAAACTGTCATATA

12023  GCTCTACCAACTGAGCTACCGAGCCTATTGCGGGAGCAGGATTTGAACCTACGACCTTCG
12024  ------------------------------------------------------------
12019  CGTCTGCCAATTCCGCCACGCCGGCTATCTTAAAACTGGGGTAGCTGGATTCGA--ACCA
12021  CGTCTGCCAATTCCGCCACGCCGGCTATCTTAAAACTGGGGTAGCTGGATTCGA--ACCA
12020  AAAATGCC--CTCATTGGTGTTAATGATCAT---ACTTTAGTAACAGAAAATGATGGTCG
12018  AGCAGACCT-TTATGAGAACTTCACAGATGT----TGATGGTATATTTGCAGCACATCCA
12022  TACCT-CTT-TTTTGTTAACCAGTAAATTATATCACGAAGATATAGAAGAATCAATCATA

12023  GGTTA-TGAGCCCGACGAGCTACCTAGCTGCTCCA-------TCCCGCGATATCTTTAAA
12024  ------------------------------------------------------------
12019  ACGCA-TGAGGGAGTCAAAGTCCCTTGCCTTACCG-------CTTGGCTATACCCCATGA
12021  ACGCA-TGAGGGAGTCAAAGTCCCTTGCCTTACCG-------CTTGGCTATACCCCATGA
12020  ACGC--TGGGTGACACGAGAGCC--TGCAATA----------------GTATACTTTCATA
12018  GGT-------GTAGTTAAGAACCCTCACGCTA----------TCCCTGAGCTTACTTATA
12022  GATAGGTGAAGAAGATAAAACCTTTTATCTCAACAACCTAACTTTATAAACTTCTTTGCA
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12023  GGA---------GGATGTGGGATTCGAACCCACGCACGCTTTTACAC--GCCTGACGGTT
12024  ------------------------------------------------------------
12019  AAAGGCG-----AGTGATGGGAATCGAACCCACGAATGTCAGAGCCACAATCTGATGTGT
12021  AAAGGCG-----AGTGATGGGAATCGAACCCACGAATGTCAGAGCCACAATCTGATGTGT
12020  AAA---------AATACTGG---T------TT--AACATTATCGCTA-----TGATACGT
12018  AAGA--------AATGCGTGAATTAGCCTATGCGGGTTTTTCGGTTT-TACATGATGAA-
12022  AAAACCTTTCATACTATTAAAAACACGATCAGCTTTTTTCTCTGTAG-AACACATTGAAA

12023  TTCAAGACCGTTCCCTTCAGCCGGACTTGGGTAATCCTCCATATAACAAAAAATATGGAC
12024  ------------------------------------------------------------
12019  TAACCACTTCACCACACCCGCCATATTAGAAAAAACACGGGCAGTAGGAATCGAACCCAC
12021  TAACCACTTCACCACACCCGCCATATTAGAAAAAACACGGGCAGTAGGAATCGAACCCAC
12020  GAAACTGGTGTCTCCTACTATTGTAATCTAGCAAGT-----CCGTATATCTTGGACCC--
12018  --------GCTTTACTTCCTGCCTATCGTGGCAGAATCCCTCTTGTTATTAAAAATAC--
12022  AAACAGTTGGTCCACTTCCTGTC-ATTAATGCAACATCGGCTCCAGAATTTAACATAC--

12023  CTTGTAGGACTCGAACCTACGACCGCTCGGTTATGAGCCGAGTGCTCTAACCAGTTGAGC
12024  ------------------------------------------------------------
12019  ACTGAAGGTTTTGGAGACCTTAGTTCTACCTTTAAACTATGCCCGTTTACTATGGAGAGA
12021  ACTGAAGGTTTTGGAGACCTTAGTTCTACCTTTAAACTATGCCCGTTTACTATGGAGAGA
12020  --TGAAGCACTCAAGTATATTGACTATGACCTTGATGTCAAAGTATTTGCAGATGGTGAA
12018  ----AAA----TAATCCCCAACAGCCTGGTACAAAAATAGTTTTAAAGCATACTCGTAG-
12022  ----GTTCTTTTATTGTACTTATAACTGGATTTTTAGTAATTGTAATATCCTCGAGTGAA

12023  TAAAGGTCCAAAGTCTCAATAAAATAAATAGCGGCGGAGGGGATCGAACCCCCGACCTCC
12024  ------------------------------------------------------------
12019  GAGGGATTCGAACCCCCGAACCCGAAGGAGCGGATTTACAGTCCGCCGCGTTTAGCCTCT
12021  GAGGGATTCGAACCCCCGAACCCGAAGGAGCGGATTTACAGTCCGCCGCGTTTAGCCTCT
12020  AAAAGACTACTAGATGTGGACGAATATGAACAGCATAAAGYTCAGATGAACT--ATCCTA
12018  --TAACATAGCAGTAACTGG-GATCGCT--TCTGATAGCCGTTTTGCTAGCATAAACGTA
12022  TTTCCCATAGATTTGACCATTAACTGATAATCTGATGACAAAATAGCAGACTTTAATAAA

12023  CGGGTATG-AACCGGACGCTCTAGCCAGCT--GAGCTACACCGCCATAAAAATATATCCA
12024  ------------------------------------------------------------
12019  TCGCTATC-TCTCCTAAGGTATAAATGGCGCGAGACGGAATCGAACCGCCGACACATGGA
12021  TCGCTATC-TCTCCTAAGGTATAAATGGCGCGAGACGGAATCGAACCGCCGACACATGGA
12020  CCGATATT-GATTATATATTAAAGGAAAATGTAAAAATATTGGTAGAATGGATAAATGAG
12018  TCTAAAT--ACTTAATGAATAGA---GAAGTAGGTTTCGGCCGAAAAG----TACTACAA
12022  TCAATATCAACTCTACTTATAGACTTACAATCAATATCTCTAAAAATGGATTTAGTTGAA

12023  TCGGGAAGACAGGATTCGAACCTGCGACACCTTGGTCCCAAACCAAGTACTCTACCAAGC
12024  ------------------------------------------------------------
12019  GCTTCAATCCATTGCTCTACCAACTGAGCTACCGAGCCTATTGCGGGAGCAGGATTTGAA
12021  GCTTCAATCCATTGCTCTACCAACTGAGCTACCGAGCCTATTGCGGGAGCAGGATTTGAA
12020  AATAAAGGCCCCTTTTC-ATCATC--ATATATCAA-TATCTGGTATAAACGGTA------
12018  ATTTTAGAG---GATTTAAATATT---AGTTTTGAACATATGCCAACTGGCATAGATGAT
12022  ATACCAAAATCCGGCTTAACCAGA---ACTATCCAACATGGTCTCAATGTCGGTAAGGGT

12023  TGAGCTACTTCCCGAAAAATATGCAC--CCTAGAGGAGTCGAACCTCTAACCGCCTGATT
12024  ------------------------------------------------------------
12019  CCTACGACCTTCGGGTTATGAGCCCG--ACGAGCTACCTAGCTGCTCCATCCCGCGATAT
12021  CCTACGACCTTCGGGTTATGAGCCCG--ACGAGCTACCTAGCTGCTCCATCCCGCGATAT
12020  --------CCTTGAATTGAAA-------AAGCGCTAACTAAC-ACACTAAATAGTG-TGT
12018  CTATCCATTGT---CTTACGTGAAA---AAGAATTGACACCAATCAAAGAACAAGAAATC
12022  TTAACAATTTCACCTTTACCTAATACTAACGAACATCCCCCACCAAGACAATAAGGAACA

12023  CGTAGTCAG---GTACTCTATCCAGTTGAGCTAAGGGTGCTAAATATTATA-----TGCC
12024  ------------------------------------------------------------
12019  CTTTAAAGGAGGATGTGGGATTCGAACCCACGCACGCTTTTACACGCCTGACG--GTTTT
12021  CTTTAAAGGAGGATGTGGGATTCGAACCCACGCACGCTTTTACACGCCTGACG--GTTTT
12020  TTTTATTA----ATATCAAATTTAATTACA---ATACTATTGCAAAAATAT----ATACT
12018  TTAAATTACCTAACTCGTAAACTAGAAGTAG--ATTACGTTGACATCCAA----------
12022  TC--ACTACC-AATTTTAAAACCAATAGCAACCATTTCGTCATAGTCCATTTGAAGATTC

12023  GAGGACCGGAATC----GAACCGGTACGATGTTTACCATCGCAGGATTTTAAGTCCTGTG
12024  ------------------------------------------------------------
12019  CAAGACCGTTCCCTTCAGCCGGACTTGGGTAATCCTCCATATAACAAAAAATAGTCCGTA
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12021  CAAGACCGTTCCCTTCAGCCGGACTTGGGTAATCCTCCATATAACAAAAAATAGTCCGTA
12020  TAAAATAAA-------AAAAGTAGAAAGATCACTTTCTACTTTTTTAAGAATAGTCCGTA
12018  CACAATCTATC-------TACAATCGTAATTGTAGGTGAAA-ATATGAAAAGTCAGATTG
12022  CATAATCGATT-------AAGAGCTCTTATTGTAGCAGCAGCATCAGTAGAACCACCCCC

12023  CGTCTGCCAGTTCCGCCACCCCGGCCTCTAACAAGCGAACGACGGGGTTCGAACCCGCGA
12024  ------------------------------------------------------------
12019  CGGGATTCGAACCCGTGTTACCGCCGTGAAAAGGCGGTGTCTTAACCCCTTGACCAACGG
12021  CGGGATTCGAACCCGTGTTACCGCCGTGAAAAGGCGGTGTCTTAACCCCTTGACCAACGG
12020  CGGGATTCGAACCCGTGTTACCGCCGTGAAAAGGCGGTGTCTTAACCCCTTGACCAACGG
12018  GAGTCACTGCAACAGCGACACAAGCCTTATC------AAGAGAAAAA-----ATCAATAT
12022  CAGTC-CTGCACAGACAGGAATGGATTTTTCTAATCTAATATGAACACCTTTATTAATAC

12023  -CCCTCACCTT-----GGCAAGGTGATGTTCTACCACTGAACTACGTTCGCACTAAAGAC
12024  ------------------------------------------------------------
12019  -ACCATATTCTTGATGGGCACGAGTGGACTCGAACCACCGACCTCACGCTTATCAGGCGT
12021  -ACCATATTCTTGATGGGCACGAGTGGACTCGAACCACCGACCTCACGCTTATCAGGCGT
12020  -ACCATATTCTTGATGGGCACGAGTGGACTCGAACCACCGACCTCACGCTTATCAGGCGT
12018  CACCATGAT-----ATCACA-----AGGTTCAAGCGAA--GTCTCCATTATGT-------
12022  CATATTGATTTTTGATTATATCTGCAGCTTTAAACACATCATTATCATTATTTAAAGGCA

12023  ACTATTTATCCTATAAAATTGTAATGCCGGC------------------------------
12024  ------TATCCTATAAAATTGTAATGCCGGC------------------------------
12019  GCGCTCTAACCACCTGAGCTACGCGCCCAAAATAACTTCTAAAATTATAAAGTTAATGCC
12021  GCGCTCTAACCACCTGAGCTACGCGCCCAAG-------CTA--------------------
12020  GCGCTCTAACCACCTGAGCTACGCGCCCAAG-------CTA--------------------
12018  --TCGTTATAAACAGTAAGGATGAAAAAAGAG-----------------------CTAT
12022  TTTTGCTACTATCAGAATCGATAACAATACAAT-----CTT---------------CCTT
             **         *

12023  ---TACATGACTTGAACACGCGACCCTCTGATTACAAATCAGATGCTCTACCAACTGAGC
12024  ---TACATGACTTGAACACGCGACCCTCTGATTACAAATCAGATGCTCTACCAACTGAGC
12019  GGCTACATGACTTGAACACGCGACCCTCTGATTACAAATCAGATGCTCTACCAACTGAGC
12021  --TTGCTTGGTTT-----T--TACTTTCTTATA-------A--------------------
12020  --TTGCTTGGTTT-----T--TACTTTCTTATA-------------------A--------
12018  TAAAGCACTATATGAA-ACAT--TCTTCCAAA--AATAGTACCTATTACACTACTTACAC
12022  TAGCTCAGAAATGGTA-ACGTAGTCATTAAGATCAATACTAACCATAATCATAGCTAATT
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12023  TAAGCCGGCAATCTACTAATGCGGGTGAAGGGACTTGAACCCCCACGCCGTTAAGCGCCA
12024  TAAGCCGGCAATCTACTAATGCGGGTGAAGGGACTTGAACCCCCACGCCGTTAAGCGCCA
12019  TAAGCCGGCAATCTACTAATGCGGGTGAAGGGACTTGAACCCCCACGCCGTTAAGCGCCA
12021  ---------AG-----TAAAGCGGGTGACGAGAATCGAACTC------------------
12020  ---------AG-----TAAAGCGGGTGACGAGAATCGAACTC------------------
12018  TATTAGATAGATAA--CAAATCGTCCT-----AAGTAAGCTTA-------CTTAGGACGA
12022  CATGATAACCATCGT-CACATCGTCCTTTAATATCTAATCCTAAATTAAGTTTGGCAGGA
                     *   **          *    * *

12023  GATCCTAAATCTGGTGCGTCTGCCAATTCCGCCACACCCGCATTTCTAAATGACCCGTAC
12024  GATCCTAAATCTGGTGCGTCTGCCAATTCCGCCACACCCGCATTTCTAAATGACCCGTAC
12019  GATCCTAAATCTGGTGCGTCTGCCAATTCCGCCACACCCGCATTTCTAAATGACCCGTAC
12021  ----------------------------GCGACAACAGC------------------
12020  ----------------------------GCGACAACAGC------------------
12018  TTTT----ATTTAGAACATAGGATAGTTTTTCCACTTTTAATCGTAA-------CCACTT
12022  GCTT----TCTCAAAAATTTTCATAAAACCTCCCTAATAAAATATAGAA-T-ATCCATAT
                                    *

12023  TGGGCTCGAACCAGTGACCCATTGATTAAAAGTCAATTGCTCTACCAACTGAGCTAACGA
12024  TGGGCTCGAACCAGTGACCCATTGATTAAAAGTCAATTGCTCTACCAACTGAGCTAACGA
12019  TGGGCTCGAACCAGTGACCCATTGATTAAAAGTCAATTGCTCTACCAACTGAGCTAACGA
12021  --------------T-----------TGGAAGGCTGTAGTTTTACCA-CTAAACTA----
12020  ------------------------TTGGAAGGCTGTAGTTTTACCA-CTAAACTA----
12018  GGTATCA------GTGACA----AATTCGGA--CAATTAAGATGTTAGCCAATCTTAAGG
12022  TATAACATAACAAATGACA----AATTCGGA--CAATTAAGATGCTAGCCAATCTTAAGG
                              *   *  *  *     *   * *  * **

12023  GTCTACGGTCCCGACGGGAATCGAACCCGCGATCTTCGCCGTGACAGGGCGACGTGATAA
12024  GTCTACGGTCCCGACGGGAATCGAACCCGCGATCTTCGCCGTGACAGGGCGACGTGATAA
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12019  GTCTACGGTCCCGACGGGAATCGAACCCGCGATCTTCGCCGTGACAGGGCGACGTGATAA
12021  ----------------------------------------CACC------------
12020  ----------------------------------------CACC------------
12018  ATA-ATAATTCCAATAAAAA----------AAGGCTAACCAAAGTTAGTC
12022  ATA-ATAATTCCAATAAAAA----------AAGGCTAACCAAAGTTAGTC
                                      *

12023  CCGCTACACTACGGGACCTATGGGAGTTAACGGGATCGAACCGCTGACCCTCTGCTTGTA
12024  CCGCTACACTACGGGACCTATGGGAGTTAACGGGATCGAACCGCTGACCCTCTGCTTGTA
12019  CCGCTACACTACGGGACCTATGGGAGTTAACGGGATCGAACCGCTGACCCTCTGCTTGTA
12021  -CGCT----------TCTATGGGAGTTAACGGGATCGAACCGCTGACCCTCTGCTTGTA
12020  -CGCT----------TCTATGGGAGTTAACGGGATCGAACCGCTGACCCTCTGCTTGTA
12018  TCCCTTTA--------TCTACTCCGCCAGTAGGACTCGAACCTACGACATCATGATTAAC
12022  TCCCTTTA--------TCTACTCCGCCAGTAGGACTCGAACCTACGACATCATGATTAAC
        * **            ***           **  *******   ***    ** **

12023  AGGCAGATGCT-CTCCCAGCTGAGCTAAACTCCCTTT--GCTAAGCGACTACCTTATCTC
12024  AGGCAGATGCT-CTCCCAGCTGAGCTAAACTCCCTTT--GCTAAGCGACTACCTTATCTC
12019  AGGCAGATGCT-CTCCCAGCTGAGCTAAACTCCCTTT--GCTAAGCGACTACCTTATCTC
12021  AGGCAGATGCT-CTCCCAGCTGAGCTAAACTCCCTTT--GCTAAGCGACTACCTTATCTC
12020  AGGCAGATGCT-CTCCCAGCTGAGCTAAACTCCCTTT--GCTAAGCGACTACCTTATCTC
12018  AGTCATGCGCTACTACCAACTGAGCTATGGCGGATTATAGCTAAGCGACTACCTTATCTC
12022  AGTCATGCGCTACTACCAACTGAGCTATGGCGGATTATAGCTAAGCGACTACCTTATCTC
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12023  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
12024  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
12019  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
12021  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
12020  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
12018  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
12022  ACAGGGGGCAACCCCCAACTACTTCCGGCGTTCTAGGGCTTAACTTCTGTGTTCGGCATG
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12023  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
12024  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
12019  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
12021  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
12020  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
12018  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
12022  AGAACAGGTGTATCTCCTAGGCAATTATCACTTAACTATTGAGCCTTATTCACTCAAAAT
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12023  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
12024  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
12019  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
12021  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
12020  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
12018  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
12022  TGAATATCTATAGTCTAACAAGAAACCGTAACGTTGTCAATATCTCTTTTTGGATAAGTC
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12023  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
12024  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
12019  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
12021  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
12020  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
12018  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
12022  CTCGAGCTATTAGTATTAGTCCGCTAAATGTGTCACCACAATTACACTCCTAACCTATCT
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12023  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
12024  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
12019  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
12021  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
12020  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
12018  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
12022  ACCTGATCATCTCTCAGGGCTCTTACTGATATAAAATCATGGGAAATCTCATCTTGAGGT
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12023           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
12024           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
12019           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
12021           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
12020           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
12018           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
12022           GGGCTTCGCACTTAGATGCTTTCAGCGCTTATCCCTTCCCTACATAGCTACCCAGCGATG
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12023           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
12024           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
12019           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
12021           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
12020           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
12018           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
12022           CCTTTGGCAAGACAACTGGTACACCAGCGGTAAGTCCACTCTGGTCCTCTCGTACTAGGA
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12023           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
12024           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
12019           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
12021           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
12020           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
12018           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
12022           GCAGATCCTCTCAAATTTCCTACGCCCGCGACGGATAGGGACCGAACTGTCTCACGACGT
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12023           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
12024           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
12019           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
12021           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
12020           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
12018           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
12022           TCTGAACCCAGCTCGCGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACCGACTA
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12023           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
12024           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
12019           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
12021           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
12020           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
12018           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
12022           CAGCCCCAGGATGCGACGAGCCGACATCGAGGTGCCAAACCTCCCCGTCGATGTGAACTC
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12023           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
12024           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
12019           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
12021           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
12020           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
12018           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
12022           TTGGGGGAGATAAGCCTGTTATCCCCAGGGTAGCTTTTATCCGTTGAGCGATGGCCCTTC
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12023           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
12024           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
12019           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
12021           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
12020           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
12018           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
12022           CATACGGAACCACCGGATCACTAAGCCCGACTTTCGTCCCTGCTCGAGTTGTAGCTCTCG
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12023           CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
12024           CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
12019           CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
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12021  CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
12020  CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
12018  CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
12022  CAGTCAAGCTCCCTTATACCTTTACACTCTACGACTGATTTCCAACCAGTCTGAGGGAAC
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12023  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
12024  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
12019  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
12021  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
12020  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
12018  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
12022  CTTTGGGCGCCTCCGTTACCTTTTAGGAGGCGACCGCCCCAGTCAAACTGCCCGTCAGAC
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12023  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
12024  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
12019  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
12021  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
12020  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
12018  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
12022  ACTGTCTCCGATAGGGATTGCCTATCTGGGTTAGAGTAGCCATAACACAAGGGTAGTATC
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12023  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
12024  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
12019  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
12021  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
12020  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
12018  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
12022  CCAACAACGCCTCAAACGAAACTGGCGTCCCGTTATCATAGGCTCCTACCTATCCTGTAC
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12023  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
12024  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
12019  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
12021  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
12020  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
12018  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
12022  ATGTGGTACAGATACTCAATATCAAACTGCAGTAAAGCTCCATGGGGTCTTTCCGTCCTG
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12023  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
12024  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
12019  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
12021  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
12020  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
12018  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
12022  TCGCGGGTAACCTGCATCTTCACAGGTACTAAAATTTCACCGAGTCTCTCGTTGAGACAG
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12023  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
12024  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
12019  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
12021  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
12020  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
12018  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
12022  TGCCCAAATCATTACGCCTTTCGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTAC
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12023  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
12024  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
12019  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
12021  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
12020  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
12018  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
12022  CTTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTTCAATTCATACCTTCGCTTA
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12023  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
12024  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
12019  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
12021  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
12020  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
12018  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
12022  CGCTAAGCACTCCTCTTAACCTTCCAGCACCGGGCAGGCGTCACCCCCTATACATCATCT
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12023  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
12024  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
12019  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
12021  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
12020  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
12018  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
12022  TACGATTTAGCAGAGAGCTGTGTTTTTGATAAACAGTTGCTTGGGCCTATTCACTGCGGC
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12023  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
12024  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
12019  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
12021  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
12020  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
12018  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
12022  TGATCTAAAATCAGCGCCCCTTCTCCCGAAGTTACGGGGCCATTTTGCCGAGTTCCTTAA
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12023  CGAGAGTTCTCTCGCTCACCTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
12024  CGAGAGTTCTCTCGCTCACCTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
12019  CGAGAGTTCTCTCGCTCACCTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
12021  CGAGAGTTCTCTCGCTCACCTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
12020  CGAGAGTTCTCTCGCTCACMTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
12018  CGAGAGTTCTCTCGCTCACCTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
12022  CGAGAGTTCTCTCGCTCACCTGAGGCTACTCGCCTCGACTACCTGTGTCGGTTTGCGGTA
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12023  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
12024  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
12019  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
12021  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
12020  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
12018  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
12022  CGGGTAGAGTATATGTATCGCTAGAAGCTTTTCTTGGCAGTGTGACATCACTAACTTCGC
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12023  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
12024  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
12019  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
12021  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
12020  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
12018  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
12022  TACTAAACTTCGCTCCTCGTCACAGCTCAATGTTAAAGATATAAGCATTTGACTCATATC
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12023  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
12024  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
12019  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
12021  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
12020  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
12018  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
12022  ACACCTCACTGTTTGACCAGACACTTCCAATCGTCTGGTTTAGTTAGCCTACTGCGTCCC
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12023  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
12024  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
12019  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
12021  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
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12020  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
12018  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
12022  TCCATCACTATATACTCTAGTACAGGAATATCAACCTGTTGTCCATCGGATACACCTTTC
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12023  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
12024  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
12019  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
12021  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
12020  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
12018  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
12022  GGTCTCTCCTTAGGTCCCGACTAACCCAGGGCGGACGAGCCTTCCCCTGGAAACCTTAGT
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12023  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
12024  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
12019  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
12021  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
12020  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
12018  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
12022  CTTACGGTGGACAGGATTCTCACCTGTCTTGCGCTACTCATACCGGCATTCTCACTTCTA
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12023  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
12024  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
12019  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
12021  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
12020  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
12018  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
12022  TGCGTTCCAGCGCTCCTCACGGTACACCTTCTTCACACATAGAACGCTCTCCTACCATGA
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12023  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
12024  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
12019  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
12021  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
12020  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
12018  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
12022  CACTTTTGTGTCATCCACAGCTTCGGTAATATGTTTTAGCCCCGGTACATTTTCGGCGCA
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12023  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
12024  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
12019  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
12021  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
12020  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
12018  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
12022  GGGTCACTCGACTAGTGAGCTATTACGCACTCTTTGAATGAATAGCTGCTTCTAAGCTAA
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12023  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
12024  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
12019  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
12021  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
12020  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
12018  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
12022  CATCCTAGTTGTCTGTGCAACCCCACATCCTTTTCCACTTAACATATATTTTGGGACCTT
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12023  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
12024  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
12019  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
12021  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
12020  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
12018  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
12022  AGCTGGTGGTCTGGGCTGTTTCCCTTTCGACTACGGATCTTAGCACTCGCAGTCTGACTG
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12023  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
12024  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
12019  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
12021  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
12020  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
12018  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
12022  CCGATTATATCTCGTTGGCATTCGGAGTTTATCTGAGATTGGTAATCCGGGATGGACCCC
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12023  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
12024  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
12019  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
12021  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
12020  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
12018  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
12022  TCACCCAAACAGTGCTCTACCTCCAAGAGACTTAACATCGACGCTAGCCCTAAAGCTATT
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12023  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
12024  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
12019  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
12021  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
12020  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
12018  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
12022  TCGGAGAGAACCAGCTATCTCCAAGTTCGTTTGGAATTTCTCCGCTACCCACAAGTCATC
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12023  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
12024  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
12019  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
12021  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
12020  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
12018  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
12022  CAAGCACTTTTCAACGTGCCCTGGTTCGGTCCTCCAGTGAGTTTTACCTCACCTTCAACC
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12023  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
12024  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
12019  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
12021  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
12020  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
12018  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
12022  TGCTCATGGGTAGGTCACATGGTTTCGGGTCTACAACATGATACTATGACGCCCTATTAA
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12023  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
12024  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
12019  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
12021  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
12020  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
12018  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
12022  GACTCGGTTTCCCTACGGCTCCGTCTCTTCAACTTAACCTCGCATCATATCGTAACTCGC
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12023  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
12024  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
12019  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
12021  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
12020  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
12018  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
12022  CGGTTCATTCTACAAAAGGCACGCTCTCACCCATTAACGGGCTCGAACTTGTTGTAGGCA
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12023  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
12024  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
12019  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
12021  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
12020  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
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12018  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
12022  CACGGTTTCAGGTTCTATTTCACTCCCCTCCCGGGGTGCTTTTCACCTTTCCCTCACGGT
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12023  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
12024  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
12019  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
12021  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
12020  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
12018  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
12022  ACTGGTTCACTATCGGTCACTAGAGAGTATTTAGGGTTGGGAGATGGTCCTCCCAGATTC
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12023  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
12024  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
12019  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
12021  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
12020  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
12018  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
12022  CGACGAGATTTCGCGTGTCTCGCCGTACTCAGGATACTGCTAAGGTTAATCTATCATTTT
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12023  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
12024  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
12019  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
12021  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
12020  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
12018  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
12022  AAATACGAGGCTGTTACTCTCTTTGGCTTACCTTCCCAGGTAATTCTTCTATAATGATTA
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12023  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
12024  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
12019  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
12021  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
12020  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
12018  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
12022  ATCCTATATCGCAGTCCTACAACCCCGAAGTGTAAACACTTCGGTTTGCCCTCCTGCCGT
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12023  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
12024  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
12019  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
12021  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
12020  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
12018  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
12022  TTCGCTCGCCGCTACTAAGGCAATCGCTTTTGCTTTCTCTTCCTGCAGCTACTTAGATGT
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12023  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
12024  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
12019  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
12021  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
12020  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
12018  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
12022  TTCAGTTCACTGCGTCTTCCTTCTCATATCCTTAACAGATATGGATACTAGTCATTAACT
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12023  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
12024  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
12019  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
12021  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
12020  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
12018  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
12022  AGTGGGTTCCCCCATTCGGACATCTCTGGATCAGCGCTTACTTACAGCTCCCCAAAGCAT
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12023  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
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12024  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
12019  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
12021  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
12020  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
12018  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
12022  TTCGTCGTTAGTCACGTCCTTCTTCGGCTTCTAGTGCCAAGGCATCCACCGTGCGCCCTT
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12023  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
12024  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
12019  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
12021  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
12020  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
12018  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
12022  ATTAACTTAACCTTATTAACCTAGTTTCTTTAAAACTAGAAAACTCATTAAATATTCACA
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12023  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
12024  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
12019  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
12021  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
12020  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
12018  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
12022  GCGTTTTCGGTTTATTTTCTTGTTACTTTCTACAATCTATTTCTAGATCGTGGAATTTGA
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12023  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
12024  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
12019  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
12021  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
12020  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
12018  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
12022  TATAGATATTCAATTTTCAATGAACAATTTGAACCTTTCGATTCAATGGAGCCTAGCGGG
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12023  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
12024  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
12019  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
12021  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
12020  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
12018  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
12022  ATCGAACCGCTGACCTCCTGCGTGCAAAGCAGGCGCTCTCCCAGCTGAGCTAAGGCCCCA
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12023  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
12024  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
12019  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
12021  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
12020  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
12018  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
12022  CAAGACCTCTCAAAACTAAACAAGACGCAAATGGCAGGTTTCCTTATCCTTAGAAAGGAG
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12023  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
12024  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
12019  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
12021  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
12020  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
12018  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
12022  GTGATCCAGCCGCACCTTCCGATACGGCTACCTTGTTACGACTTCACCCCAATCATCTAT
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12023  CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
12024  CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
12019  CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
12021  CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
12020  CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
12018  CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
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12022   CCCACCTTAGGCGGCTGGCTCCTAAAAGGTTACCTCACCGACTTCGGGTGTTACAAACTC
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12023   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
12024   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
12019   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
12021   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
12020   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
12018   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
12022   TCGTGGTGTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGCGGCGTGCTGAT
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12023   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
12024   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
12019   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
12021   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
12020   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
12018   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
12022   CCGCGATTACTAGCGATTCCGACTTCATGTAGGCGAGTTGCAGCCTACAATCCGAACTGA
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12023   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
12024   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
12019   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
12021   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
12020   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
12018   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
12022   GATTGGCTTTAAGAGATTAGCTTGCCGTCACCGGCTTGCGACTCGTTGTACCAACCATTG
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12023   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
12024   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
12019   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
12021   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
12020   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
12018   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
12022   TAGCACGTGTGTAGCCCAGGTCATAAGGGGCATGATGATTTGACGTCATCCCCACCTTCC
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12023   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
12024   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
12019   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
12021   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
12020   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
12018   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
12022   TCCGGTTTATTACCGGCAGTCTCGCTAGAGTGCCCAACTTAATGATGGCAACTAACAATA
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12023   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
12024   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
12019   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
12021   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
12020   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
12018   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
12022   GGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGAGCTGACGACAACCA
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12023   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
12024   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
12019   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
12021   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
12020   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
12018   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
12022   TGCACCACCTGTCACTTCTGCTCCGAAGAGAAAGCCTATCTCTAGGCCGGTCAGAAGGAT
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12023   GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
12024   GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
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12019  GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
12021  GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
12020  GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
12018  GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
12022  GTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAAACCACATGCTCCACCGCTTG
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12023  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
12024  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
12019  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
12021  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
12020  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
12018  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
12022  TGCGGGCCCCCGTCAATTCCTTTGAGTTTCAACCTTGCGGTCGTACTCCCCAGGCGGAGT
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12023  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
12024  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
12019  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
12021  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
12020  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
12018  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
12022  GCTTAATGCGTTAGCTGCGGCACTAAGCCCCGGAAAGGGCCTAACACCTAGCACTCATCG
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12023  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
12024  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
12019  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
12021  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
12020  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
12018  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
12022  TTTACGGCGTGGACTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGAGCCTCA
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12023  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
12024  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
12019  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
12021  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
12020  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
12018  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
12022  GCGTCAGTTACAGACCAGAGAGCCGCTTTCGCCACCGGTGTTCCTCCATATATCTACGCA
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12023  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
12024  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
12019  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
12021  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
12020  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
12018  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
12022  TTTCACCGCTACACATGGAATTCCACTCTCCCCTTCTGCACTCAAGTCCTCCAGTTTCCA
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12023  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
12024  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
12019  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
12021  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
12020  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
12018  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
12022  AAGCGTACAATGGTTAAGCCACTGCCTTTAACTTCAGACTTAAAGAACCGCCTGCGCTCG
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12023  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
12024  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
12019  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
12021  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
12020  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
12018  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
12022  CTTTACGCCCAATAAATCCGGACAACGCTCGGGACCTACGTATTACCGCGGCTGCTGGCA
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12023           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
12024           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
12019           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
12021           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
12020           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
12018           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
12022           CGTAGTTAGCCGTCCCTTTCTGGTTAGTTACCGTCACTTGGTAGATTTTCCACTCCTACC
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12023           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
12024           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
12019           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
12021           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
12020           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
12018           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
12022           AACGTTCTTCTCTAACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGT
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12023           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
12024           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
12019           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
12021           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
12020           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
12018           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
12022           TGCTCGGTCAGACTTCCGTCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTC
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12023           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
12024           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
12019           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
12021           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
12020           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
12018           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
12022           TGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGTCG
                ************************************************************

12023           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
12024           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
12019           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
12021           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
12020           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
12018           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
12022           CCTTGGTGAGCCTTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCACAGTGAA
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12023           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
12024           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
12019           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
12021           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
12020           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
12018           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
12022           GCAATTGCTCCTTTTAAATAACTAACATGTGTTAATTACTCTTATGCGGTATTAGCTATC
                ************************************************************

12023           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
12024           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
12019           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
12021           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
12020           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
12018           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
12022           GTTTCCAATAGTTATCCCCCGCTATGAGGCAGGTTACCTACGCGTTACTCACCCGTTCGC
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12023           AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
12024           AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
12019           AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
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12021  AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
12020  AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
12018  AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
12022  AACTCATCAGTCTAGTGTAAACACCAAACCTCAGCGTTCTACTTGCATGTATTAGGCACG
       ************************************************************

12023  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
12024  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
12019  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
12021  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
12020  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
12018  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
12022  CCGCCAGCGTTCGTCCTGAGCCAGGATCAAACTCTCATTAAAAGTTTGAGCTTTGCTCTT
       ************************************************************

12023  TTCTGTCTCGCTGACAGATTTATTGTTTTTT-GTCATTGACGGATTTACAATGTAAATCC
12024  TTCTGTCTCGCTGACAGATTTATTGTTTTTTTGTCATTGACGGATTTACAATGTAAATCC
12019  TTCTGTCTCGCTGACAGATTTATTGTTTTTT-GTCATTGACGGATTTACAATGTAAATCC
12021  TTCTGTCTCGCTGACAGATTTATTGTTTTTTTGTCATTGACGGATTTACAATGTAAATCC
12020  TTCTGTCTCGCTGACAGATTTATTGTTTTTTTGTCATTGACGGATTTACAATGTAAATCC
12018  TTCTGTCTCGCTGACAGATTTATTGTTTTTT-GTCATTGACGGATTTACAATGTAAATCC
12022  TTCTGTCTCGCTGACAGATTTATTGTTTTTT-GTCATTGACGGATTTACAATGTAAATCC
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12023  ACCCTGCACATTCGTTCGTCTTGTTCAGTTTTCAAAGGTCTAATGATATATCATAAAAAT
12024  ACCCTGCACATTCGTTCGTCTTGTTCAGTTTTCAAAGGTCTTTGCCTCTCTTGAGACAAC
12019  ACCCTGCACATTCGTTCGTCTTGTTCAGTTTTCAAAGGTCTTTGCCTCTCTTGAGACAAC
12021  ACCCTGCACATTCGTTCGTCTTGTTCAGTTTTCAAAGGTCTTTGCCTCTCTTGAGACAAC
12020  ACCCTGCACATTCGTTCGTCTTGTTCAGTTTTCAAAGGTCTTTGCCTCTCTTGAGACAAC
12018  ACCCTGCACATTCGTTCATCTTGTTCAGTTTTCAAAGGTCTTTGCCTCTCTTGAGACAAC
12022  ACCCTGCACATTCGTTCGTCTTGTTCAGTTTTCAAAGGTCTTTGCCTCTCTTGAGACAAC
       ***************** ********************     * * *    * **

12023  ATATCCATCGGGAAGACAGGATTCGAACCTG-CGACACCTTGGTCCCAAACCAAGTACTC
12024  TTCTATATTCTAGCAAACTTATTCTGCTTTGTCAACTACTTTTTTTTAAGTTGTTAACTA
12019  TTCTATATTCTAGCAAACTTATTCTGCTTTGTCAACTACTTT-TTTTAAGTTGTTAACTA
12021  TTCTATATTCTAGCAAACTTATTCTGCTTTGTCAACTACTTT-TTTTAAGTTGTTAACTA
12020  TTCTATATTCTAGCAAACTTATTCTGCTTTGTCAACTACTTT-TTTTAAGTTGTTAACTA
12018  TTCTATATTCTAGCAAACTTATTCTGCTTTGTCAACTACTTT-TTTTAAGTTGTTTATAA
12022  TTCTATATTCTAGCAAACTTATTCTGCTTTGTCAACTACTTT-TTTTAAGTTGTTAACTA
        * *  **       *    ****     ** * **  ***  *   **       *

12023  TACCAAGCTG--A-GCTACT-TCCCGAAAAA---TATGCACC---CTAGAGGAGTCGAAC
12024  CGCGTTACTAGAA-GCTGCTCTCTCGAGACAACTTATTCATTATACTAAATATTTCTACT
12019  CGCGCTAATAGAA-ACTGCTCTCTCGAGACAACTTATTCATTATACTAAATATTTCTACT
12021  CGCGCTAATAGAA-ACTGCTCTCTCGAGACAACTTATTTAGTTTACTACATCATCTCTTA
12020  CGCGCTAATAGAA-ACTGCTCTCTCGAGACAACTTATTTAGTTTACTACATCATCTCTTA
12018  AATGATAATACAATATTAGGTTCGCTTAAGAACTCATTTAGTATACTATAATTTTTTATT
12022  CGCGCTAATAGAA-ACTGCTCTCTCGAGACAACTTATTTAGTTTACTACATCATCTCTTA
              *   *   *    ** *   * *    **  *     *** *

12023  CTCTAACCGCCTGATTCGTA-GTCAGGTACTCTATCC-------AGTTGA----GCTAAG
12024  TCCTGTCAATACTATTTTTGCATTTTTTCTTTTATTTTTAAA-AAGTTAATATTATTTTAT
12019  TCCTGTCAATACTATTTTTGTA---TTTTATAAATTTAGTAT-AGACATAACTATTCCTC
12021  CTTTGTCAACTCTTTTTTCATACT-TTTTCTACATTTTCTGA-AAATGTAGATCAGGCTC
12020  CTTTGTCAACTCTTTTTTCATACT-TTTTCTACATTTTCTGA-AAATGTAGATAGAGCGC
12018  TGTTGTCAATAGGTTTTAAAAA----------AATCTCAGAGAAAACCCTGAGATTTTT
12022  CTTTGTCAACTCTTTTTTCATACT-TTTTCTACATTTTCTGAAAAAAGTTTCCTGTTGGC
          *  *       **                *

12023  GGTGCTAAAT--------ATTATATGCCGA-------GGACCGGAATC-------G---A
12024  AGTAACTAAC--------CTTCTATACTTGTTGA-ATGGATAGCATTT-------T---T
12019  TATATTCAATTAAGAGAAATTATATAACCACTATTGAGAAATGTAGTC-------T---A
12021  AA-GCTTAAC---GATTCTTTTTAAAATCATTA-----AATTTTAAAA-------C---A
12020  AAGAAAAAAAGAGGTCTCACCTCTTTTTATTTCTTAGTAACTACTACA-------A---A
12018  TAAATT--ATGTTACAAAGTT--AATTTCCTT-----TAGCTTCAATT---------AAA
12022  TAACACCAATAACATAGAGTTTAAAATTCCATAC--CTAAATTTATTTTATTAGTAAAAA
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12023   ACCGGTACGATGTTTACC-A--TCGCAGGATTTTAAGTCCTGTGCGTCTGC--CAGTTCC
12024   ACCGTTGTCATGTTCAT--A--TTTCATCTTCTTAATTCACAAATTTAAACTTCATCTTC
12019   GCGATTAAATTCTTTGCTCA--TCGAA-AATATCCAATAAATATAATAATGCATAAAACG
12021   AATTTCAGACATGTTGC------CAAA-GTTTTGATATTATTACTATAAT--ATAGTTTG
12020   TCTATTAGGATCGTTACCTT--CAGAATAACTTTCAACACCCTCTATAGT-TGCAATTGT
12018   CCTAGTTCGCCATCTTCACG-CTTGTAAAGGACATTTGTCGTATTATCTTCTGCATCT--
12022   AATAAAAGATGGGCTAGCCATCTTTTATAATATTTGTTTTTTATATTCTTCAGCTTCTTG
                                      *                   *

12023   G-CCA--------CCCCGGCCTCTAACAAGCGAACGACGGGGTTCGAA-CCCGCGACCCT
12024   A-TAAAAAATACCCTTCAAATTTTATCTAAATTTGAAGGGTATTTGAAATTTATAAAGTT
12019   C-CTGCTTACGAAATATAAACAAA-ATTGTTTGCAT--TTCGTAAACAAGCGTTACCTAT
12021   T-AGAGGAGAATAATATGGGCCAA-GAACCTATCAT--CGAATATCAAAATAT----CAA
12020   T-TTATGAACAGTTTTTCGCTCACTGTTACTCATAGGATCCATATGGTAAGGTTCATTAG
12018   --GTATAGATAAAGAAATCATGACCTAAAAGTTCCATTTGCAACAATGCTTCCTCAACAT
12022   GGGTGTAGATAAAACAAA-ATGACCAGGGGTAATCTCGTGCATTTGACGTTCTTGTCCGT

12023   CAC--CTTGGCAAGGTGATGTTCTACCACTGAACTACGT-TCGCACTAAAGACACTATT-
12024   CTT--TAAAAATATATGATGACTTATTTTTTATCTTCTTCTTGCATTTTTTCTTTGATTT
12019   TTA--ACAATATATGATGAGTGTTCCCGCTGAGAATAATTCTCAGCGGTAGACCAGAGCT
12021   TAA--AGTGTATGGGGAAAATGTTGCGGTTGAAGACA----TTAACCTTAAAATTTACCC
12020   TCT--CTAAAACACGCCTAGCTATTTTTTTAGAAAAA----TCAATTAAAGTTTCTGTAC
12018   CCA--TTGGTTTTAGATTAACATTCTTAGTACGTACAAT--T-CTTTGGCTTACTGCTTC
12022   CTTGCTCAATAGCTGGATTATACGGCTGGTGAACACGTT--GACGTTCACTCTCCGGATC
                                        *

12023   ------------------------------------------------------------
12024   CATCGTATGATAACGCTCTTGCTTTATCTTCA---TCATTTTCTGTCTCAGGCATTTTAC
12019   AGACTAAGAATCGATTGATTCCATCATCATAACACTCAACAAAATTGATAAAAATTATAC
12021   TGGT---GATTTTGTTTGTTTCATCGGTA-------CGAGTGGATCAGGTAAAACAACAT
12020   GATGCTCAACGTAGTCATGGACATTAATGGA----TACTGAAAAACTCTTAGAAAAGCGG
12018   TTCATCTGGCTCAGCC-----TCAAATTCTGTTGTGAAAAC---TTGACTTGCTGGAATC
12022   TGGTTCTGGAATAGCTGATAATAGACTCTTCGTATAAGGGTGGATTGGATTGTTATAAAC

12023   ------------------------------------------------------------
12024   CTGTCTCAAAAATCGATTTAATCTGAGCAGCATCAA-----GAGTCTCATATTTTAAGAG
12019   TAATTCA-ATAATTGCCATTGGGGCAGCATCGCCAC--GGCGTGGTTCTGT-TTTAAGAA
12021   TAATGCGTATGGTTAACCATATGTTAAAACCAACAA--ATGGTACTCTATTATTTAAGGG
12020   TCATGAAGATAATT----TTGTGCTAACAACTGCAACGATTTTAATACTTT-TCCATGAT
12018   TTTTCACGATATT--------TTTTCGCAATTTTA--------GTTTTATT-TTTACGA-
12022   ATCATCAGATGTTC---CAACTTCTAACAGTTTCCCCCAATGCATAACACC-GATACGAT

12023   ------------------------------------------------------------
12024   GGCTTCTGCAATTAATTTATGAGTATCACGGTTTTCGTTGATAATATCAGCTGCC--TTA
12019   TACGAGTGTATCCTCCG--TTACGTTCAGCATAACGAGGTGCGATGTCGTC-AAA--AAG
12021   AAAAGATATTTCTACTA--TTAACCCCATTGAATTAAGACGCAGAATTG---GAT--ATG
12020   AACCAATGATGCGCCCAGCTTCTGGCGTTTCTATTTGGAGATTTATTTGTC-GCT--TAC
12018   ---------ATTTGAC------GCTCAATTTT-----ATCAACAACTAAGTCAAT-----
12022   CTGAAATGTATTTTACC--ATAGACAAATCATGTGCGATAAACAAATAAGTCAATCCTTG

12023   ------------------------------------------------------------
12024   TTACGTGCTTCATTAAGAAGGTGACGAACTTCATCATCAATAAGTTGTGCAGTTTGAGCA
12019   TTTTTGAAGAGCTGTTGTTGATGTAT-ATTT-ATCAGAAGCTTCATCATAGTTTTCTGAT
12021   TTATCCAAAACATTGGTTTAATGCCTCATATGACCATTTACGAAAATATAGTTCT-TGTA
12020   TTGTCGTAG--TTTCTATTGTTGCAT-CTAAATCCATCTCATAGATGATATTTTC----A
12018   TGACCCATACATATCTTGTGAAACATCTTCTGCTCGTAAAGTAATAGAATCTATTAAG--
12022   TTCTCTTTGCAATTTTTGCATTAAATTAACAACTTGTGCTTGGATTGAAACATCTAAGGC

12023   ------------------------------------------------------------
12024   GAATATGATTTTTCAGGTGACATTTGACCA--GCCATCATTGCGTGGTTGCCTTCGTATT
12019   GCAATTTCATTACGTACATAAGCAGCAGCT--TGACGACGAGCATGTAAATCACCACGTT
12021   CCAAAATTATTGAAATGGTCAGAAGAAGCT--AAAAGA-GCTAAAGCAAGGGAACTTATT
12020   ACGTATTTAGTCACCTGAGCAGCTGCTACT--TCAATATTAGGAAGTAGGTCAATTTTTT
12018   ----ATTGTTACTTCAACTTTTGCGGTCTT---CTCTCTGTATACTTTGAGGTTGACTCT
12022   AGATATTGGTTCATCAGCAATGATAAATTTAGGCTCTACTGCTAAAGCACGTGCAATCCC
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12023 ----------
12024 GAACTGGTCCAAGTTTCTCGCTCATACCATATTCAGTTACCATAGCGCGGGCCATAGCAG
12019 TACCTAGAGTAATCATTTTTTCAACTGTTTTACGGATTTCTTTAGCACGTGCTTCAGTAG
12021 AAATTAGTTGAATTACCCGAAGAA-TATTTGGATCGCTACCCTAGTGAGTTGTCTGGCGG
12020 CAATAGCTTCACTTGTAGTTACAACGTTTTTATCATCAATTTTTGGAAGT--TCTGGTTG
12018 AGTATCTAATTCTTGTGCTTC-----ATTAAAGTATTTTTCAACTTTAGAGAGTTTGGTC
12022 GATACGTTGTCGTTGTCCACCTGAAAATTCATGCGGATAACGTGTTAAATGATCTTTATT

12023 ----------
12024 TGGCTTGTTCGAAGTCATTTGAGGCACCTGTTGTCTGAGCGTTGAAAATAATTTCTTCCG
12019 TTACAATTGATTCGTTGATAAGAAGATCGGTTGTCAAATCA--CGAAGCATTGCCTTACG
12021 TCAGCAACAACGTATCGGTGTCATTCGCGCTCTTGCAGCAGACCAAGATATTATTTTAAT
12020 T----GATACGTCTTCTTTTTCAAGCGT-TTCATCAACCTCCTCTATATATTCTTCCACC
12018 TCAACATACTCA--CGAATAGCTTCTG----TTACTTCGATGTTTTCACCACGAAT-ACT
12022 TAACCCTACAAGATCTAATAGGGCCTGAACTTTACTATCACGATCTGATTTTGATTTAGC

12023 ----------
12024 CTACACGTCCTCCCATAAGACCTGCTAATTGCTCTTTCATATCATCTTTTGAAAGAAGCA
12019 TTGTGAGCTAGT-------GCGTCCTAGTTTACGGTAAGCCATTATGTCCTCCTATTTTA
12021 GGATGAGCCTTTT-----GGAGCTCTGGATCCTATTACTAGAGAAGGTATTCAAGACTTA
12020 ACATCTACGCTA-------GACGGTACATTCTTAATATTTTTTAACG--CTACCGATTCA
12018 GTATTTAATCAT----ATGAGTACCTCTTTCTTGCGTTGTTAACGCTTTCTATACTCTTA
12022 TAATTTATGTAT----ATCTAAACCT-TCTGCTACGATATCACGAATCTTCATACGGCCG

12023 ----------
12024 TTTGATCTTCTTTAGGT----AAAGCAATCATATATCCACCTGCACGACCACGTGGTACG
12019 TTTATCGTTTTTTAATC----CAAGACCTAGATCGGCAAGTTTGATTTTAACTTCTTCAA
12021 GTCAAGTCTCTTCAGG------AAGAAATGGG--GAAAACTATCATCTTAGTTACT-CAT
12020 TTAATATCAGTTACTT----------CGTCGGT-GATACCTTCTATTTCAACTTTTGCTG
12018 TTATAACC-GCTT-----TCATGAAAA----------
12022 TTTAAGCTAGCCTGAGGATCCTGAAAAATCATCTGAGCGTCTTTACGAAAACTATGTAAT

12023 ----------
12024 ATAGTAACTTTATGAACAACTCGCGCATTTGAAAGAATCAAACCGACAATTGTGTGCCCA
12019 GACTCTTACGTCCTAAGTTTCGGACTTTCATCATTTCAGGCTCAGTTTTTTCTG-TTAAA
12021 GA---T-ATGGATGAAGCCCTCAAGTT--AGCAACAAAAATT--ATTGTTATGG-ACAAT
12020 GC---TTTTTACCAAAGCCCAAAAAACCTTTTTTCTCACGTGATACAACTTTTATATGTG
12018 ----------
12022 GCTTTACCTTTCAGATGTGAGATCACTTCTCCATTAAAGGTAATTTCTCCATCAGAAATA

12023 ----------
12024 GCTTCATGGTAAGCAACCATAGCTCTTTCTCTTTCAGAAATAGTACGATCTTTTTTAGAA
12019 TCAAATACTGTATTAATTCCAGCACGTTTTAAACAGTTATATGAGCGCACTGACAAATCA
12021 GGTAAAATGGTCCAAGAAGGGACACCCAATGATCTCTTACATCATCCTGCTA--------
12020 CCCTCAATCGTGAAATGTTTAACTCTTGTAGTCCTTTTTCAATAGCTTCTTCTACAGTCG
12018 ----------
12022 TCATAAAGTTTTAAAATTGAACGTCCAACGGTTGTCTTTCCTGATCCAGATTCCCCAACT

12023 ----------
12024 GGACCAGCAATTACACGGTCTTCTGCTTCATCAATATCTGAAGCATCAATAACTTTTTTA
12019 AGTTCCTCAATTGTCCGGTCAAGCACTTTCTCATCGTTCACTTTCTCTGTTTCCTTCATT
12021 ----------
12020 CTCCTGTAAATAATACC----------
12018 ----------
12022 AATCCAAACACTTCACCTTCATAAATGTCAAAACTAACATTATCAATTGCTCTCACTTCA

12023 ----------
12024 TTTCGTCGCGCAGCAACTAAAGCAGCTTCATTGAGAACATTCTCCAAATCAGCACCAACA
12019 ACTTCAGTTGCTTTAGCAACCTCTGTTAAATCAGTAAACAAGTTTAAGTGTTCAATTAAG
12021 ----------
12020 ----------
12018 ----------
12022 TTAGCTTTTCCTTTATTGAAGGTCAAAGAAACATTTTTGACTTCAACTAATTTTTTTCGA

12023 ----------
12024 AATCCTGGGGTTTGTTGAGCTACTACTTTTAAGTCAACATTATCTGCTAATGGTTTATTT...
12019 ACGCGAGCTGAAAGACCAAGAGCATCCTCAGGAATGA----------
12021 ----------
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12020           ------------------------------------------------------------
12018           ------------------------------------------------------------
12022           TTTTCAGTCATTAGGCT-------------------------------------------
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It will be understood that the invention has been described by way of example only and modifications may be made whilst remaining within the scope and spirit of the invention.

TABLE I – THEROETICAL MOLECULAR WEIGHTS FOR GBS PROTEINS

GBS #	expected mol. weight (dalton)		
	GST-fusion	His-fusion	Native
1	78425	53460	49720
2	40035	15070	11330
3	90305	65340	61600
4	43115	18150	14410
5	158835	133870	130130
6	39265	14300	10560
7	44985	20020	16280
8	56315	31350	27610
9	50265	25300	21560
10	96465	71500	67760
11	91515	66550	62810
11d	85905	60940	57200
12	64455	39490	35750
13	40475	15510	11770
14	33325	8360	4620
15	44765	19800	16060
16	73475	48510	44770
17	46745	21780	18040
18	54335	29370	25630
19	46085	21120	17380
20	47625	22660	18920
21	56535	31570	27830
21 long	66435	41470	37730
22	60055	35090	31350
23	60165	35200	31460
24	58405	33440	29700
25	50265	25300	21560
26	118245	93280	89540
28	63795	38830	35090
29	50595	25630	21890
30	44215	19250	15510
31	63795	38830	35090
31d	58735	33770	30030
32	40585	15620	11880
33	71495	46530	42790
34	69295	44330	40590
35	56535	31570	27830
36	59065	34100	30360
37	46965	22000	18260
38	61815	36850	33110
39	65225	40260	36520
41	75235	50270	46530
42	46745	21780	18040
43	58955	33990	30250
44	52355	27390	23650
45	43555	18590	14850
46	59835	34870	31130
47	84255	59290	55550
48	86455	61490	57750
48d	106695	81730	77990
49	59615	34650	30910
50	94155	69190	65450

51	47075	22110	18370
52	55435	30470	26730
53	110215	85250	81510
54	73365	48400	44660
55	36295	11330	7590
56	34865	9900	6160
57	51145	26180	22440
58	128805	103840	100100
59	99215	74250	70510
60	63575	38610	34870
61	68085	43120	39380
62	105485	80520	76780
63	64125	39160	35420
64	112745	87780	84040
65	72485	47520	43780
66	49715	24750	21010
67	120335	95370	91630
68	131225	106260	102520
68d	103065	78100	74360
69	53895	28930	25190
70	74465	49500	45760
70d	59725	34760	31020
71	56755	31790	28050
72	75565	50600	46860
73	72815	47850	44110
74	131225	106260	102520
74d	95475	70510	66770
75	114725	89760	86020
76	198875	173910	170170
77	78535	53570	49830
78	48835	23870	20130
79	58185	33220	29480
79d	50815	25850	22110
80	81835	56870	53130
81	89205	64240	60500
82	40475	15510	11770
83	62585	37620	33880
84	122645	97680	93940
85	70175	45210	41470
86	84035	59070	55330
87	44435	19470	15730
88	73365	48400	44660
89	143325	118360	114620
90	93495	68530	64790
91	88325	63360	59620
92	193595	168630	164890
93	95585	70620	66880
94	77435	52470	48730
95	60605	35640	31900
96	57195	32230	28490
97	138375	113410	109670
98	82055	57090	53350
99	60715	35750	32010
100	53015	28050	24310
101	59395	34430	30690
102	40695	15730	11990
103	56975	32010	28270

104	120005	95040	91300
105	179735	154770	151030
105dNterm	127265	102300	98560
105dCterm	81285	56320	52580
106	85795	60830	57090
107	89535	64570	60830
108	64565	39600	35860
109	75125	50160	46420
109d	70725	45760	42020
110	53895	28930	25190
111 / 190	60165	35200	31460
112	63905	38940	35200
113	59175	34210	30470
114	51915	26950	23210
115	98225	73260	69520
116	73475	48510	44770
117	47515	22550	18810
118	42235	17270	13530
119	109225	84260	80520
120	71385	46420	42680
121	65115	40150	36410
122	46855	21890	18150
123	68305	43340	39600
124	54115	29150	25410
125	57305	32340	28600
126	56865	31900	28160
127	80845	55880	52140
128	39925	14960	11220
129	43775	18810	15070
130	82275	57310	53570
130d	63245	38280	34540
131	89755	64790	61050
132	49055	24090	20350
133	54445	29480	25740
134	42015	17050	13310
135	65225	40260	36520
136	54885	29920	26180
137	63465	38500	34760
138	40145	15180	11440
139	38165	13200	9460
140	43445	18480	14740
141	49935	24970	21230
142	79745	54780	51040
143	33545	8580	4840
144	49165	24200	20460
145	63025	38060	34320
146	107025	82060	78320
147	156965	132000	128260
148	41905	16940	13200
149	62365	37400	33660
150	54665	29700	25960
151	50412	25447	21707
151L	50045	25080	21340
152	45535	20570	16830
153	46965	22000	18260
154	101525	76560	72820
155	62585	37620	33880

156	61265	36300	32560
157	74025	49060	45320
158	52025	27060	23320
159	41025	16060	12320
160	82825	57860	54120
161	95365	70400	66660
162	42015	17050	13310
163	69405	44440	40700
164	42345	17380	13640
165	43555	18590	14850
166	38055	13090	9350
167	50375	25410	21670
168	32555	7590	3850
169	43445	18480	14740
170	64015	39050	35310
170d	59945	34980	31240
171	49825	24860	21120
172	62365	37400	33660
173	96795	71830	68090
174	45095	20130	16390
175	59175	34210	30470
176	55435	30470	26730
177	66215	41250	37510
178	62365	37400	33660
179	58515	33550	29810
180	37615	12650	8910
181	63685	38720	34980
182	90085	65120	61380
182d	87225	62260	58520
183	57855	32890	29150
184	46415	21450	17710
185	40695	15730	11990
186	85685	60720	56980
187	56205	31240	27500
188	61595	36630	32890
189	60165	35200	31460
191	116705	91740	88000
192	69625	44660	40920
193	98005	73040	69300
194	49385	24420	20680
195	81065	56100	52360
195L	147615	122650	118910
195L N-term	91405	66440	62700
196	69515	44550	40810
197	99325	74360	70620
198	73805	48840	45100
199	158285	133320	129580
200	132325	107360	103620
201	74538	49573	45833
202	157295	132330	128590
203	61705	36740	33000
204	39705	14740	11000
205	55985	31020	27280
206	56645	31680	27940
207	44765	19800	16060
208	59725	34760	31020
209	62145	37180	33440

209d	56425	31460	27720
210	60935	35970	32230
210d	53675	28710	24970
211	64895	39930	36190
212	60825	35860	32120
213	45205	20240	16500
214	38935	13970	10230
215	45205	20240	16500
216	91515	66550	62810
217	36075	11110	7370
218	81065	56100	52360
219	56535	31570	27830
220	54555	29590	25850
220	50155	25190	21450
221	41465	16500	12760
222	47405	22440	18700
223	42895	17930	14190
224	45865	20900	17160
225	56645	31680	27940
226	44875	19910	16170
227	46195	21230	17490
228	46525	21560	17820
229	35855	10890	7150
230	51915	26950	23210
231	60935	35970	32230
231d	58735	33770	30030
232	41795	16830	13090
233	35635	10670	6930
234	43115	18150	14410
235	58295	33330	29590
235d	48395	23430	19690
236	46525	21560	17820
237	44215	19250	15510
238	59725	34760	31020
239	63905	38940	35200
240	51475	26510	22770
241	45095	20130	16390
242	43225	18260	14520
243	119455	94490	90750
244	48065	23100	19360
245	48615	23650	19910
246	49605	24640	20900
246d	45975	21010	17270
247	58955	33990	30250
248	92505	67540	63800
248d	70835	45870	42130
249	103835	78870	75130
250	136505	111540	107800
251	52135	27170	23430
252	51695	26730	22990
253	74245	49280	45540
254	59615	34650	30910
255	69075	44110	40370
256	47845	22880	19140
257	60495	35530	31790
258	67975	43010	39270
259	79415	54450	50710

260	48175	23210	19470
261	55765	30800	27060
262	75345	50380	46640
263	63465	38500	34760
264	47185	22220	18480
265	56315	31350	27610
266	51365	26400	22660
267	88655	63690	59950
268	50265	25300	21560
269	60495	35530	31790
270	59285	34320	30580
271	56315	31350	27610
272	118355	93390	89650
272d	98885	73920	70180
273	70945	45980	42240
274	56205	31240	27500
275	47515	22550	18810
276	147945	122980	119240
277	87005	62040	58300
277d	75675	50710	46970
278	52245	27280	23540
279	79415	54450	50710
280	88655	63690	59950
281	74465	49500	45760
281d	71495	46530	42790
282	44765	19800	16060
283		20240	16500
284	67645	42680	38940
285	57525	32560	28820
286	41355	16390	12650
287	61045	36080	32340
287d	57085	32120	28380
288	53675	28710	24970
288d	51035	26070	22330
289	65005	40040	36300
289 long	71825	46860	43120
290	47405	22440	18700
291	63795	38830	35090
292	103505	78540	74800
293	115935	90970	87230
293d N-term	73805	48840	45100
293d C-term	70835	45870	42130
294	75785	50820	47080
295	89425	64460	60720
296	60385	35420	31680
297	100205	75240	71500
298	54335	29370	25630
299	62255	37290	33550
300	130895	105930	102190
301	54885	29920	26180
302	80075	55110	51370
303	53235	28270	24530
304	75125	50160	46420
305	78645	53680	49940
306	67975	43010	39270
307	86675	61710	57970
308	59285	34320	30580

309	62695	37730	33990
310	58845	33880	30140
311	76445	51480	47740
312	64785	39820	36080
313	65995	41030	37290
314	52135	27170	23430
315	51695	26730	22990
316	41795	16830	13090
317	179295	154330	150590
317d N-term	115935	90970	87230
317d C-term	92160	67402	63360
318	70065	45100	41360
319	61925	36960	33220
320	57965	33000	29260
321	83705	58740	55000
322	76628	51663	47923
323	86345	61380	57640
324	86345	61380	57640
325	82605	57640	53900
326	91515	66550	62810
326L	172695	147730	143990
326L N-term	113955	88990	85250
327	279175	254210	250470
327d N-term	139915	114950	111210
327d C-term	167965	143000	139260
328	97602	72637	68897
329	113955	88990	85250
330	83595	58630	54890
331	60825	35860	32120
332	75675	50710	46970
333	63465	38500	34760
333d	57965	33000	29260
334	38275	13310	9570
335	43555	18590	14850
336	67645	42680	38940
337	75235	50270	46530
338	54995	30030	26290
339	76665	51700	47960
339d	72925	47960	44220
340	86565	61600	57860
341	38385	13420	9680
342	61595	36630	32890
343	60385	35420	31680
344	55875	30910	27170
345	40585	15620	11880
346	53895	28930	25190
347	55325	30360	26620
348	58405	33440	29700
349	98335	73370	69630
350	53895	28930	25190
351	82165	57200	53460
352	111315	86350	82610
352d	105485	80520	76780
353	55325	30360	26620
354	42345	17380	13640
355	52135	27170	23430
356	59065	34100	30360

357	40255	15290	11550
358	60495	35530	31790
359	78865	53900	50160
360	73695	48730	44990
361	109005	84040	80300
362	125945	100980	97240
362d N-term	63355	38390	34650
362d C-term	91295	66330	62590
363	53125	28160	24420
364	75015	50050	46310
365	102075	77110	73370
366	68415	43450	39710
367	76885	51920	48180
368	44765	19800	16060
369	142115	117150	113410
370	94595	69630	65890
371	65555	40590	36850
372	55105	30140	26400
373	50265	25300	21560
374	57525	32560	28820
375	66875	41910	38170
376	48065	23100	19360
377	73805	48840	45100
378	58955	33990	30250
379	68855	43890	40150
380	47405	22440	18700
381	66875	41910	38170
382	50815	25850	22110
383	57085	32120	28380
384	77985	53020	49280
385	75675	50710	46970
386	39485	14520	10780
387	54555	29590	25850
388	45645	20680	16940
389	43005	18040	14300
390	62255	37290	33550
391	54775	29810	26070
392	71385	46420	42680
393	55765	30800	27060
394	59725	34760	31020
395	72375	47410	43670
396	34865	9900	6160
397	113625	88660	84920
397d	100865	3740	72160
398	56755	31790	28050
399	55435	30470	26730
400	74135	49170	45430
401	59395	34430	30690
402	78095	53130	49390
403	64455	39490	35750
404	61595	36630	32890
405	45975	21010	17270
406	36955	11990	8250
407	82715	57750	54010
407d	71715	46750	43010
408	45315	20350	16610
409	70395	45430	41690

409d	59600	34842	30800
410	62475	37510	33770
411	41355	16390	12650
412	35965	11000	7260
413	59175	34210	30470
414	50375	25410	21670
415	46195	21230	17490
416	42455	17490	13750
417	77985	53020	49280
418	42125	17160	13420
419	47515	22550	18810
420	67755	42790	39050
421	62915	37950	34210
422	60165	35200	31460
423	74245	49280	45540
424	89975	65010	61270
424	77325	52360	48620
425	116045	91080	87340
426	83815	58850	55110
427	41135	16170	12430
428	55325	30360	26620
429	59175	34210	30470
430	53785	28820	25080
431	54005	29040	25300
432	65665	40700	36960
433	40915	15950	12210
434	44545	19580	15840
642	91845	66880	63140
643	78975	54010	50270
644	49605	24640	20900
645	59725	34760	31020
646	61595	36630	32890
647	55875	30910	27170
648	59835	34870	31130
649	76115	51150	47410
650	51475	26510	22770
651	53345	28380	24640
652	49715	24750	21010
653	44655	19690	15950
654	51255	26290	22550
655	65995	41030	37290
656	57525	32560	28820
657	62805	37840	34100
658	60165	35200	31460
659	60275	35310	31570
660	71495	46530	42790
661	60605	35640	31900
662	62695	37730	33990
663	89535	64570	60830
664	45315	20350	16610
665	41135	16170	12430
666	47075	22110	18370
667	53162	28197	24457
668	43555	18590	14850
669	48505	23540	19800
670	45315	20350	16610
671	36940	12182	8140

672	40130	15372	11330
673	41450	16692	12650
674	45300	20542	16500
675	55970	31212	27170
676	65650	40892	36850
677	54320	29562	25520
678	77750	52992	48950
679	60480	35722	31680
680	64440	39682	35640
681	93040	68282	64240
682	84790	60032	55990
683	15950	44655	19690
684	11880	40585	15620
685	16280	44985	20020
686	21340	50045	25080
687	9350	38055	13090
689	55105	3740	26400

TABLE II – PRIMERS USED TO AMPLIFY GBS*nnn* PROTEINS

Forward primers begin 5'-GGGGACAAGTTTGTACAAAAAAGCAGGC-3' and continue with the sequences indicated in the table below; reverse primers begin 5'-GGGGACCACTTTGTACAAGAAAGCTGGGTT-3' and continue with the sequences indicated in the table. The primers for GBS1 are thus:

Fwd: GGGGACAAGTTTGTACAAAAAAGCAGGC**TCTCAATCTCATATTGTTTCAG**

Rev: GGGGACCACTTTGTACAAGAAAGCTGGGTT**ATTTTTAGACATCATAGACA**

The full forward primer sequences are given in the sequence listing as SEQ IDs 10968-11492. The reverse primer sequences are SEQ IDs 11493-12017.

GBS	Forward	Reverse
1	TCTCAATCTCATATTGTTTCAG	ATTTTTAGACATCATAGACA
2	TCTAATTACATTATTACATTTTTG	GGGAATGCCTACAAA
3	TCTGATACTAGTTCAGGAATATC	TTTTTTACTATACTTTTTGT
4	TCTGATACAAGTGATAAGAATACT	TTCCTTTTTAGGCTTACT
5	TCTATTTTTCTTCATAGTCCAC	ATTAGCTTCATTTGTCAG
6	TCTGAATGGGTGTTATTAACTC	AGTTTCTTCTTTAAAATCAT
7	TCTACAAATTCTTATTTTAGCAA	CTCTGAAGCTGTAAAACC
8	TCTGTATCAGTTCAGGCGT	TTTATCAATGTTTGAAACG
9	TCTGCTGCTCTAGGACAAC	TAGTAAATCAAGTTTTTGCA
10	TCTTTTGTTGTTGCCTTATT	ATCCCTTCTATTTTCGA
11	TCTCCACCTATGGAACGT	ATGTAGTGACGTTTCTGTG
11d	TCTCAGAAAGTCTATCGGG	ATGTAGTGACGTTTCTGTG
12	TCTAGTGAGAAGAAAGCAAAT	ATTGGGTGTAAGCATT
13	TCTTCTTGGAATTATTGGAG	CTTAACTCTACCCGTCC
14	TCTGCAATGATTGTAACCAT	TTTTCTCTTATTAAAGAATT
15	TCTGCATCTTATACCGTGAA	ATACCAGCCGTTACTATT
16	TCTGCCGAGAAGGATAAA	TTTAGCTGCTTTTTTAATG
17	TCTGTTTATAAAGTTATTCAAAA	AAATACTACATTTACAGGTG
18	TCTAAGCCTAACAGTCAACA	TTGGTTATTCTCCTTTAAT
19	TCTGATGATAACTTTGAAATGC	ATTATATTTTTGGATATTTC
20	TCTGCAGTGATTGCAAGTC	GGGCTTTTTCTTAAAAA
21	TGTGCTGCATCAAAC	GTTGGCATCCCTTTT
21 Long+A527	TGTGCTGCATCAAAC	CTTTTGATGGGATTGG

22	TGTACTAAACAAAGCCAG	TTGATTTAACGATTTGA
23	TGTCAATTAACCGATAC	TTTATCTCCTCTAAAATAATG
24	TGCTCAAATGATTCAT	CTTTGATAAGTCAGACCA
25	TCTAAAAGTTCACAAGTTACTACT	GTAACCCCAAGCTGAT
26	TCTAGTCATTATTCCATAAAATT	TGATTTTGCAATATCAA
28	TCTAATCATATGCTGATTGAG	TTTTTGTAATTTAAGTACTAA
29	TCAGTTTGGATGTTAAC	TTCTTTTATATTAAGAGCTT
30	TCAACAAATGCAGATG	ATTCGGATAAATGTAGC
31	TGTTTTGTCATTATTGATAG	TCCATTTTTATCCTCAC
31d	TCTCTAACTTGGTTTTTATTAGA	TCCATTTTTATCCTCAC
32	TCTGGTTTAAAAGTGACTGAA	ATGACCTCTACTTTCCA
33	TCTCATCATTTAGGTAAGGAA	CTTGTAATCACTTGGAC
34	TCTGTTAGTAATCGCTACAATC	ATTAATCATGGTATTGGT
35	TCTAATCAAGAAGTTTCAGC	CCATTGTGGAATATCA
36	TCTCGAGTTTTAGCGGATA	TTTGTAAAGCAGTTCTT
37	TCTGTATTATTTTACCAATCACA	ATCATTCATATGATCTCTAGA
38	TTAGGAGTGGTAGTTCAT	ATTTTGATTGATTCTACTC
39	TTTTTATTGTTAGTATTAGC	TTTTGTTTTTTTCAAATA
41	TCTGTTTATCTAGCGGTTAGA	ATCTTCAACGTCCTCC
42	TATAACAGTTTAGTTAGAAGTC	AAAGTCAAAGGAAACTT
43	TTTAAAGGGTTTACATATT	TTCTTTATCTAATTTATAATAG
44	TTTAATACAATTGGTCG	TTGCAATGTTTTTTCT
45	TCTATGGAAAAAATTAGGATT	TAAACTTTGGATAATCTGT
46	TCTAGAGATGAGCAAGAAATA	GTTGAAATTTTGATATGA
47	TCTCAACAGATAGGTCTTTATAA	CTCCTTTACTATATAGCTAACT
48	TTTCTCTATAATTACTTCAAT	TTGTTTGTGAAGTAAAAC
49	TCTAATAAGGCATTATTAGAGG	TGATAATATCTCCATATTTT
50	TCTACACATTTAGTTGACTTAAC	GCATTGGCGCCATA
51	TCTAGTAAACAACACATTTATCTA	TTCTACACGACTTTTATTC
52	TCTCAAGAAACTCATCAGTTG	AAGACCTCCTCGAGAT
53	TCTGCAGAAGACATTGTTACA	TGTTTTTTCTTTCTGTTG
54	TATAATTTTTCGACTAATGA	TGGATTAGTTTGACCTG
55	TCTGACACAGTGTCTTATCCT	TTTATCGTAAGCACTTAGG
56	TCTGTGGAGCAAGTGGCCA	CTCCTTCCAGGCATCG
57	TCTCAAGAACTAAGTAACTTTGA	GTAAAAGTATCTTAAATAGTCA
58	TCTACTGAAACGTTTGAAGG	TGCCATTCCTCCTCT
59	TCTGATGAAGCAACAACTAA	TGTTACCTTTTTATTTTCT
60	TCTAATAAAGATAATCAAAAAACT	TTTTTCATGCGATTGA
61	TGTTTCTTTTTTATTCCA	GAGACGTTTCTTATACCTT
62	TATTACTTTGATGGTAGTTT	TGTACCATATGTTCTCTCT
63	TCTGTTCAATCATTAGCAAA	AAAAGTTGGACTACTTTC
64	TTTAAAGGTAATAAGAAGTTG	TCGTTTTCCACCC
64d	TCTAGTCAAGTTGACTCTGTTA	TCGTTTTCCACCC
65	TCTCAAAACCAGGTGACTG	ATTTGGGTAAATATAGTAAA
66	TTAAGATTTTATAACAACGA	TTTACGACTAACCTCAAC
67	TCTAATGTTTTAGGGGAAA	AATTCCTTTTGGTGG
68	TCCCAAAAGACTTTTG	GGCAGAATACACCTTC
68d	TCCCAAAAGACTTTTG	GGCTGACGTCGACGCA
69	TCTAAAGTTTTAGCCTTTGA	AACTCTCTTAATATATTCTTCT
70	TCTGAAATGGCTTTAG	GTCTTTTTCAATATTCTGT
70d	TCTACTAACTTATTGAGTAGAATCA	GTCTTTTTCAATATTCTGT
71	TGTAGCTCAAAATCTCAT	CTTCTCCTTAGGAGTAACG
72	TCTAGTTTATCTATTAAAGATGCC	ATTATTATCAATTAATAACTCTT
73	TCTATCAAAGAGGCGGTAA	GTCAAACATACTTCCAAA
74	TCTAAAGAGGATAAAAAGCTAG	TTTCGTCGTATAAGCA
74d	TCTAGTGTTTCAGGTAGTAGTG	TTTCGTCGTATAAGCA
75	TCTAAAAAATTAAAACACTCAA	TGTCCTCATTTTTTCAG

76	TCTGATGAAGTTACAACTTCAG	AATACTTGCTGGAACAG
77	TTATTCCAAAGTAAAATAAA	GTCTTTCTTCAATTTTGG
78	TCTCATAACCATCACTCAGAACACATGT	GTCGTGATTTTTATGAGT
79	TCTCCCAAGAATAGGATAAA	CCCAAACTGGCATAAC
79d	TCTAGTCAGTATGAGTCACAGA	CCCAAACTGGCATAAC
80	TCTGCAGAAGTGTCACAAGA	TGAAGGACGTTTGTTG
81	TCTTTTGATGGATTTTT	TTTTTTTAGTTTAAGGCTA
82	TCTACAAATGAAAAACGAAC	GTCCACCTTCCGAT
83	TCTGAAATTAAACTCAAAAATATT	AACATTGTTTTTCCTTTC
84	TCTCATACTCAAGAACACAAAA	ATGGTGATGATGACCT
85	TCTCCTAAGAAGAAATCAGATAC	ATTAACATTTTGAGGGT
86	TCTGCAGAACTAACTCTTTTAA	TTTTGCAAAATCAACA
87	TCTGCGGATACATATAATAACTA	GAATAAATAACTGTATTTTTT
88	TCTTACCAAAAAATGACG	ATTTTCATTAATTTCCTCT
89	TCTGAAGAGCTTACCAAAAC	GATAGCTAATTGGTCTGT
90	TCTAGATATACAAATGGAAATTT	TAAAAGATGAGCTTCTCG
91	TCTAAAAAAGGACAAGTAAATG	AATTTCAATATAGCGACG
92	TCTGATTCTGTCATAAATAAGC	CTTGTTTGTCTTTACCTT
93	TCTGAATTTTCACGAGAAA	ATTATCCTTCAAAGCTG
94	TACCAATTAGGTAGCTATAA	TGTGTCATATAATGTAACCA
95	TCTGTTAATACAAAAACACTTCT	TGATCTTAATTTTCGAG
96	TCTGGTCAGTCTAAAAATGAAG	CCAAACAGGTTGATCT
97	TCTAGCCAGGAGGTATATG	ATTTACATCAGACTGTGAC
98	TCTGAAACTATTAATCCAGAAA	TTTATGGCCAATAACA
99	TCTACAAGTATGAACCATCAA	TTTTTTAGTAGTTGTCAATT
100	TCTAAGGGGCCAAAAGTAG	GTAAGCTGAATTTTCGA
101	TCTATTACTTTAGAAAAATTTATAGA	ACGAGAGTGGTTATTGG
102	TCTGCCTTTTACTTTGGCA	TTTCTTCACTCTTTCTAGAG
103	TCTATTTTTTCCTTGATCAT	CGGCCAGTTTTTTCTT
104	TCTGGTGAAACCCAAGATA	AACACCTGGTGGGCGT
105	TTAACAATTCATGGACC	ACTATTTCTAATTGCTCTG
105d	TTAACAATTCATGGACC	TGGTCCCGGTGCGCCA
105d	TCTCAAGGACCTCCCGGTG	ACTATTTCTAATTGCTCTG
106	TCTCAAAATCAAAATTCACA	CTTAGCAGATTCATCCC
107	TCTCTGGAGCCTTTTATTT	TTTACTATTTGAAAATTGG
108	TCTGGTAATCGTTCAGATAAG	TTTCATAGGAACTTGTATT
109	TCTATCCAGCAGATCAACT	GTCCACACCTGCGACT
109d	TCTAAACGGGTTCGCTATG	GTCCACACCTGCGACT
110	TCTGTAAAATTAGTATTCGCAC	TTTACCTAAGTAATATTCTGA
111.19	TCTGTTAGCGTTGATAAGGC	TCCCCGTCTTTTTTGT
112	TCTACAATTAAAAATCTCACTG	GTCGTAATCATAAAAGCC
113	TCTAGTAAAATCAAAATTGTAACG	TTCATAACGAACCATAAC
114	TCTAATCTTTTAATTATGGGTT	TTTGAGTTCTAGCAACG
115	TTTCAATACTATTTAAAAGG	TTTTTTATCTTCTTCTTGC
116	TCTACCGAGGAGCCATTAA	TTTTAAAACCTGGTAAAC
117	TCTGAACAATCACAAAAAACA	TCAGCTCGTACTGTTT
118	TCTATGGTGACGGTGCTGG	GTCCTCCTCAATTGGT
119	TCTAGTCAGCCGGTAGGGG	CTCTTTTATACGCGATG
120	TCTGGTGGAGCATTTGCTA	GTTATTTGCTCGTTGTT
121	TCTAATAAAGATAATCAAAAAACT	TTTCTCAAATGTTTTCAT
122	TCTGCTGCCACCAAGAAAG	TTTCAAATGATCTACAGC
123	TCTACAACAAATGTAATGGC	GGCTAGTGTCTGTCCG
124	TCAATGAATTTTTCATTT	ACCATCTATTTTTACCCC
125	TCTACAAAATATCAGCGAATG	AGAACCCGCACTCTCA
126	TCTACTAAGCAAGCAATGTC	GAACGCAACGGCTGCT
127	TCTACAAAAGAATATCAAAATTAT	TTTCATATCAAAAACTATCG
128	TCGACTAATTCGTTAAA	TTCTTTATCTCTTAATGCTT

129	TTTGAAATAGTATTGGAAA	CACAACAGTTATTTTTTCA
130	TCTATATTTTCTATTTTTTATTATGT	AGGCCCTTCTGAGTAG
130d	TCTAAAAAACAACTTCACAAC	AGGCCCTTCTGAGTAG
131	TCTAAAACAGATATTGAAATAGC	AAATAATCCAATGGCTG
132	TCTATTAAATATTATCATTTGCA	CTTTTCAAGCTTTTTCC
133	TCTGCTTTACGGAACCTTG	AAAATGATCAGTTTGAGG
134	TCTACTATTTCTCAACAACAATAC	TTTTTGGCTTAAGAAAG
135	TCTGAAAAAAAGAGTAGTTCAAC	CTTACGATACATTTTAAATTG
136	TCTAATCAATTATCAGAAATCA	TTCTTTTTTTACTTTAGCG
137	TCTCAAGAGTATAAAACAAAAGAG	CCATTGCAATCCAGCA
138	TCTGCTGTATTTACACTCGTC	ATGTTTATGGCTTGCT
139	TCTGGCGGCAAGATAAAAT	TTTTTGATAAATCCCC
140	TCTGATGGGTTAAAGAATAATG	ATATGTGTATTCATCCTTT
141	TCTGATGTTGTAATTAGTGGAG	TACTTCTATTTTTCCATCTG
142	TTCGAATTAAGAGAAAGA	GTAATGCAATAAATCAAAA
143	TCTAGCTTTTTAGTGATTTCA	GGATTTTAGTTTCGCA
144	TATACGCATAGTGGAAC	CCCATTGATTTCGTCG
145	TCTGTTATTATCAGGGGCG	TACCTCTTTCAATACCAC
146	TCTGTTAGTCGTTCTCCGA	ATTACCGTTAGGTACTGTA
147	TCTGAGGAGCAAGAATTAAA	GGTATGGTTAACAGAATC
148	TCTATTCTAACAAAAGCAAGT	ATATACCCTAGACTTTTTGA
149	TCTAGTGGGCGTTCATGGA	AGGAGTTTTATTGATGATAT
150	TCTGATACCCCTAATCAACTA	AAATGATTGTGGAAAAA
151	TGCAGGAGCTGTCCGC	ATCAAAGAAGTTGACATTG
151 Long	TCTGTCCGCATTGGTAAAG	ATCAAAGAAGTTGACATTG
152	TCTAACTGCTTAGAAAATGAA	GTTAGATAAATTAACCAGTG
153	TCTAACAACTCCAGCA	CCCTTTGCTTCGTTGT
154	TCTGGAAAGGTCAGTGCAG	TTCCACAAGTCCGATT
155	TCTATTTTATTTTCAGATGAAC	TTGTTTGATTCGTCCT
156	TCTGCATCAGATGTTCAGA	ACTACCAAACTGCTGG
157	TCTAGTGACGTTGACAAATA	TTGTGTATTTTTAGTTAGGT
158	TCTATGACCATTTACTTCAATA	GTGGATAAAATTCGAAA
159	TCTCAAACTATTTTGACGC	CAGACTGACTAGGAGCT
160	TCTGATGAATATCTACGTGTCG	GACTTGTAATTGATTCGC
161	TCTGATGAGGTGGACTATAACA	GAAGGCACCACCACCT
162	TCTATTTTCTTGCTCTTAGTTG	GTTGTATAGATGAGTTAATCTG
163	TCTGAAACTGTCATTCAACTTG	ACGGTTTTTAAAGAATG
164	TATTTTTTAACAACAAAAAA	TTTTTCTTTATCTTCTGTG
165	TCTCCAATTTTTATTGGTTT	CGATTTTGTAAGAGCTT
166	TCTGCATCTTATACCGTGAA	CGACGAAGCTATTTCT
167	TCTACAATTTATATTGCTTGG	TAAGGCTTGCATTTTG
168	TCTGTTGGATTGATGTTGG	TTTTCCTAAAAATTTTCC
169	TGGAAACAAATCACAG	GGCATCTCCTAGCTTT
170	TCTGCAATAGTTTTTACTTTTTT	TGATAAAGGTAGTTCTACAC
170d	TCTGGTTCTTATCATTTAACAA	TGATAAAGGTAGTTCTACAC
171	TCTGCTAGACCCAAACAGT	TTTTAGATGTTTTTGTGG
172	TACACTCATATTGTTGAAAA	ATGATTGATAATTTTAAGC
173	TCTAATAGTACTGAGACAAGTGC	TGCTTTTTGATATGCC
174	TCTGCTTATGTCGTCAATTT	TAAAATAAAGTTCAGAAAAG
175	TCTGAATTACCTTCGTTTATC	TTTCTCCCTTGACTTTC
176	TCTAAACATCCGATACTTAATG	CTTTTTCTCAGATGCTT
177	TCTAATTATCCTTTTGCGA	GACATTGAAACGGAAT
178	TCTGGACTACGCGGAGTAT	TTTTATCAATGATGTTGA
179	TCTGCTATTGGAGCAGCTG	CATATGACGCAAACGC
180	TCTGATAAAGAAGGGATAGAGG	AGCCTCTTTTCTTGTT
181	TCTAAAGAAAAATCACAAACTG	ACGATTATCAACAAAGTT
182	TCTCAAAATAATAAAAAAGTAAAA	CATTCTTTTAAATACAAATC

182d	TCTCAAAATAATAAAAAAGTAAAA	GGGTTTGAAAGTTTTC
183	TCAAATGGTCAATCTAGC	TTTAACTTTAATTACTGGAAT
184	TCTAAGGATTCAAAAATCCC	TTTTTTAATAAGCTTCGA
185	TCTGGGCAACCATCTACAT	TTTTTTGTAAACTTCCTG
186	TCTCATTCACAGGATAGCA	CTTAGATACATTGTTTTTTTC
187	TCTGGACGAGGAGAAGTATC	CTTTCTTTTCTTACTTGC
188	TCACAATCTTCTCAAAA	TTTATTATTTTTAATACTTGAA
189	TCTGATAAGTCAGCAAACCC	CTTCAACTGTTGATAGAGC
191	TCTATCACGACATTACAGACT	TCCTTTAGCAGGAGCT
192	TCTAGATATTTAACTGCTGGT	GTTATACATGTTGTCTGAAG
193	TCTATAAAATATCAAGATGATTTT	CCAAATAATAACACGTTT
194	TTAGAAGTCAGAGAGCAG	GCTATCCCTTTCCAAT
195	TCTATTATGGAGACGGGTA	TGTATTTTTAATTTGTTTTC
195L	TCTTTGAATAATAAAGGTGTCG	TGTATTTTTAATTTGTTTTC
195LN	TCTTTGAATAATAAAGGTGTCG	CAAACTTTTAACATTTAATG
196	TCTATTTCCTCAAATTTTTACG	ATAGTGTAAGCTACCAGC
197	TCTAATTTTTATAAGCTCTTG	GTCATCATATTCCTGAAA
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199	TTTTTAAAAGAAATTGAAA	ATTGGTCATTTCTTGAG
200	TTTCGTAAATATAATTTTGA	AACAGATTTATTGGTTGG
201	TCTAGCGATACCTTTAATTTT	AGACTCATCAACTTTTTCT
202	TCTATGCTGATTAAGTCGC	GAACCCTGAAGGGTAG
203	TGTGGTAAAACTGGACT	CCAATTGTATTTTTCAAC
204	TCTAAGACAGGAGCACCCGT	ATTTATACTACCTGTTGAATC
205	TGCGAGTCAATTGAGC	TTTAAATTTGTAGTCTTTAATA
206	TCTACAAATACTTTGAAAAAAGA	CTCTTTTACTTTTCCAAAA
207	TCTAATTTATTTAAACGTTCCT	CCCTCCCTTAAGAGAA
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213	TCTAAACACACCAGTAAAGAA	TTTTTCCTCTACTTTCTTA
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215	TTAATAAAAGGATTATTGTCA	CAATAACTTCTGTAAAATAAA
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217	TCTAACACTAACATCCCTAGC	TGCATTTTTCCCTTCT
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220d	TACTATGCGAATCACAG	TGCATATAAGTTTTTTAGC
221	TCTAGTTTAGCATTGCAAAT	CTCATCTAAAGTGCTATCC
222	TCTACATTTTATAAAAAGACGG	CTCGTATTTAGGCAACT
223	TCTAAGAAAATACGAAGCTATAC	ATTGGATATGCCATAAA
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225	TCTGGTATGTCTAATAAGGAAAT	TTCTTTACTATAAACATCTTCA
226	TCTAACAAACTTATTACAGAAAA	AGCATTTAAAGTTGAATGT
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229	TCTGAACGTCGGGTAAGTC	TACTTCTTTCTCTTTCAATT
230	TTTTTAATCGATTTTATTT	CTTAGTGTTCCGATATGA
231	TCATTAATTATTCTTACGGT	TCTTGTTTTAAGAGCAGA
231d	TCTTTATACGTTGTTAAACA	TCTTGTTTTAAGAGCAGA
232	TGGCTAAGTAAGCATGAG	ATCATGTTTTCCCTCAA
233	TTCCCAGCTAGCTGTC	ATCTGATATATCCGTTTTAT

234	TCTATAGAAATTGCTGTATTAATT	TTTTTTGTCTCCTTTTTTA
235	TCTATTCGATTTCTTATTCTTG	AAAGACACGATAAACATAAG
235d	TCTGACTCAACCACAGTCTC	AAAGACACGATAAACATAAG
236	TCTGCAGACCTTACAAGTCA	ATTTGCAACTTCTTGTATA
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239	TCTGTTAGTGCTGCTATTGAA	TTCTCCTCCCCCATTA
240	TCTAAGAAGCTTACTTTTATTTG	ATCCAAACGAGTGAAAT
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242	TCTCATAATATATTAAGATTTTTAGG	CTTTCTAAGTTTATTAAACATA
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244	TCTCATGAAAATGTTAAAAAAG	AAACAACTCCATTATTTTT
245	TCTAAGTCAACGGTAACAAA	TAAACGTTGAAGAGCAT
246	AGGAAACGTTTTTCCT	CTTATCATATCTTGTTAAATCA
246d	TCTAACCATAAGGGAAAAGTA	CTTATCATATCTTGTTAAATCA
247	TCTGCTAAACAATTAATTGGT	TTGCCATGGGTTATAG
248	TCTTTGATGGTGTTGTTATTC	AGAATTAAAATTTTCATGC
248d	TCTAAAACTTATTTGTCAAATG	AGAATTAAAATTTTCATGC
249	TGGGCTTACCATACTG	TTTTTTAGATGTTTTATGTG
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251	TCTCAATATTTTTTGAAACAAG	TTTCAAACTCCAGCCA
252	TTTATTTCAGGTTATATCAA	GGAGTGCCTTTCTACT
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254	TCTATTGAAAAGGGAGTTG	ATCGTCAACCTTAACG
255	TCTATTGTTGGTAGAGAAATCA	TTTTACTTGACGTCTCAC
256	TATCATGTAAAAATTGATCA	GTCTTCCATTAATATTCCC
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258	TCTGAACGTTATACAGATAAAATG	ATTTTTTTGAATAATATAATCC
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261	TCTATAAAGAAAGCTGAAAATC	CGAAACGTCAGGTAAA
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263	TCTCAGCCTTCTAAACTACTTC	ATCAGCATTTCTACGAA
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265	TCTCTTGCTTCCCTGATTT	TTTACTGTTCCTTTCGC
266	TCTCATCAATCAAATCATTATC	GAGATTAATTTGATTATATTTTT
267	TCTATCTTTATTATCGGACAA	AACATCATTTCCTCCC
268	TCTAAAGAATTTATTAAAGAATGG	GTTGATAGTTCCAAAACG
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270	TTAAATGATGCAATAACAA	CATCAATAGCCGAGCTG
271	TTGCTGGATTATCCTC	TTTATTTTCCAAATGACA
272	TCTGTATTTATGGCAAATAAGA	TTCACTCGGAGTTGGAG
272d	TCTATGAGTTCTCTGGAAGTT	TTCACTCGGAGTTGGAG
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274	TCTGTTCATGATTTTGGTGA	GTTTTTTAATGGTTTGC
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276	TCTCAATCAGACATTAAAGCA	CTGATCTCTTGTTGATGC
277	TCTATTTGGAGGGGGGAAA	AAGCAGGGGAGCAATA
277d	TCTACCAAATTTGACTGGG	AAGCAGGGGAGCAATA
278	TCTGTTACGTTTTTCTTAT	CTGAGCAACACCTGTC
279	TCTAAAAAGAAAAGTTTAATTAGC	GGCAATTTTGTGGCAA
280	TTTGATTTTTTTAAGAAAA	TTGCTTAGTTAATGGCT
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281d	TCTGGTTTTTCGTTTTTGA	AGGCGTTGAATATAATTC
282	TCTCTATTCTCAGATGAAACAA	CTTTTCAACTCCAAACA
283	TCTGTTAAATTAAAATCGTTACTG	GAGTTGTCTTTTTTTGTC
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285	TTAGGTGAAAGCAAATC	CTTTGTCTGCTTCACTT
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287d	TCTAACAATCGTTCAAAGC	TTGGTTAATCGTCTTG
288	TCTAAAAAGTTTTTAAAAGTTTT	TTTAGTTACTTTCATAAATGG
288d	TGGAATAATCATCAGTCA	TTTAGTTACTTTCATAAATGG
289	TCTCAATCTAAAGGGCAAA	ATATAATTCCTCTAAAACTAGC
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290	TATTACTTATCAAAAGAAAAGG	ATTCCTTGAACACGAA
291	TCTCAAGTATTAAATGACAATGG	GTGCCATTCATTCTCT
292	TTGAATCGTAAAAAAAGG	TTGTCCTGTGAACTGTG
293	TCTATGGGTCTAGCAACAA	AGGGTTTATTTGTTGAAG
293d N-term	TCTATGGGTCTAGCAACAA	TCCTGATTTATCCACTG
293d C-term	TCTGTTACAGCTAAACACGG	AGGGTTTATTTGTTGAAG
294	TCTGGTCATTTTAGTGAAAAA	CAAAATACCTAAGCTAGC
295	TCTAGCGACATAAAAATCAT	ACGAACTTCCATAACC
296	TCTAAAGGTATTATTTTAGCG	GGCTTCTCCAATCAAA
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299	TTTGAAATACTTAAACCTG	TTTCTCCGCCCAGTCA
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304	TCTAACGAAATCAAATGCCC	GTCTTTTAGAGCATCGA
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317	TCTAATAAGCCATATTCAATAG	ATCTTCTCCTAACTTACCC
317d N-term	TCTAATAAGCCATATTCAATAG	ACTAGCTAGATTCTTAACGC
317d C-term	TCTGACTTGAATGGCAATAT	ATCTTCTCCTAACTTACCC
318	TCTATTGATTTTATTATTTCTATTG	GCCTCTTTCTCCAAAT
319	TTAAAACATTTTGGTAGTAA	ATGTCCTGTTATATCTTCTT
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324	TCTGGAAGTAAATCAGCTTC	TTTTTTATAAGCATGTGTA
325	TCTGCTTGGCAACTTGTTC	ATGAGACATAAGGTCTTG
326	TCTGGCATCTCAGACTTACC	GTTGGAGCTCCTACTG
326L	TCTAAATTCAAATCTGGGG	GTTGGAGCTCCTACTG
326L N-term	TCTAAATTCAAATCTGGGG	CATTTCTTTGGTTAAAGC
327	TCTGGAGGGAAAATGAATC	TATCTCGAGTGCTATTTG
327d N-term	TCTGGAGGGAAAATGAATC	CTCTTCATCGACATAGTAA
327d C-term	TCTGGCAACTTCAAAGCAT	TATCTCGAGTGCTATTTG
328	TCTGACCAAGTCGGTGTCC	ATTTTACAGTAGTGGAGTTT
329	TCTAAATCAAAGACCTCTTCTA	TGTCCTCATTTTTTCA
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331	TCTACCAGAACAGTAGCAAT	CCCCCTGTTTTTAAAAT
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333	TCTATTGATATACAAAAAATAAAA	TTTAAAATAATGATACATCTC
333d	TCTGGATCATTGAGGGCAA	TTTAAAATAATGATACATCTC
334	TCTAATTTAGTAAAAGTGAATAGTG	TAACCCCGTCTCAACA
335	TCTGAAGAAGAAAAATATTTTGA	TATTTTCGTTTTCTCAAA
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338	TCTGCTATAATAGACAAAAAG	GAAATCATAGCTTCCC
339	TCGAAACCGATTAAGAT	ACCTTTTACTTTTGGTAGT
339d	TCTCAAGTCATGCGCTATG	ACCTTTTACTTTTGGTAGT
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352	TCTACTTTTTTTAAAAAGCTAAA	ATCTCCTATTGTAATTTTGA
352d	TCTGGTACAGATAGTAAATTTGG	ATCTCCTATTGTAATTTTGA
353	TCTACAATGTTAAAAATTGAAA	CACCTCTTTTGTCAGA
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359	TCAAGAAATAATTACGGT	ACGCAGTCCCATTTTC
360	TCTATAATGAAGGCGGTCT	CTGGCATGAGGTCTCA
361	TCTAGCGTATATGTTAGTGGA	CCTTTTTTCAATAATAGC
362	TCTACTAAACCACAGGGGG	ATCTTTAATCTTACCATCC
362d N-term	TCTACTAAACCACAGGGGG	TGCTGCTACTGCAATG
362 C-term	TCTGGTAATGAAGGAAATATCAC	ATCTTTAATCTTACCATCC
363	TCTCTCGAATTAAAAAATATTG	TAAATTCCTTTGTTGTAATA
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424	TCTATGAAAGATTTTATTGAATG	GCCATTCTTACCTCCT
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653	TCTAAAATTTTAGGTACACCA	AAAGAAAAGATGTGCC
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661	TGTCAGTCAAACCACA	ATCATACGAATGCAAC
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663	TGTGGAAGTAAATCAGC	ATTATTTTTATAAGCATGTG
664	TCTGTTAAATTAAAATCGTTACTG	GAGTTGTCTTTTTTTGTC
665	TCTATTGCTGGTCCTAGTG	GATAAGCACTTTCCTTAA
666	TTATTTTTTGGAAATTGG	GCCTAAAAACCAATCA
667	TCTGCTGTATTTACACTCGTC	ATGTTTATGGCTTGCT
668	TTTTATATGAAAGAACAACA	TTGTATCTTCTCCTGACC
669	TCAATTATTATTGGGTTAA	ATATACCCTAGACTTTTTGA
670	TCTCCTAAATTAACCCTAGTCT	GGCTTTAAAGTTCGATA
671	TCTAGTCTTGCGAAGGCAG	TTTATCGTAAGCACTTAGG
672	TCTGTATTTACACTCGTCTTACA	ATGTTTATGGCTTGCTT
673	TCTGGAGGATTTTATATGAAAG	TTGTATCTTCTCCTGACC
674	TCTGTTAAATTAAAATCGTTACTG	GAGTTGTCTTTTTTTGTCT
675	TCTGGTTCATCAGACAAACA	TTCAACTTGATTGCCA
676	TCTGTAGTTAAAGTTGGTATTAACG	TTTTGCAATTTTTGC
677	TCTGTATTAGAAGTACATGCTGA	TTTTAATGCTGTTTGAA
678	TCTGAGACACCAGTAATGGC	TTTTTTAGCTAAGGCTG
679	TCTGCTAACAAGCAGGATC	TTTTGCTAAACCTTCTG
680	TCTAATAAGTCCAGTAACTCTAAG	ATTCATATTAACACGATGC
681	TCTGCTTTTGATGTAATTATGC	TTTGCGTTTTGGAGGG
682	TCTATTAACTATGAGGTTAAAGC	TGCACCTTGATGGCGA
683	TCTGTAATTGTTGAACTTAGTTTG	CCATAATATTTGATGCTG
684	TCTCTTAGGAAGTATAAGCAAA	TTCTAATCCTACAGCATG
685	TCTAAAATTTGTCTGGTTGG	AAAAATTCCTCCTAAATTAA
686	TCTGACTTTTATGATATCAATCTT	AAAGTTTTGACTATTACTGATAG
687	TATGCTATTATGCAAAAAG	TGGGGGAGATAGTTATG
688	TCTGCAATCGTTTCAGCAG	TTGACAGAAAGCTAATTG

TABLE III – RESULTS FOR *in vivo* GBS CHALLENGE

GBS #	% survival	
	Pre-immune	Post-immune
1	18.7	22.2
4gst	19.4	37.2
4his	25.0	75.0
8	14.3	42.1
10	29.1	36.0
15	30.0	60.9

GBS #	% survival	
	Pre-immune	Post-immune
110	11.1	30.0
113	17.6	29.4
114	40.0	52.2
117	27.8	36.8
119	36.4	52.2
139	23.1	26.7

16	33.3	53.8
18	29.4	50.0
21	5.9	10.0
22	36.8	63.1
24	38.5	41.4
25	28.6	85.7
32	20.0	25.0
35	0.0	17.6
45	26.7	37.5
48	20.0	25.0
52	14.2	17.3
53	23.8	29.2
54	22.7	44.0
55	50.0	52.9
57	33.3	55.6
58	6.7	11.8
62	15.8	36.4
63	21.4	42.9
65	3.7	23.3
67	23.5	27.8
71	13.3	26.7
73	28.6	39.1
80	38.8	56.5
84	33.3	37.5
85	30.8	62.5
90	14.3	22.7
94	25.0	30.0
95	16.7	23.1
98	5.9	11.1
100	26.9	42.9
103	16.7	52.9
106	10.0	18.2

150	21.6	44.4
153	25.0	30.0
155	22.6	36.8
157	14.3	31.8
158	22.6	40.0
163	29.6	37.9
164	25.0	43.8
173	17.9	38.7
176	20.0	38.9
177	21.7	33.3
181	5.0	21.7
186	41.2	52.6
188	11.8	23.5
189	21.4	31.6
195	32.1	64.7
206	33.3	50.0
211	30.8	33.3
232	50.0	57.1
233	34.8	55.2
236	57.1	70.6
243	46.7	52.9
263	15.4	35.7
273	61.5	75.0
276	23.8	44.4
296	25.0	28.6
297	13.3	23.5
298	20.0	22.2
302	30.0	52.2
304	33.3	40.9
305	42.1	70.0
316	38.5	42.9
318	7.1	15.8

TABLE IV – COMPARISON OF GBS*nnn* NUMBERING AND SEQ ID NUMBER

GBS numbering	Sequence listing
GBS1	SEQ ID 3532 & 8736
GBS2	SEQ ID 4530 & 8818
GBS3	SEQ ID 6266 & 8958
GBS4	SEQ ID 2 & 8786
GBS5	SEQ ID 2598 & 8674
GBS6	SEQ ID 398 & 8496
GBS7	SEQ ID 8790 & 9798
GBS8	SEQ ID 8694
GBS9	SEQ ID 4540 & 8822
GBS10	SEQ ID 8718
GBS11	SEQ ID 5884 & 8930
GBS12	SEQ ID 8764 & 9692
GBS13	SEQ ID 8484
GBS14	SEQ ID 5406 & 8892
GBS15	SEQ ID 4 & 8710
GBS16	SEQ ID 944 & 8538
GBS17	SEQ ID 1770 & 8602
GBS18	SEQ ID 6860 & 9002
GBS19	SEQ ID 4422 & 8812
GBS20	SEQ ID 308 & 8488
GBS21	SEQ ID 8762

GBS numbering	Sequence listing
GBS345	SEQ ID 2442
GBS346	SEQ ID 2768
GBS347	SEQ ID 2766
GBS348	SEQ ID 8658
GBS349	SEQ ID 2360
GBS350	SEQ ID 8698
GBS351	SEQ ID 2970
GBS352	SEQ ID 8692
GBS353	SEQ ID 3454
GBS354	SEQ ID 8754
GBS355	SEQ ID 8752
GBS356	SEQ ID 8724
GBS357	SEQ ID 8720
GBS358	SEQ ID 3184
GBS359	SEQ ID 3948
GBS360	SEQ ID 3926
GBS361	SEQ ID 8770
GBS362	SEQ ID 8768
GBS363	SEQ ID 3816
GBS364	SEQ ID 1452
GBS365	SEQ ID 1398

GBS22	SEQ ID 8584
GBS23	SEQ ID 8512
GBS24	SEQ ID 1694 & 8598
GBS25	SEQ ID 3180 & 8714
GBS26	SEQ ID 8820
GBS27	SEQ ID 8774
GBS28	SEQ ID 8738
GBS29	SEQ ID 8744
GBS30	SEQ ID 8860
GBS31	SEQ ID 8702
GBS32	SEQ ID 8910 & 10142
GBS33	SEQ ID 5734 & 8912
GBS34	SEQ ID 5750 & 8916
GBS35	SEQ ID 8908
GBS36	SEQ ID 8542
GBS37	SEQ ID 8564
GBS38	SEQ ID 2122 & 8642
GBS39	SEQ ID 8480
GBS40	SEQ ID 8654
GBS41	SEQ ID 1176 & 8562
GBS42	SEQ ID 4856 & 8850
GBS43	SEQ ID 672 & 8520
GBS44	SEQ ID 9000
GBS45	SEQ ID 9018
GBS46	SEQ ID 1834 & 8608
GBS47	SEQ ID 8588
GBS48	SEQ ID 8594 & 8596
GBS49	SEQ ID 8494 & 9490
GBS50	SEQ ID 1236 & 8566
GBS51	SEQ ID 5410
GBS52	SEQ ID 3920
GBS53	SEQ ID 8586
GBS54	SEQ ID 3442
GBS55	SEQ ID 9020 & 10338
GBS56	SEQ ID 2510 & 8668
GBS57	SEQ ID 8854
GBS58	SEQ ID 8664
GBS59	SEQ ID 3744
GBS60	SEQ ID 8760
GBS61	SEQ ID 8776
GBS62	SEQ ID 2244
GBS63	SEQ ID 390
GBS64	SEQ ID 374
GBS65	SEQ ID 8544
GBS66	SEQ ID 3028
GBS67	SEQ ID 3746
GBS68	SEQ ID 4012
GBS69	SEQ ID 4916
GBS70	SEQ ID 3718
GBS71	SEQ ID 8906
GBS72	SEQ ID 1348
GBS73	SEQ ID 220
GBS74	SEQ ID 5872
GBS75	SEQ ID 8926
GBS76	SEQ ID 5862
GBS77	SEQ ID 3256
GBS78	SEQ ID 3262
GBS79	SEQ ID 3264
GBS80	SEQ ID 8780

GBS366	SEQ ID 8574
GBS367	SEQ ID 1340
GBS368	SEQ ID 1598
GBS369	SEQ ID 4822
GBS370	SEQ ID 8844
GBS371	SEQ ID 4926
GBS372	SEQ ID 4956
GBS373	SEQ ID 5062
GBS374	SEQ ID 8878
GBS375	SEQ ID 326
GBS376	SEQ ID 5380
GBS377	SEQ ID 5468
GBS378	SEQ ID 5570
GBS379	SEQ ID 8918
GBS380	SEQ ID 156
GBS381	SEQ ID 8934
GBS382	SEQ ID 8610
GBS383	SEQ ID 4738
GBS384	SEQ ID 8836
GBS385	SEQ ID 1094
GBS386	SEQ ID 9038
GBS387	SEQ ID 8558
GBS388	SEQ ID 9040
GBS389	SEQ ID 8516
GBS390	SEQ ID 8952
GBS391	SEQ ID 8522
GBS392	SEQ ID 6220
GBS393	SEQ ID 8966
GBS394	SEQ ID 8960
GBS395	SEQ ID 6276
GBS396	SEQ ID 8468
GBS397	SEQ ID 6262
GBS398	SEQ ID 8806
GBS399	SEQ ID 1960
GBS400	SEQ ID 3154
GBS401	SEQ ID 3170
GBS402	SEQ ID 4236
GBS403	SEQ ID 8798
GBS404	SEQ ID 8800
GBS405	SEQ ID 8508
GBS406	SEQ ID 8506
GBS407	SEQ ID 6484
GBS408	SEQ ID 9042
GBS409	SEQ ID 6678
GBS410	SEQ ID 4064
GBS411	SEQ ID 9044
GBS412	SEQ ID 9046
GBS413	SEQ ID 272
GBS414	SEQ ID 8946
GBS415	SEQ ID 8944
GBS416	SEQ ID 6044
GBS417	SEQ ID 1874
GBS418	SEQ ID 5146
GBS419	SEQ ID 2638
GBS420	SEQ ID 2104
GBS421	SEQ ID 2108
GBS422	SEQ ID 714
GBS423	SEQ ID 6884
GBS424	SEQ ID 4874

GBS81	SEQ ID 2706
GBS82	SEQ ID 2898
GBS83	SEQ ID 8772
GBS84	SEQ ID 4182
GBS85	SEQ ID 216
GBS86	SEQ ID 2978
GBS87	SEQ ID 3452
GBS88	SEQ ID 5694
GBS89	SEQ ID 2682
GBS90	SEQ ID 8476
GBS91	SEQ ID 8938
GBS92	SEQ ID 8964 & 10238
GBS93	SEQ ID 2848
GBS94	SEQ ID 1592
GBS95	SEQ ID 2224
GBS96	SEQ ID 2130
GBS97	SEQ ID 800
GBS98	SEQ ID 8746
GBS99	SEQ ID 4240
GBS100	SEQ ID 8782
GBS101	SEQ ID 6902
GBS102	SEQ ID 6894
GBS103	SEQ ID 6
GBS104	SEQ ID 8778
GBS105	SEQ ID 1400
GBS106	SEQ ID 8502
GBS107	SEQ ID 6026
GBS108	SEQ ID 8532
GBS109	SEQ ID 4116
GBS110	SEQ ID 6832
GBS111	SEQ ID 8842
GBS112	SEQ ID 8904
GBS113	SEQ ID 300
GBS114	SEQ ID 8968
GBS115	SEQ ID 5164
GBS116	SEQ ID 5152
GBS117	SEQ ID 8962
GBS118	SEQ ID 2508
GBS119	SEQ ID 8814
GBS120	SEQ ID 8874
GBS121	SEQ ID 3826
GBS122	SEQ ID 9006
GBS123	SEQ ID 6310
GBS124	SEQ ID 260
GBS125	SEQ ID 3872
GBS126	SEQ ID 6736
GBS127	SEQ ID 8816
GBS128	SEQ ID 752
GBS129	SEQ ID 8990
GBS130	SEQ ID 9004
GBS131	SEQ ID 6198
GBS132	SEQ ID 8730
GBS133	SEQ ID 474
GBS134	SEQ ID 9008
GBS135	SEQ ID 8882
GBS136	SEQ ID 1188
GBS137	SEQ ID 3960
GBS138	SEQ ID 9052
GBS139	SEQ ID 884

GBS425	SEQ ID 3978
GBS426	SEQ ID 3976
GBS427	SEQ ID 6958
GBS428	SEQ ID 3398
GBS429	SEQ ID 3402
GBS430	SEQ ID 8840
GBS431	SEQ ID 8902
GBS432	SEQ ID 8534
GBS433	SEQ ID 2558
GBS434	SEQ ID 8590
GBS435	SEQ ID 484
GBS436	SEQ ID 8472
GBS437	SEQ ID 466
GBS438	SEQ ID 362
GBS439	SEQ ID 900
GBS440	SEQ ID 8536
GBS441	SEQ ID 936
GBS442	SEQ ID 940
GBS443	SEQ ID 998
GBS444	SEQ ID 1776
GBS445	SEQ ID 8634
GBS446	SEQ ID 2048
GBS447	SEQ ID 1654
GBS448	SEQ ID 8592
GBS449	SEQ ID 1634
GBS450	SEQ ID 1630
GBS451	SEQ ID 2098
GBS452	SEQ ID 2062
GBS453	SEQ ID 8636
GBS454	SEQ ID 1734
GBS455	SEQ ID 1690
GBS456	SEQ ID 1684
GBS457	SEQ ID 8656
GBS458	SEQ ID 8650
GBS459	SEQ ID 2152
GBS460	SEQ ID 2148
GBS461	SEQ ID 2394
GBS462	SEQ ID 2778
GBS463	SEQ ID 8688
GBS464	SEQ ID 8684
GBS465	SEQ ID 8682
GBS466	SEQ ID 2694
GBS467	SEQ ID 2350
GBS468	SEQ ID 8660
GBS469	SEQ ID 2998
GBS470	SEQ ID 2988
GBS471	SEQ ID 2924
GBS472	SEQ ID 2910
GBS473	SEQ ID 2882
GBS474	SEQ ID 2878
GBS475	SEQ ID 2856
GBS476	SEQ ID 8690
GBS477	SEQ ID 3112
GBS478	SEQ ID 3432
GBS479	SEQ ID 3460
GBS480	SEQ ID 3504
GBS481	SEQ ID 8734
GBS482	SEQ ID 8740
GBS483	SEQ ID 3606

GBS140	SEQ ID 8632
GBS141	SEQ ID 1768
GBS142	SEQ ID 8600
GBS143	SEQ ID 9054
GBS144	SEQ ID 2238
GBS145	SEQ ID 8700
GBS146	SEQ ID 8696
GBS147	SEQ ID 8526
GBS148	SEQ ID 9010
GBS149	SEQ ID 8732
GBS150	SEQ ID 3736
GBS151	SEQ ID 3188
GBS152	SEQ ID 3952
GBS153	SEQ ID 3904
GBS154	SEQ ID 4024
GBS155	SEQ ID 8796
GBS156	SEQ ID 4646
GBS157	SEQ ID 4812
GBS158	SEQ ID 5504
GBS159	SEQ ID 8628
GBS160	SEQ ID 8924
GBS161	SEQ ID 8922
GBS162	SEQ ID 168
GBS163	SEQ ID 224
GBS164	SEQ ID 1102
GBS165	SEQ ID 3672
GBS166	SEQ ID 8712
GBS167	SEQ ID 4214
GBS168	SEQ ID 9016
GBS169	SEQ ID 4346
GBS170	SEQ ID 8982
GBS171	SEQ ID 6720
GBS172	SEQ ID 6704
GBS173	SEQ ID 8788
GBS174	SEQ ID 6150
GBS175	SEQ ID 62
GBS176	SEQ ID 8478
GBS177	SEQ ID 8876
GBS178	SEQ ID 6078
GBS179	SEQ ID 8848
GBS180	SEQ ID 3062
GBS181	SEQ ID 1924
GBS182	SEQ ID 3774
GBS183	SEQ ID 4796
GBS184	SEQ ID 1978
GBS185	SEQ ID 1046
GBS186	SEQ ID 8470
GBS187	SEQ ID 844
GBS188	SEQ ID 3410
GBS189	SEQ ID 6986
GBS190	SEQ ID 8842
GBS191	SEQ ID 1814
GBS192	SEQ ID 8618
GBS193	SEQ ID 2382
GBS194	SEQ ID 3912
GBS195	SEQ ID 8
GBS196	SEQ ID 4944
GBS197	SEQ ID 5486
GBS198	SEQ ID 8896

GBS484	SEQ ID 3562
GBS485	SEQ ID 3552
GBS486	SEQ ID 3762
GBS487	SEQ ID 3756
GBS488	SEQ ID 3732
GBS489	SEQ ID 3730
GBS490	SEQ ID 3704
GBS491	SEQ ID 3698
GBS492	SEQ ID 3252
GBS493	SEQ ID 3244
GBS494	SEQ ID 3238
GBS495	SEQ ID 8722
GBS496	SEQ ID 8716
GBS497	SEQ ID 3876
GBS498	SEQ ID 3858
GBS499	SEQ ID 8758
GBS500	SEQ ID 4022
GBS501	SEQ ID 4106
GBS502	SEQ ID 1406
GBS503	SEQ ID 8580
GBS504	SEQ ID 4578
GBS505	SEQ ID 4566
GBS506	SEQ ID 8832
GBS507	SEQ ID 8830
GBS508	SEQ ID 4644
GBS509	SEQ ID 8828
GBS510	SEQ ID 8826
GBS511	SEQ ID 4892
GBS512	SEQ ID 4970
GBS513	SEQ ID 4974
GBS514	SEQ ID 8862
GBS515	SEQ ID 8864
GBS516	SEQ ID 8866
GBS517	SEQ ID 8868
GBS518	SEQ ID 9012
GBS519	SEQ ID 5068
GBS520	SEQ ID 8870
GBS521	SEQ ID 5228
GBS522	SEQ ID 322
GBS523	SEQ ID 8492
GBS524	SEQ ID 8894
GBS525	SEQ ID 5430
GBS526	SEQ ID 5414
GBS527	SEQ ID 5524
GBS528	SEQ ID 8898
GBS529	SEQ ID 5670
GBS530	SEQ ID 5630
GBS531	SEQ ID 5588
GBS532	SEQ ID 1324
GBS533	SEQ ID 8914
GBS534	SEQ ID 8550
GBS535	SEQ ID 8568
GBS536	SEQ ID 1288
GBS537	SEQ ID 5798
GBS538	SEQ ID 8920
GBS539	SEQ ID 158
GBS540	SEQ ID 8482
GBS541	SEQ ID 184
GBS542	SEQ ID 9048

GBS199	SEQ ID 1162
GBS200	SEQ ID 8936
GBS201	SEQ ID 4550
GBS202	SEQ ID 8666
GBS203	SEQ ID 6478
GBS204	SEQ ID 1996
GBS205	SEQ ID 18
GBS206	SEQ ID 8552
GBS207	SEQ ID 3822
GBS208	SEQ ID 3916
GBS209	SEQ ID 3918
GBS210	SEQ ID 3738
GBS211	SEQ ID 4680
GBS212	SEQ ID 8750
GBS213	SEQ ID 8500
GBS214	SEQ ID 8498
GBS215	SEQ ID 9022
GBS216	SEQ ID 8606
GBS217	SEQ ID 9024
GBS218	SEQ ID 8652
GBS219	SEQ ID 8646
GBS220	SEQ ID 2730
GBS221	SEQ ID 9028
GBS222	SEQ ID 3842
GBS223	SEQ ID 8794
GBS224	SEQ ID 9026
GBS225	SEQ ID 8834
GBS226	SEQ ID 4966
GBS227	SEQ ID 5030
GBS228	SEQ ID 5050
GBS229	SEQ ID 9056
GBS230	SEQ ID 1296
GBS231	SEQ ID 5810
GBS232	SEQ ID 5830
GBS233	SEQ ID 4722
GBS234	SEQ ID 1106
GBS235	SEQ ID 8560
GBS236	SEQ ID 6162
GBS237	SEQ ID 8706
GBS238	SEQ ID 4246
GBS239	SEQ ID 8980
GBS240	SEQ ID 8986
GBS241	SEQ ID 9030
GBS242	SEQ ID 9032
GBS243	SEQ ID 8678
GBS244	SEQ ID 6554
GBS245	SEQ ID 8994
GBS246	SEQ ID 6864
GBS247	SEQ ID 8856
GBS248	SEQ ID 454
GBS249	SEQ ID 8620
GBS250	SEQ ID 8634
GBS251	SEQ ID 2258
GBS252	SEQ ID 8648
GBS253	SEQ ID 2526
GBS254	SEQ ID 2710
GBS255	SEQ ID 2966
GBS256	SEQ ID 3424
GBS257	SEQ ID 3550

GBS543	SEQ ID 8932
GBS544	SEQ ID 5880
GBS545	SEQ ID 44
GBS546	SEQ ID 9014
GBS547	SEQ ID 12
GBS548	SEQ ID 8614
GBS549	SEQ ID 8612
GBS550	SEQ ID 4720
GBS551	SEQ ID 4710
GBS552	SEQ ID 1086
GBS553	SEQ ID 1088
GBS554	SEQ ID 1138
GBS555	SEQ ID 8748
GBS556	SEQ ID 5968
GBS557	SEQ ID 774
GBS558	SEQ ID 1192
GBS559	SEQ ID 1196
GBS560	SEQ ID 1268
GBS561	SEQ ID 8518
GBS562	SEQ ID 8676
GBS563	SEQ ID 2296
GBS564	SEQ ID 2300
GBS565	SEQ ID 8950
GBS566	SEQ ID 694
GBS567	SEQ ID 680
GBS568	SEQ ID 6300
GBS569	SEQ ID 8956
GBS570	SEQ ID 8972
GBS571	SEQ ID 8970
GBS572	SEQ ID 3300
GBS573	SEQ ID 3304
GBS574	SEQ ID 8726
GBS575	SEQ ID 8810
GBS576	SEQ ID 4418
GBS577	SEQ ID 8808
GBS578	SEQ ID 4382
GBS579	SEQ ID 4378
GBS580	SEQ ID 1932
GBS581	SEQ ID 8622
GBS582	SEQ ID 8624
GBS583	SEQ ID 1962
GBS584	SEQ ID 8708
GBS585	SEQ ID 8672
GBS586	SEQ ID 6444
GBS587	SEQ ID 8976
GBS588	SEQ ID 8804
GBS589	SEQ ID 8514
GBS590	SEQ ID 8510
GBS591	SEQ ID 630
GBS592	SEQ ID 8504
GBS593	SEQ ID 514
GBS594	SEQ ID 8978
GBS595	SEQ ID 6738
GBS596	SEQ ID 6712
GBS597	SEQ ID 6686
GBS598	SEQ ID 6674
GBS599	SEQ ID 6662
GBS600	SEQ ID 8988
GBS601	SEQ ID 8578

GBS258	SEQ ID 3752
GBS259	SEQ ID 8756
GBS260	SEQ ID 4162
GBS261	SEQ ID 1530
GBS262	SEQ ID 8572
GBS263	SEQ ID 1616
GBS264	SEQ ID 8824
GBS265	SEQ ID 4554
GBS266	SEQ ID 4652
GBS267	SEQ ID 4980
GBS268	SEQ ID 5038
GBS269	SEQ ID 5534
GBS270	SEQ ID 1998
GBS271	SEQ ID 8570
GBS272	SEQ ID 22
GBS273	SEQ ID 5994
GBS274	SEQ ID 774
GBS275	SEQ ID 2308
GBS276	SEQ ID 8942
GBS277	SEQ ID 8954
GBS278	SEQ ID 8524
GBS279	SEQ ID 6292
GBS280	SEQ ID 6254
GBS281	SEQ ID 4458
GBS282	SEQ ID 4444
GBS283	SEQ ID 9034
GBS284	SEQ ID 6456 & 8974
GBS285	SEQ ID 8802
GBS286	SEQ ID 9036
GBS287	SEQ ID 5354
GBS288	SEQ ID 5374
GBS289	SEQ ID 8616
GBS290	SEQ ID 8680
GBS291	SEQ ID 8530
GBS292	SEQ ID 8998
GBS293	SEQ ID 8582
GBS294	SEQ ID 8604
GBS295	SEQ ID 2722
GBS296	SEQ ID 2658
GBS297	SEQ ID 3024
GBS298	SEQ ID 8704
GBS299	SEQ ID 3268
GBS300	SEQ ID 4170
GBS301	SEQ ID 8576
GBS302	SEQ ID 8670
GBS303	SEQ ID 8554
GBS304	SEQ ID 5846
GBS305	SEQ ID 208
GBS306	SEQ ID 212
GBS307	SEQ ID 8992
GBS308	SEQ ID 8880
GBS309	SEQ ID 3386
GBS310	SEQ ID 286
GBS311	SEQ ID 3964
GBS312	SEQ ID 4660
GBS313	SEQ ID 4090
GBS314	SEQ ID 8556
GBS315	SEQ ID 1766
GBS316	SEQ ID 2000

GBS602	SEQ ID 8948
GBS603	SEQ ID 6132
GBS604	SEQ ID 5282
GBS605	SEQ ID 5302
GBS606	SEQ ID 8884
GBS607	SEQ ID 5314
GBS608	SEQ ID 8886
GBS609	SEQ ID 8888
GBS610	SEQ ID 8890
GBS611	SEQ ID 6028
GBS612	SEQ ID 8474
GBS613	SEQ ID 5092
GBS614	SEQ ID 8872
GBS615	SEQ ID 6052
GBS616	SEQ ID 8940
GBS617	SEQ ID 1824
GBS618	SEQ ID 6600
GBS619	SEQ ID 6608
GBS620	SEQ ID 6620
GBS621	SEQ ID 864
GBS622	SEQ ID 8640
GBS623	SEQ ID 8996
GBS624	SEQ ID 9050
GBS625	SEQ ID 2812
GBS626	SEQ ID 8858
GBS627	SEQ ID 8852
GBS628	SEQ ID 8784
GBS629	SEQ ID 6950
GBS630	SEQ ID 4502
GBS631	SEQ ID 4492
GBS632	SEQ ID 4488
GBS633	SEQ ID 8728
GBS634	SEQ ID 3066
GBS635	SEQ ID 8838
GBS636	SEQ ID 4772
GBS637	SEQ ID 8626
GBS638	SEQ ID 8984
GBS639	SEQ ID 8546
GBS640	SEQ ID 6780
GBS641	SEQ ID 900
GBS642	1312
GBS643	1772
GBS644	1956
GBS645	2726
GBS646	3348
GBS647	3770
GBS648	4934
GBS649	5076
GBS650	5446
GBS651	5602
GBS652	5610
GBS653	5760
GBS654	6096
GBS655	6656
GBS656	9324
GBS657	10782
GBS658	8802
GBS659	9344
GBS660	9410

GBS317	SEQ ID 4210
GBS318	SEQ ID 8548
GBS319	SEQ ID 892
GBS320	SEQ ID 916
GBS321	SEQ ID 8846
GBS322	SEQ ID 8540
GBS323	SEQ ID 2102
GBS324	SEQ ID 8490
GBS325	SEQ ID 8900
GBS326	SEQ ID 8630
GBS327	SEQ ID 5856
GBS328	SEQ ID 6016
GBS329	SEQ ID 8928
GBS330	SEQ ID 8792
GBS331	SEQ ID 922
GBS332	SEQ ID 1004
GBS333	SEQ ID 1786
GBS334	SEQ ID 1784
GBS335	SEQ ID 1782
GBS336	SEQ ID 1886
GBS337	SEQ ID 2010
GBS338	SEQ ID 8638
GBS339	SEQ ID 2080
GBS340	SEQ ID 8594 & 8596
GBS341	SEQ ID 2280
GBS342	SEQ ID 2266
GBS343	SEQ ID 8644
GBS344	SEQ ID 8662

GBS661	9428
GBS662	9286
GBS663	9294
GBS664	9034
GBS665	10546
GBS666	10610
GBS667	9052
GBS668	9036
GBS669	9010
GBS670	10730
GBS671	9020
GBS672	9052
GBS673	9036
GBS674	9034
GBS675	10634
GBS676	10692
GBS677	10746
GBS678	9330
GBS679	9404
GBS680	6668
GBS681	4264
GBS682	6762
GBS683	9290
GBS684	9614
GBS685	10454
GBS686	2774
GBS687	4620
GBS688	10224

TABLE V – NUCLEOTIDES DELETED IN EXPRESSION OF GBS*nnn* PROTEINS

GBS	Deleted nucleotides
11d	1-153
31d	1-129
64d	1-165
68d	2029-2796
70d	1-402
74d	1-975
79d	1-201
105dN	2689-4119
105dC	1-2688
105d	1-2688
109d	1-120
130d	1-518
170d	1-111
182d	1596-1674
195C	1-1710
195N	1711-3243
209d	757-912
210d	1-99 & 777-879
220d	1-120
231d	1-54
235d	1-270
246d	1-75
248d	1-591

GBS	Deleted nucleotides
272d	1-531
277d	1-318
281d	1-54
287d	1-108
288d	1-72
293C	1-1229
293N	1230-2379
317N	1729-4107
317C	1-2379
326N	1707-2652
326dN	2326-3927
327N	3034-6831
327C	1-3033
333d	1-150
339d	1-111
352d	1-158
362N	1707-2652
362C	1-1706
397d	1-348
399d	1-111
407d	1174-1473
409d	1-297
424d	1327-1671

TABLE VI – PREDICTED FUNCTIONS FOR CERTAIN SEQ IDs

SEQ ID	Function
6	manganese ABC transporter, ATP-binding protein (psaB)
12	iron (chelated) ABC transporter, permease protein (psaC)
18	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
26	chorismate binding enzyme (pabB)
30	probable transposase (insertion sequence IS861)
42	peptidase, M20/M25/M40 family
44	drug transporter
50	ribosomal protein L11 (rplK)
54	ribosomal protein L1 (rplA)
62	peptide ABC transporter, permease protein
66	peptide ABC transporter, permease protein
78	uridylate kinase (pyrH)
84	ribosome recycling factor (frr)
104	PhoH family protein (phoH)
110	MutT/nudix family protein superfamily
116	tetracenomycin polyketide synthesis O-methyltransferase TcmP
134	phosphopantetheine adenylyltransferase (coaD)
140	PDZ domain protein
144	5-nucleotidase family protein
156	VanZF-related protein
158	ABC transporter, ATP-binding/permease protein
162	ABC transporter, ATP-binding/permease protein
168	BioY family protein
180	acetyl-CoA acetyltransferase
188	endonuclease III (nth)
196	glucokinase (gki)
200	rhodanese family protein
204	elongation factor Tu family protein (typA)
212	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-
216	cell division protein DivIB
220	cell division protein FtsA (ftsA)
224	cell division protein FtsZ (ftsZ)
236	ylmH protein (ylmH)
240	cell division protein DivIVA (divIVA)
244	isoleucyl-tRNA synthetase (ileS)
252	MutT/nudix family protein
256	ATP-dependent Clp protease, ATP-binding subunit ClpE (clpE)
268	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cycloh
274	exodeoxyribonuclease VII, large subunit (xseA)
278	exodeoxyribonuclease VII, small subunit (xseB)
282	geranyltranstransferase (ispA)
286	hemolysin A
290	transcriptional repressor
296	DNA repair protein RecN (recN)
300	degV family protein (degV)
322	peptide ABC transporter, permease protein (oppC)
326	peptide ABC transporter, ATP-binding protein (oppD)
328	peptide ABC transporter, ATP-binding protein (oppF)
348	4-diphosphocytidyl-2C-methyl-D-erythritol kinase (ispE)
352	adc operon repressor AdcR (adcR)
356	zinc ABC transporter, ATP-binding protein (adcC)
370	tyrosyl-tRNA synthetase (tyrS)
374	penicillin-binding protein 1B (pbp1B)
378	DNA-directed RNA polymerase, beta subunit (rpoB)
382	dna-directed rna polymerase beta' chain

390	competence protein CglA (cglA)
406	acetate kinase (ackA)
410	transcriptional regulator
418	pyrroline-5-carboxylate reductase (proC)
422	glutamyl-aminopeptidase (pepA)
432	thioredoxin family protein
436	tRNA binding domain protein (pheT)
440	methyltransferase
442	single-strand DNA-binding protein, authentic point mutation (ssbB)
454	GAF domain protein (lytS)
466	lrgB protein (lrgB)
474	oligopeptide ABC transporter, permease protein
476	peptide ABC transporter, ATP-binding protein
480	peptide ABC transporter, ATP-binding protein (oppF)
484	PTS system, IIABC components (treB)
488	alpha amylase family protein (treC)
494	transcriptional regulator, BglG family
506	transcriptional regulator, BglG family
508	PTS system, IIB component
514	PTS system, IIC component
518	transketolase, N-terminal subunit (tktA)
528	ribosomal protein S15 (rpsO)
546	cysteinyl-tRNA synthetase (cysS)
554	RNA methyltransferase, TrmH family, group 3
562	DegV family protein (degV)
572	ribosomal protein S9 (rpsI)
576	integrase, phage family
580	transcriptional regulator
596	recombination protein
626	transcriptional regulator MutR
630	transporter
640	amino acid ABC transporter, permease protein (opuBB)
642	glycine betaine/L-proline transport ATP binding subunit (proV)
654	lectin, alpha subunit precursor
662	transcriptional regulator
664	acetyltransferase, GNAT family
666	acetyltransferase, GNAT family (rimJ)
670	acetyltransferase, GNAT family
676	transcriptional regulator, tetR family domain protein
680	ABC transporter efflux protein, DrrB family
690	IS1381, transposase OrfA/OrfB, truncation
714	magnesium transporter, CorA family
718	oxidoreductase, Gfo/Idh/MocA family
722	valyl-tRNA synthetase (valS)
730	acetyltransferase, GNAT family
746	methyltransferase
750	bacteriophage L54a, integrase
754	DNA-damage-inducible protein J
774	cation efflux system protein
778	oxidoreductase, aldo/keto reductase family
784	alcohol dehydrogenase, zinc-containing
790	3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylas
804	ribonucleoside-diphosphate reductase, alpha subunit (nrdE)
808	nrdI protein (nrdI)
812	Ribonucleotide reductases
824	elaA protein (elaA)
828	RNA methyltransferase, TrmA family
832	RecX family protein
840	-identity (jag)

844	membrane protein, 60 kDa (yidC)
856	UTP-glucose-1-phosphate uridylyltransferase (galU)
864	rhomboid family protein
884	MORN motif family
892	transcriptional regulator
896	adenylosuccinate lyase (purB)
908	phosphoribosylaminoimidazole carboxylase, catalytic subunit (purE)
912	phosphoribosylamine--glycine ligase (purD)
916	phosphosugar-binding transcriptional regulator
920	acetyl xylan esterase
922	ROK family protein (gki)
926	N-acetylneuraminate lyase (nanA)
936	sugar ABC transporter, permease protein
940	sugar ABC transporter, permease protein (msmF)
952	LysM domain protein, authentic frameshift
956	zoocin A endopeptidase
958	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydr
962	acetyltransferase, GNAT family family
964	phosphoribosylglycinamide formyltransferase (purN)
968	phosphoribosylformylglycinamidine cyclo-ligase (purM)
972	amidophosphoribosyltransferase (purF)
980	phosphoribosylformylglycinamidine synthase
984	phosphoribosylaminoimidazole-succinocarboxamide synthase (purC)
1042	oligoendopeptidase F (pepF)
1060	ebsC protein
1068	hydrolase, haloacid dehalogenase-like family
1076	riboflavin synthase, beta subunit (ribH)
1082	riboflavin biosynthesis protein RibD (ribD)
1086	Mn2+/Fe2+ transporter, NRAMP family
1094	peptidase, U32 family
1116	HPr(Ser) kinase/phosphatase (hprK)
1130	oxidoreductase
1148	signal recognition particle-docking protein FtsY (ftsY)
1152	Cof family protein
1156	Cof family protein
1172	vicX protein (vicX)
1176	sensory box sensor histidine kinase (vicK)
1180	DNA-binding response regulator (vicR)
1184	amino acid ABC transporter, ATP-binding protein
1188	amino acid ABC transporter, amino acid-binding protein (fliY)
1192	amino acid ABC transporter, permease protein
1196	amino acid ABC transporter, permease protein
1208	DNA-binding response regulator (vicR)
1210	threonyl-tRNA synthetase (thrS)
1214	glycosyl transferase, group 1
1218	glycosyl transferase, group 1 (cpoA)
1222	alpha-amylase (amy)
1230	proline dipeptidase (pepQ)
1238	haloacid dehalogenase-like hydrolase superfamily
1244	mannonate dehydratase (uxuA)
1248	glucuronate isomerase
1254	transcriptional regulator, GntR family
1268	sodiumgalactoside symporter family protein
1270	D-isomer specific 2-hydroxyacid dehydrogenase family protein
1282	transcriptional regulator, LysR family
1290	ABC transporter, ATP-binding protein (potA)
1296	DedA family protein
1308	MutT/nudix family protein family
1310	phosphoserine phosphatase SerB (serB)

1312	septation ring formation regulator EzrA
1320	hydrolase, haloacid dehalogenase-like family (gph)
1340	sensor histidine kinase (vncS)
1348	transmembrane protein Vexp3 (vex3)
1352	ABC transporter, ATP-binding protein (vex2)
1358	transmembrane protein Vexp1 (vex1)
1366	transposase
1374	integrase, phage family
1390	holin 2
1398	minor structural protein
1400	host specificity protein
1404	minor structural protein
1406	PblA
1486	homeobox protein drg11
1488	reverse transcriptase
1496	p22 erf-like protein
1498	gp157
1500	tropomyosin 2
1512	gp49 homologous
1526	transcriptional regulator-related protein
1566	chorismate mutase
1572	PTS system component
1576	PTS system, IIB component
1580	PTS system IIA component
1584	lactose phosphotransferase system repressor (lacR)
1594	adhesion lipoprotein (lmb)
1602	GTP pyrophosphokinase (relA)
1606	2`,3`-cyclic-nucleotide 2`-phosphodiesterase (cpdB)
1616	iron ABC transporter, iron-binding protein
1620	DNA-binding response regulator
1630	PTS system component
1634	PTS system component (manM)
1638	PTS system component (manL)
1642	PTS system component
1658	response regulator BlpR (blpR)
1676	phosphate transport system regulatory protein PhoU
1680	phosphate ABC transporter, ATP-binding protein (pstB)
1684	phosphate ABC transporter, permease protein (pstA)
1690	phosphate ABC transporter, permease protein (pstC)
1694	probable hemolysin precursor
1704	ribosomal protein L11 methyltransferase (prmA)
1710	transcriptional regulator, MerR family (skgA)
1714	acetyltransferase, GNAT family
1716	MutT/nudix family protein
1722	spermidine N1-acetyltransferase
1726	ATPase, AAA family
1736	ABC transporter domain protein
1738	Helix-turn-helix domain protein
1748	integrase, phage family
1756	Helix-turn-helix domain protein
1762	bacteriophage L54a, integrase
1768	LPXTG-motif cell wall anchor domain protein
1776	membrane protein
1778	conjugal transfer protein
1780	IS1381, transposase OrfA/OrfB, truncation
1802	transcriptional regulator (rstR-1)
1806	transcriptional regulator
1808	FtsK/SpoIIIE family protein
1814	aggregation substance

1818	mercuric reductase
1822	transcriptional regulator, MerR family
1824	Mn2+/Fe2+ transporter, NRAMP family
1830	ABC transporter, ATP-binding protein (epiF)
1848	Helix-turn-helix domain protein
1850	type 2 phosphatidic acid phosphatase(PAP2), family
1858	Abortive infection protein family
1868	aminotransferase, class-V
1874	glutathione reductase (gor)
1882	chorismate synthase (aroC)
1886	3-dehydroquinate synthase (aroB)
1900	sulfatase family protein
1914	ABC transporter, ATP-binding protein
1920	smf protein (Smffamily)
1924	transferrin receptor
1928	iron compound ABC transporter, ATP-binding protein
1932	iron compound ABC transporter, permease protein
1942	acetyltransferase, CysE/LacA/LpxA/ NodL family
1952	GTP-binding protein
1958	carbon starvation protein A
1960	response regulator (lytR)
1962	GAF domain protein (lytS)
2000	extracellular protein
2004	diarrheal toxin (yukA)
2024	carbamoyl-phosphate synthase, large subunit (carB)
2028	carbamoyl-phosphate synthase, small subunit (carA)
2032	aspartate carbamoyltransferase (pyrB)
2036	dihydroorotase, multifunctional complex type (pyrC)
2040	orotate phosphoribosyltransferase (pyrE)
2048	membrane protein
2062	phosphate ABC transporter, permease protein (pstA-2)
2064	phosphate ABC transporter, ATP-binding protein (pstB)
2070	phosphate transport system regulatory protein PhoU
2072	aminopeptidase N (pepN)
2076	DNA-binding response regulator (arlR)
2080	sensor histidine kinase (arlS)
2088	signal recognition particle protein (ffh)
2102	peptide ABC transporter, peptide-binding protein
2104	integrase/recombinase, phage integrase family
2108	sensor histidine kinase
2112	DNA-binding response regulator (vicR)
2118	ABC transporter, ATP-binding protein
2122	nisin-resistance protein
2130	lipoprotein
2136	gid protein (gid)
2140	transcriptional regulator, GntR family
2142	GMP synthase (guaA)
2152	branched-chain amino acid ABC transporter, permease protein (livM)
2154	branched-chain amino acid ABC transporter, ATP-binding protein (livG)
2156	branched-chain amino acid ABC transporter, ATP-binding protein (livF)
2160	acetoin utilization protein AcuB
2174	DNA polymerase III, delta prime subunit (holB)
2186	copper homeostasis protein (cutC)
2190	phosphoserine aminotransferase (serC)
2202	methylated-DNA--protein-cysteine S-methyltransferase (ogt)
2208	exodeoxyribonuclease III (xth)
2214	PTS system, IIC component
2224	tellurite resistance protein TehB (tehB)
2246	icaA protein

2250	acetyltransferase, GNAT family
2258	oxidoreductase, short chain dehydrogenase/reductase family (fabG)
2266	oxidoreductase, Gfo/Idh/MocA family family
2268	glyoxalase family protein
2272	UDP-N-acetylglucosamine pyrophosphorylase (glmU)
2276	MutT/nudix family protein
2284	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase (mtf)
2296	phosphatidate cytidylyltransferase (cdsA)
2300	membrane-associated zinc metalloprotease
2308	autolysin (flgJ)
2312	DNA polymerase III, alpha subunit, Gram-positive type
2320	nitroreductase family protein superfamily
2326	4-hydroxy-2-oxoglutarate aldolase/2-deydro-3-deoxyphosphogluconate aldo
2328	carbohydrate kinase, PfkB family
2336	oxidoreductase, short chain dehydrogenase/reductase family (fabG)
2338	PTS system, IIA component (manL)
2342	glucuronyl hydrolase
2346	PTS system, IIB component (manL)
2350	PTS system, IIC component (manM)
2364	sugar binding transcriptional regulator RegR (regR)
2368	polypeptide deformylase (def)
2380	oxidoreductase, Gfo/Idh/MocA family
2382	endopeptidase O (pepO)
2394	Na+/H+ antiporter
2404	transcriptional regulator
2410	replication initiation protein RepRC
2412	bacteriophage L54a, antirepressor
2416	e11
2422	replicative DNA helicase (dnaB)
2432	GTP-binding protein
2440	arpR protein
2444	gene 17 protein
2458	integrase/recombinase, phage integrase family
2468	bacteriophage L54a, phage D3 terminase
2472	protease
2500	PblB
2504	sensor histidine kinase
2514	N-acetylmuramoyl-L-alanine amidase
2518	KH domain protein
2522	ribosomal protein S16 (rpsP)
2526	permease
2528	ABC transporter, ATP-binding protein
2538	carbamoyl-phosphate synthase, large subunit
2540	carbamoyl-phosphate synthase, small subunit (carA)
2550	transcriptional regulator, LysR family
2554	ribosomal protein L27 (rpmA)
2562	ribosomal protein L21 (rplU)
2572	glycerophosphoryl diester phosphodiesterase
2582	nitroreductase family protein
2586	dipeptidase (pepV)
2614	GTP-binding protein HflX (hflX)
2618	galactose-1-phosphate uridylyltransferase (galT)
2626	oxidoreductase, short chain dehydrogenase/reductase family
2630	single-stranded-DNA-specific exonuclease RecJ (recJ)
2638	adenine phosphoribosyltransferase (apt)
2646	Bcl-2 family protein
2654	oxidoreductase, DadA family protein
2658	glucose-1-phosphate thymidylyltransferase (rfbA)
2664	dTDP-4-dehydrorhamnose 3,5-epimerase (rfbC)

2682	hyaluronidase
2686	mutator MutT protein (mutX)
2690	MutT/nudix family protein
2694	membrane protein
2702	acetolactate synthase (ilvK)
2706	adherence and virulence protein A (pavA)
2714	ABC transporter, permease protein (rbsC)
2722	metallo-beta-lactamase superfamily protein
2734	ribose 5-phosphate isomerase (rpiA)
2738	phosphopentomutase (deoB)
2742	purine nucleoside phosphorylase, family 2 (deoD)
2750	purine nucleoside phosphorylase (deoD)
2762	capsular polysaccharide biosynthesis protein Cps4A (cps4A)
2768	cpsb protein
2770	cpsc protein
2772	CpsE
2774	CpsF
2776	CpsVG
2778	CpsVH
2780	CpsVM
2782	CpsVN
2784	glycosyl transferase domain protein
2786	glycosyl transferase, family 2/glycosyl transferase family 8
2790	CpsVK
2794	CpsL
2796	neuB protein
2798	UDP-N-acetylglucosamine 2-epimerase
2800	hexapeptide transferase family protein
2802	NeuA
2808	uracil-DNA glycosylase (ung)
2818	DNA topoisomerase IV, B subunit (parE)
2822	DNA topoisomerase IV, A subunit (parC)
2826	branched-chain amino acid aminotransferase (ilvE)
2842	glycerol kinase (glpK)
2848	aerobic glycerol-3-phosphate dehydrogenase (glpD)
2874	ABC transporter, ATP-binding protein
2882	PTS system component (bglP)
2886	glutamate 5-kinase (proB)
2890	gamma-glutamyl phosphate reductase (proA)
2898	cell division protein FtsL (ftsL)
2904	penicillin-binding protein 2X (pbpX)
2910	phospho-N-acetylmuramoyl-pentapeptide-transferase (mraY)
2914	ATP-dependent RNA helicase, DEAD/DEAH box family (deaD)
2918	ABC transporter, substrate-binding protein
2924	amino acid ABC transporter, permease protein
2928	amino acid ABC transporter, ATP-binding protein
2932	thioredoxin reductase (trxB)
2940	NAD+ synthetase (nadE)
2944	aminopeptidase C (pepC)
2952	recombination protein U (recU)
2966	Uncharacterized protein family UPF0020 family
2974	autoinducer-2 production protein LuxS (luxS)
2978	KH domain protein
2986	ABC transporter, ATP-binding protein
2994	DNA-binding response regulator (vraR)
3000	guanylate kinase (gmk)
3004	DNA-directed RNA polymerase, omega subunit
3008	primosomal protein N (priA)
3012	methionyl-tRNA formyltransferase (fmt)

3016	Sun protein (sun)
3020	protein phosphatase 2C
3032	sensor histidine kinase
3034	DNA-binding response regulator (vraR)
3036	cof family protein/peptidyl-prolyl cis-trans isomerase, cyclophilin typ
3040	S1 RNA binding domain protein (rpsA)
3044	pyruvate formate-lyase-activating enzyme
3062	PTS system, IIB component (celA)
3066	PTS system, cellobiose-specific IIC component (celB)
3068	formate acetyltransferase (pfl)
3072	transaldolase
3080	cysteine synthase A (cysK)
3088	comF operon protein 1 (comFA)
3092	competence protein ComF
3096	ribosomal subunit interface protein (yfiA)
3104	tryptophanyl-tRNA synthetase (trpS)
3108	carbamate kinase (arcC)
3116	ornithine carbamoyltransferase (argF)
3124	arginine deiminase (arcA)
3134	transcriptional regulator, Crp/Fnr family
3138	inosine-5'-monophosphate dehydrogenase (guaB)
3140	MutR
3142	transporter
3146	recF protein (recF)
3158	peptidase, M16 family
3166	ABC transporter, ATP-binding protein
3170	ABC transporter, ATP-binding protein
3178	LysM domain protein (lytN)
3180	immunodominant antigen A (isaA)
3184	L-serine dehydratase, iron-sulfur-dependent, alpha subunit (sdhA)
3188	L-serine dehydratase, iron-sulfur-dependent, beta subunit (sdhB)
3202	DHH subfamily 1 protein
3206	ribosomal protein L9 (rplI)
3210	replicative DNA helicase (dnaB)
3216	ribosomal protein S4 (rpsD)
3224	transcriptional regulator, TetR family
3236	membrane protein
3238	choline transporter (proWX)
3240	glycine betaine/L-proline transport ATP binding subunit (proV)
3242	DNA-binding response regulator
3244	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family
3246	ornithine carbamoyltransferase (argF)
3248	carbamate kinase (arcC)
3252	membrane protein
3256	sensory box histidine kinase VicK
3258	DNA-binding response regulator
3268	Helix-turn-helix domain protein
3278	integrase
3284	ribosomal protein L33 (rpmG)
3288	ribosomal protein L32 (rpmF)
3300	YitT family protein
3304	YitT family protein
3320	DNA mismatch repair protein MutS (mutS)
3324	cold-shock domain family protein-related protein
3336	drug transporter
3340	Holliday junction DNA helicase RuvA (ruvA)
3352	recA protein (recA)
3386	oxidoreductase, Gfo/Idh/MocA family
3390	acetyltransferase, GNAT family

3394	anaerobic ribonucleoside-triphosphate reductase activating protein (nrd
3412	ABC transporter, permease protein (rbsC)
3414	ABC transporter, ATP-binding protein (nrtC)
3416	PTS system, mannose-specific IIAB components (manL)
3420	Cof family protein
3432	xanthine/uracil permease family protein
3440	acetyltransferase, GNAT family
3442	transcriptional regulator (cps4A)
3448	HIT family protein (hit)
3460	ABC transporter, permease protein
3472	Uncharacterized BCR, YhbC family COG0779 superfamily
3484	ribosomal protein L7A family
3496	esterase
3500	transcriptional repressor, CopY (copY)
3504	cation-transporting ATPase, E1-E2 family
3508	cation-binding protein-related protein
3520	DNA polymerase I (polA)
3534	DNA-binding response regulator (saeR)
3536	sensor histidine kinase (saeS)
3562	drug resistance transporter, EmrB/QacA subfamily
3566	peptidase M24 family protein
3570	peptidase M24 family protein (pepQ)
3572	cytidine/deoxycytidylate deaminase family protein
3584	translation elongation factor P (efp)
3592	N utilization substance protein B (nusB)
3596	sugar-binding transcriptional regulator, LacI family (scrR)
3600	sucrose-6-phosphate dehydrogenase (scrB)
3606	PTS system IIABC components (scrA)
3610	fructokinase (scrK)
3614	mannose-6-phosphate isomerase, class I (manA)
3622	phospho-2-dehydro-3-deoxyheptonate aldolase (aroH)
3626	holo-(acyl-carrier-protein) synthase (acpS)
3630	alanine racemase (alr)
3634	autolysin (usp45)
3636	ATP-dependent DNA helicase RecG (recG)
3642	shikimate 5-dehydrogenase (aroE)
3652	Cof family protein
3668	ferredoxin-related protein
3676	peptidase t (pepT)
3684	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (mur
3692	iron compound ABC transporter, substrate-binding protein
3698	FecCD transport family protein (sirB)
3704	iron compound ABC transporter, permease protein (sirB)
3710	inorganic pyrophosphatase, manganese-dependent (ppaC)
3714	pyruvate formate-lyase-activating enzyme (pflA)
3718	CBS domain protein
3730	acid phosphatase
3736	LPXTG-motif cell wall anchor domain protein
3738	LPXTG-site transpeptidase family protein
3742	LPXTG-site transpeptidase family protein
3744	cell wall surface anchor family protein
3746	cell wall surface anchor family protein
3752	glycosyl transferase, group 1 family protein domain protein
3754	EpsQ protein
3756	polysaccharide extrusion protein
3768	dTDP-glucose 4-6-dehydratase
3782	glycosyl transferase domain protein
3788	dTDP-4-dehydrorhamnose reductase (rfbD)
3796	RNA polymerase sigma-70 factor (rpoD)

3802	DNA primase (dnaG)
3816	ABC transporter, ATP-binding protein Vexp2 (vex2)
3818	permease
3820	transmembrane protein Vexp3
3822	transmembrane protein Vexp3
3832	endopeptidase O (pepO)
3834	endopeptidase O (pepO)
3840	serine protease, subtilase family
3842	exotoxin 2
3844	CylK
3854	glycine cleavage system T protein
3856	CylE
3858	ABC transporter homolog CylB
3862	acyl carrier protein homolog AcpC (acpP)
3864	3-oxoacyl-(acyl-carrier-protein) reductase (fabG)
3868	CylD
3876	membrane protein
3912	LPXTG-site transpeptidase family protein
3916	LPXTG-site transpeptidase family protein
3918	LPXTG-site transpeptidase family protein
3920	LPXTG-motif cell wall anchor domain protein
3928	chaperonin, 33 kDa (hslO)
3932	Tn5252, Orf 10 protein
3934	transposase OrfAB, subunit B
3948	psr protein
3952	shikimate kinase (aroK)
3964	enolase (eno)
3972	MutT/nudix family protein
3976	glycosyl transferase, group 1
3978	preprotein translocase, SecA subunit (secA)
3986	preprotein translocase SecY family protein
3990	glycosyl transferase, family 8
3992	glycosyl transferase, family 2
3998	glycosyl transferase, family 8
4000	glycosyl transferase, family 2/glycosyl transferase family 8
4002	glycosyl transferase, family 8
4012	LPXTG-motif cell wall anchor domain protein (clfB)
4016	transcriptional regulator
4018	excinuclease ABC, B subunit (uvrB)
4022	Abortive infection protein family
4024	amino acid ABC transporter, amino acid-binding protein/permease protein
4026	amino acid ABC transporter, ATP-binding protein
4034	GTP-binding protein, GTP1/Obg family (obg)
4042	aminopeptidase PepS (pepS)
4050	ribosomal small subunit pseudouridine synthase A (rsuA)
4060	lactoylglutathione lyase (gloA)
4064	glycosyl transferase family protein
4072	alkylphosphonate utilization operon protein PhnA (phnA)
4078	glucosamine--fructose-6-phosphate aminotransferase (isomerizing) (glmS)
4090	Phosphofructokinase
4094	DNA polymerase III, alpha subunit (dnaE)
4098	transcriptional regulator, GntR family
4102	ABC transporter, ATP-binding protein
4106	ABC transporter, ATP-binding protein
4116	FtsK/SpoIIIE family protein
4122	Helix-turn-helix domain protein
4152	Helix-turn-helix domain protein
4158	excisionase
4160	transposase

4166	chloramphenicol acetyltransferase (cat)
4174	PilB-related protein
4178	acetyltransferase
4182	Leucine Rich Repeat domain protein
4190	nucleoside diphosphate kinase (ndk)
4206	Protein of unknown function superfamily
4218	hydrolase, haloacid dehalogenase-like family (pho2)
4226	oxygen-independent coproporphyrinogen III oxidase
4236	phosphoglucomutase/phosphomannomutase family protein (femD)
4240	Gram-positive signal peptide, YSIRK family domain protein
4256	cobyric acid synthase (cobQ)
4260	lipoate-protein ligase A (lplA)
4264	branched-chain alpha-keto acid dehydrogenase E3 component, lipoamide de
4266	pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltr
4270	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase be
4286	magnesium transporter, CorA family
4294	exonuclease RexB (rexB)
4302	phenylalanyl-tRNA synthetase, beta subunit (pheT)
4324	ATP synthase F1, epsilon subunit (atpC)
4328	ATP synthase F1, beta subunit (atpD)
4332	ATP synthase F1, gamma subunit (atpG)
4338	ATP synthase F1, alpha subunit (atpA)
4342	ATP synthase F1, delta subunit (atpH)
4346	ATP synthase F0, B subunit (atpF)
4350	ATP synthase, F0 subunit A (atpB)
4354	proton-translocating ATPase, c subunit-related protein
4360	glycogen synthase (glgA)
4362	glycogen biosynthesis protein GlgD (glgD)
4366	1,4-alpha-glucan branching enzyme (glgB)
4368	pullulanase
4382	ribonuclease BN
4396	acetyltransferase, GNAT family
4398	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
4402	thiamine-phosphate pyrophosphorylase (thiE)
4406	phosphomethylpyrimidine kinase (thiD)
4410	transcriptional regulator, Deg family (tenA)
4414	ABC transporter, ATP-binding protein
4426	S-adenosylmethionine synthetase (metK)
4440	DNA polymerase III, gamma and tau subunits (dnaX)
4444	GAF domain protein
4448	uridine kinase (udk)
4452	ATP-dependent RNA helicase, DEAD/DEAH box family
4458	peptidoglycan GlcNAc deacetylase (pgdA)
4462	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent (gapN)
4466	phosphoenolpyruvate-protein phosphotransferase (ptsI)
4470	phosphocarrier protein hpr
4474	NrdH-redoxin-related protein
4478	ribonucleoside-diphosphate reductase 2, alpha subunit (nrdE)
4498	glycosyl transferase, family 8
4504	alanyl-tRNA synthetase (alaS)
4512	alkyl hydroperoxide reductase, subunit F (ahpF)
4516	alkyl hydroperoxide reductase, subunit C (ahpC)
4520	ribosomal protein S2 (rpsB)
4524	translation elongation factor Ts (tsf)
4532	transcriptional regulator CtsR (ctsR)
4536	ATP-dependent Clp protease, ATP-binding subunit (clpC)
4540	deoxynucleoside kinase
4544	NifR3/Smm1 family protein
4548	chaperonin, 33 kDa (hslO)

4558	glutamate--cysteine ligase (gshA)
4562	Helix-turn-helix domain, fis-type protein
4566	perfringolysin O regulator protein (pfoR)
4570	adenylosuccinate synthetase (purA)
4578	SgaT protein (sgaT)
4582	PTS system, IIB component (sgaT)
4586	PTS system, IIA component (mtlA)
4590	hexulose-6-phosphate synthase
4594	hexulose-6-phosphate isomerase
4598	L-ribulose-5-phosphate 4-epimerase (araD)
4606	sugar binding transcriptional regulator RegR
4610	D-isomer specific 2-hydroxyacid dehydrogenase family protein (serA)
4622	transcriptional regulator, BglG family
4632	glycine betaine/L-proline transport ATP binding subunit (proV)
4636	amino acid ABC transporter, permease protein
4644	Na+/H+ exchanger family protein (kefB)
4648	glyoxylase family protein
4652	LPXTG-site transpeptidase family protein
4656	DNA gyrase, A subunit (gyrA)
4660	L-lactate dehydrogenase (ldh)
4664	NADH oxidase (nox)
4680	lipoprotein (bmpD)
4690	pantothenate kinase (coaA)
4694	ribosomal protein S20 (rpsT)
4698	amino acid ABC transporter, amino acid-binding protein (aatB)
4702	amino acid ABC transporter, ATP-binding protein
4726	ribosomal large subunit pseudouridine synthase B (rluB)
4734	Uncharacterized ACR, COG1354
4738	integrase/recombinase, phage integrase family (xerD)
4742	CBS domain protein
4746	phosphoesterase
4750	HAM1 protein
4768	transcriptional regulator, biotin repressor family
4792	amino acid ABC transproter, permease protein
4796	amino acid ABC transporter, substrate-binding protein
4798	6-aminohexanoate-cyclic-dimer hydrolase
4800	transcription elongation factor GreA (greA)
4804	Uncharacterized BCR, YceG family COG1559
4812	UDP-N-acetylmuramate--alanine ligase (murC)
4822	Snf2 family protein
4828	GTP-binding protein (b2511)
4832	primosomal protein DnaI (dnaI)
4844	sensor histidine kinase (arlS)
4846	DNA-binding response regulator (arlR)
4852	heat shock protein HtpX (htpX)
4870	potassium uptake protein, Trk family
4874	ABC transporter, ATP-binding protein
4888	phosphoglycerate kinase (pgk)
4896	transcriptional regulator, MerR family
4900	glutamine synthetase, type I (glnA)
4904	secreted 45 kd protein (usp45)
4908	metallo-beta-lactamase superfamily protein
4916	glycoprotease family protein
4926	glycoprotease family protein (gcp)
4938	ribosomal protein S14p/S29e (rpsN)
4952	exonuclease (dnaQ)
4956	transcriptional regulator, merR family
4958	cyclopropane-fatty-acyl-phospholipid synthase (cfa)
4970	1,4-dihydroxy-2-naphthoate octaprenyltransferase (menA)

4972	pyridine nucleotide-disulphide oxidoreductase (ndh)
4974	cytochrome d oxidase, subunit I (cydA)
4976	cytochrome d ubiquinol oxidase, subunit II (cydB)
4980	transport ATP-binding protein CydD
4988	polyprenyl synthetase (ispB)
4990	X-pro dipeptidyl-peptidase (pepX)
4998	drug transporter
5002	universal stress protein family
5004	glycerol uptake facilitator protein (glpF)
5012	cppA protein (cppA)
5034	exodeoxyribonuclease V, alpha subunit (recD)
5038	Signal peptidase I
5042	ribonuclease HIII (rnhC)
5062	transcriptional regulator
5068	maltose ABC transporter, permease protein (malD)
5072	maltose ABC transporter, permease protein (malC)
5088	ABC transporter, ATP-binding protein
5092	ABC transporter, permease protein
5106	spspoJ protein (spo0J)
5114	DNA polymerase III, beta subunit (dnaN)
5118	Diacylglycerol kinase catalytic domain (presumed) protein
5138	transcription-repair coupling factor (mfd)
5142	S4 domain protein
5156	MesJ/Ycf62 family protein
5160	hypoxanthine phosphoribosyltransferase (hpt)
5164	cell division protein FtsH (ftsH)
5172	hydrolase, haloacid dehalogenase-like family (b2690)
5178	transcriptional regulator, MarR family
5182	3-oxoacyl-(acyl-carrier-protein) synthase III (fabH)
5190	enoyl-(acyl-carrier-protein) reductase (fabK)
5194	malonyl CoA-acyl carrier protein transacylase (fabD)
5198	3-oxoacyl-[acyl-carrier protein] reductase (fabG)
5200	3-oxoacyl-(acyl-carrier-protein) synthase II (fabF)
5202	acetyl-CoA carboxylase, biotin carboxyl carrier protein (accB)
5206	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
5210	acetyl-CoA carboxylase, biotin carboxylase (accC)
5214	acetyl-CoA carboxylase, carboxyl transferase, beta subunit (accD)
5218	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit (accA)
5224	seryl-tRNA synthetase (serS)
5234	PTS system, mannose-specific IID component
5246	ribosomal large subunit pseudouridine synthase, RluD subfamily (rluD)
5254	GTP pyrophosphokinase (relA)
5266	ribose-phosphate pyrophosphokinase (prsA)
5270	aminotransferase, class-V
5274	DNA-binding protein
5282	Domain of unknown function
5290	platelet activating factor
5296	transcriptional regulator, AraC family
5302	voltage-gated chloride channel family protein
5318	spermidine/putrescine ABC transporter, ATP-binding protein (potA)
5320	UDP-N-acetylenolpyruvoylglucosamine reductase (murB)
5324	bifunctional folate synthesis protein (folK)
5328	dihydroneopterin aldolase (folB)
5332	dihydropteroate synthase (folP)
5336	GTP cyclohydrolase I (folE)
5344	rarD protein (rarD)
5348	homoserine kinase (thrB)
5354	Polysaccharide deacetylase family (icaB)
5362	osmoprotectant transporter, BCCT family (opuD)

5384	thiol peroxidase (psaD)
5388	hydrolase
5390	transcriptional regulator, GntR family
5402	gls24 protein
5424	uncharacterized domain 1
5440	cation efflux family protein
5454	dihydroorotate dehydrogenase A (pyrDa)
5458	beta-lactam resistance factor (fibB)
5462	beta-lactam resistance factor (fibA)
5474	HD domain protein
5482	cation-transporting ATPase, E1-E2 family
5486	fructose-1,6-bisphosphatase (fbp)
5488	iron-sulfur cluster-binding protein
5492	peptide chain release factor 2 (prfB)
5496	cell division ABC transporter, ATP-binding protein FtsE (ftsE)
5504	carboxymethylenebutenolidase-related protein
5506	metallo-beta-lactamase superfamily protein
5514	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
5520	asparaginyl-tRNA synthetase (asnS)
5526	inosine-uridine preferring nucleoside hydrolase (iunH)
5528	general stress protein 170
5534	Uncharacterised protein family superfamily
5538	Uncharacterized BCR, COG1481
5546	zinc ABC transporter, zinc-binding adhesion liprotein (adcA)
5560	isochorismatase family protein (entB)
5566	3-hydroxybutyryl-CoA dehydrogenase
5572	pyruvate phosphate dikinase (ppdK)
5574	glutamyl-tRNA(Gln) amidotransferase, C subunit (gatC)
5580	glutamyl-tRNA(Gln) amidotransferase, A subunit (gatA)
5594	GTP-binding protein
5612	iojap-related protein
5626	transcriptional regulator SkgA (skgA)
5630	glycerol uptake facilitator protein (glpF)
5634	dihydroxyacetone kinase family protein
5638	dihydroxyacetone kinase family protein
5640	transcriptional regulator, tetR family
5646	dihydroxyacetone kinase family protein
5654	glutamine amidotransferase, class I
5666	peptidase, M20/M25/M40 family
5668	ABC transporter, ATP-binding protein
5686	pur operon repressor (purR)
5690	cmp-binding-factor 1 (cbf1)
5694	competence-induced protein Ccs50 (ccs50)
5702	ribulose-phosphate 3-epimerase (rpe)
5710	rRNA (guanine-N1-)-methyltransferase (rrmA)
5712	dimethyladenosine transferase (ksgA)
5718	primase-related protein
5726	endosome-associated protein
5728	CG17785 gene product
5734	dltD protein (dltD)
5738	D-alanyl carrier protein-related protein
5742	dltB protein (dltB)
5754	DNA-binding response regulator (arlR)
5756	ribosomal protein L34 (rpmH)
5766	penicillin-binding protein 4 (pbp4)
5770	intein-containing protein
5774	NifU family protein
5778	aminotransferase, class-V
5782	Uncharacterized protein family (UPF0051) family

5786	ABC transporter, ATP-binding protein
5790	glycosyl transferase domain protein (llm)
5794	transcriptional regulator MecA (mecA)
5798	undecaprenol kinase
5806	amino acid ABC transporter, amino acid-binding protein/permease protein
5808	amino acid ABC transporter, ATP-binding protein
5834	riboflavin biosynthesis protein RibF (ribF)
5850	type I restriction-modification system, S subunit
5860	lipoprotein
5862	aggregation substance
5866	ID479
5896	type II DNA modification methyltransferase Spn5252IP (spn5252IMP)
5916	ribosomal protein L10 (rplJ)
5922	ATP-dependent Clp protease, ATP-binding subunit ClpC (clpC)
5926	homocysteine S-methyltransferase (mmuM)
5932	transcriptional regulator, TetR family
5938	GTP-binding protein (cgpA)
5952	thymidylate synthase (thyA)
5956	condensing enzyme, FabH-related
5960	hydroxymethylglutaryl-CoA reductase, degradative
5974	gene_idK21C13.21~pir||T04769~strong similarity to unknown protein, put
5976	FMN-dependent dehydrogenase family protein
5980	phosphomevalonate kinase
5986	diphosphomevalonate decarboxylase (mvaD)
5990	mevalonate kinase (mvk)
5994	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase family (PhoR1
6002	GTP pyrophosphokinase (relA)
6006	transposase for insertion sequence element is904
6016	5'-nucleotidase family
6018	polypeptide deformylase (def)
6022	NADP-specific glutamate dehydrogenase (gdhA)
6026	ABC transporter, ATP-binding/permease protein
6028	ABC transporter, ATP-binding/permease protein
6030	acetyltransferase, GNAT family family
6032	ABC transporter, ATP-binding protein
6040	degV family protein (degV)
6056	carbohydrate kinase, PfkB family (fruB)
6064	beta-lactam resistance factor (fibB)
6070	2-dehydropantoate 2-reductase
6076	PTS system component
6078	pyridine nucleotide-disulphide oxidoreductase family protein (trxB)
6082	tRNA (guanine-N1)-methyltransferase (trmD)
6092	c5a peptidase precursor
6100	ParA
6102	transposase family protein (orfA)
6116	Tn5252, relaxase
6120	Tn5252, Orf 10 protein
6124	mercuric reductase
6126	transcriptional regulator, MerR family
6132	cation transport ATPase, E1-E2 family
6138	cation-transporting ATPase, E1-E2 family
6140	cation-transporting ATPase, E1-E2 family
6144	cation-transporting ATPase, E1-E2 family
6146	transcriptional repressor, CopY (copY)
6150	cadmium resistance transporter
6158	membrane protein
6162	flavoprotein (dfp)
6170	lipoate-protein ligase A
6174	FMN oxidoreductase (nemA)

6178	Bacterial luciferase superfamily
6182	glycine cleavage system H protein (gcvH)
6186	Domain of unknown function
6194	lipoate-protein ligase A (lplA)
6198	formate--tetrahydrofolate ligase (fhs)
6202	cardiolipin synthetase (cls)
6220	aminotransferase, class II (aspB)
6222	RNA methyltransferase, TrmH family, group 2
6232	60 kda chaperonin
6242	purine nucleoside phosphorylase (deoD)
6248	deoxyribose-phosphate aldolase (deoC)
6254	Lyme disease proteins of unknown function
6258	ribosomal large subunit pseudouridine synthase, RluD subfamily (rluD)
6262	penicillin-binding protein 2A (pbp2A)
6266	pathenogenicity protein
6268	transcription antitermination protein NusG (nusG)
6272	glycosyl transferase, family 8
6276	glycosyl transferase, family 8
6284	sugar transporter family protein
6292	sensory box histidine kinase
6306	homocysteine S-methyltransferase (metH)
6310	glycerol dehydrogenase
6312	DNA topology modulation protein FlaR
6316	translation initiation factor IF-1 (infA)
6320	adenylate kinase (adk)
6326	ribosomal protein L15 (rplO)
6330	ribosomal protein L30 (rpmD)
6336	ribosomal protein S5 (rpsE)
6344	ribosomal protein L6 (rplF)
6348	ribosomal protein S8 (rpsH)
6352	ribosomal protein S14 (rpsN)
6356	ribosomal protein L5 (rplE)
6360	ribosomal protein L24 (rplX)
6366	ribosomal protein L14 (rplN)
6368	ribosomal protein S17 (rpsQ)
6372	ribosomal protein L29 (rpmC)
6374	ribosomal protein L16 (rplP)
6378	ribosomal protein S3 (rpsC)
6382	ribosomal protein L22 (rplV)
6386	ribosomal protein S19 (rpsS)
6390	ribosomal protein L2 (rplB)
6394	ribosomal protein L23 (rplW)
6398	ribosomal protein L4/L1 family (rplD)
6402	ribosomal protein L3 (rplC)
6408	ribosomal protein S10 (rpsJ)
6414	MATE efflux family protein
6418	threonine synthase (thrC)
6428	Uncharacterized BCR, COG1636 superfamily
6436	4-alpha-glucanotransferase (malQ)
6440	glycogen phosphorylase family protein (malP)
6444	glycerol-3-phosphate transporter (glpT)
6452	rhodanese family protein
6458	ammonium transporter
6464	DNA repair protein RadA (radA)
6472	oxidoreductase, pyridine nucleotide-disulfide, class I
6478	ribose ABC transporter, periplasmic D-ribose-binding protein (rbsB)
6484	ribose ABC transporter, ATP-binding protein (rbsA)
6486	ribose ABC transporter protein (rbsD)
6488	ribokinase (rbsK)

6498	ABC transporter, ATP-binding protein
6502	DNA-binding response regulator (vicR)
6506	argininosuccinate synthase (argG)
6508	argininosuccinate lyase (argH)
6514	bacteriophage L54a, repressor protein
6528	soluble transducer HtrXIII
6542	probable transposase (insertion sequence IS861)
6544	ABC transporter, ATP-binding/permease protein
6550	ABC transporter, ATP-binding/permease protein
6560	Serine hydroxymethyltransferase
6568	HemK protein (hemK)
6572	peptide chain release factor 1 (prfA)
6576	thymidine kinases
6580	4-oxalocrotonate tautomerase (dmpI)
6588	oxidoreductase
6594	oxidoreductase
6600	formate/nitrite transporter family protein
6608	xanthine permease (pbuX)
6612	xanthine phosphoribosyltransferase (xpt)
6616	guanosine monophosphate reductase (guaC)
6620	drug resistance transporter, EmrB/QacA subfamily
6622	oxidoreductase
6624	Kup system potassium uptake protein (kup)
6636	O-methyltransferase
6642	oligoendopeptidase F (pepF)
6646	competence protein CoiA (coiA)
6650	major facilitator superfamily protein superfamily
6652	ribosomal small subunit pseudouridine synthase A (rsuA)
6658	glucosamine-6-phosphate isomerase (nagB)
6662	nodulin-related protein, truncation
6664	S-adenosylmethioninetRNA ribosyltransferase-isomerase (queA)
6674	permease, GntP family
6684	6-phospho-beta-glucosidase (bglA)
6686	PTS system, beta-glucosides-specific IIABC components
6688	transcription antiterminator LicT (licT)
6704	esterase
6706	sugar-binding transcriptional repressor, LacI family
6708	hydrolase, haloacid dehalogenase-like family
6712	DNA internalization-related competence protein ComEC/Rec2
6716	competence protein CelA (celA)
6720	acyltransferase family protein
6732	ATP-dependent RNA helicase DeaD (deaD)
6736	lipoprotein, YaeC family
6738	ABC transporter, permease protein
6752	diacylglycerol kinase (dgkA)
6768	formamidopyrimidine-DNA glycosylase (mutM)
6776	epidermin immunity protein F
6788	glycyl-tRNA synthetase, beta subunit (glyS)
6790	acyl carrier protein phosphodiesterase
6800	SsrA-binding protein (smpB)
6822	D-alanine--D-alanine ligase
6824	recombination protein RecR (recR)
6830	penicillin-binding protein 2b
6832	phosphoglycerate mutase (gpmA)
6836	triosephosphate isomerase (tpiA)
6856	phosphoglycerate mutase family protein
6860	D-alanyl-D-alanine carboxypeptidase family
6864	autolysin
6868	heat-inducible transcription repressor HrcA (hrcA)

6872	heat shock protein GrpE (grpE)
6876	chaperone protein dnak
6880	dnaJ protein (dnaJ)
6884	transcriptional regulator, gntR family domain protein
6888	tRNA pseudouridine synthase A (truA)
6892	phosphomethylpyrimidine kinase (thiD)
6910	galactose-6-phosphate isomerase, LacA subunit (lacA)
6922	tagatose 1,6-diphosphate aldolase (lacD)
6932	sugar ABC transporter, ATP-binding protein (msmK)
6936	glucan 1,6-alpha-glucosidase (dexB)
6940	UDP-glucose 4-epimerase (galE)
6942	response regulator (citB)
6950	citrate carrier protein (citS)
6954	malate oxidoreductase (tme)
6958	bacterocin transport accessory protein
6976	transposase family protein (orfA)
6980	pXO1-128
6986	adhesion lipoprotein (lmb)
6994	DNA-directed RNA polymerase, alpha subunit (rpoA)
6998	ribosomal protein L17 (rplQ)
7040	probable dna-directed rna polymerase delta subunit
7044	CTP synthase (pyrG)
7058	bacteriocin transport accessory protein
7074	translation initiation factor IF-3 (infC)
7100	adenosine deaminase
8468	preprotein translocase, SecE subunit
8476	antigen, 67 kDa
8486	Lipase/Acylhydrolase
8492	peptide ABC transporter, permease protein (oppB)
8494	competence protein CglB (cglB)
8502	peptide ABC transporter, peptide-binding protein
8504	oxidoreductase
8510	amino acid ABC transporter, permease protein (opuBB)
8522	abc transporter atp-binding protein ybhf
8530	glycerol-3-phosphate dehydrogenase (NAD(P)+) (gpsA)
8538	sugar ABC transporter, sugar-binding protein
8544	secreted 45 kd protein (usp45)
8556	phosphoglycerate mutase family protein
8566	glycosyl hydrolase, family 3
8576	N-acetylmuramoyl-L-alanine amidase
8596	sensory box histidine kinase (withHAMPandPASd)
8608	aminoglycoside 6-adenylyltransferase
8622	iron compound ABC transporter, permease protein (sirB)
8636	phosphate ABC transporter, permease protein (pstC-2)
8650	branched-chain amino acid transport system II carrier protein (brnQ)
8658	PTS system, IID component
8662	replisome organiser-related protein
8674	alkaline amylopullulanase
8676	exfoliative toxin A
8690	glycerol uptake facilitator protein (glpF)
8698	ABC transporter, ATP-binding protein
8706	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (pgs
8708	cobalt transport protein
8730	integral membrane protein
8734	yadS protein
8736	cell wall surface anchor family protein
8748	polysaccharide biosynthesis protein
8752	glycosyl transferase domain protein
8764	endopeptidase O

8770	beta-ketoacyl-acyl carrier protein synthase II
8772	ABC transporter, ATP-binding protein
8776	penicillin-binding protein
8778	cell wall surface anchor family protein
8780	cell wall surface anchor family protein
8786	LPXTG-motif cell wall anchor domain protein
8788	6-aminohexanoate-cyclic-dimer hydrolase
8796	NLP/P60 family protein
8802	DNA/RNA non-specific endonuclease
8806	hydroxyethylthiazole kinase (thiM)
8826	PTS system component
8832	sugar ABC transporter, permease protein
8836	potassium uptake protein, Trk family (trkA)
8850	lemA protein (lemA)
8856	cobalt transport protein
8882	spermidine/putrescine ABC transporter, spermidine/putrescine-binding pr
8884	spermidine/putrescine ABC transporter, permease protein (potC)
8906	ABC transporter, substrate-binding protein
8908	lipoprotein
8916	sensor histidine kinase
8930	TrsK-like protein (traK)
8936	R5 protein
8962	chromosome assembly protein homolog
8978	ribose ABC transporter, permease protein (rbsC)
8980	permease
8982	sensor histidine kinase (arlS)
8986	hydrolase, haloacid dehalogenase-like family (gph)
8994	dephospho-CoA kinase
8996	oxalateformate antiporter
9004	sensory box protein
9006	host cell surface-exposed lipoprotein
9012	PAP2 family protein
9034	GtrA family protein
9050	lipoprotein signal peptidase (lspA)
9280	alcohol dehydrogenase, zinc-containing (adh)
9284	trigger factor (tig)
9290	fructose-bisphosphate aldolase (fba)
9292	DAK2 domain protein
9296	oligopeptide ABC transporter, permease protein
9298	N-acetylglucosamine-6-phosphate deacetylase (nagA)
9300	transcriptional regulator, DeoR family (lacR)
9302	PTS system, mannose-specific IIC component (manM)
9306	Phosphoglucose isomerase
9310	aspartate--ammonia ligase (asnA)
9312	amino acid ABC transporter, ATP-binding protein
9314	DNA-binding protein HU (hup)
9316	DHH subfamily 1 protein
9318	chloride channel
9320	integrase (int)
9324	DNA/RNA non-specific endonuclease
9326	PTS system component
9328	cell division protein, FtsW/RodA/SpoVE family (ftsW)
9330	LPXTG-motif cell wall anchor domain protein
9332	peptide chain release factor 3 (prfC)
9334	ABC transporter, ATP-binding protein
9336	superoxide dismutase [mn-fe]
9340	phenylalanyl-tRNA synthetase, alpha subunit (pheS)
9342	amino acid ABC transporter, permease protein
9344	phosphate ABC transporter, phosphate-binding protein (pstS)

9346	NOL1/NOP2/sun family protein (sun)
9348	Abortive infection protein family
9350	permease
9352	N-acetylmuramoyl-L-alanine amidase domain protein (usp45)
9354	ABC transporter, ATP-binding protein
9356	phosphoglucomutase (pgm)
9358	oxidoreductase, short chain dehydrogenase/reductase family
9360	phosphate acetyltransferase
9362	gls24 protein
9364	ribosomal protein S1 (rpsA)
9368	dTDP-glucose 4,6-dehydratase (rfbB)
9370	excinuclease ABC, C subunit (uvrC)
9372	MATE efflux family protein
9378	amino acid permease (rocE)
9380	DNA-binding response regulator TrcR (trcR)
9382	16S rRNA processing protein RimM (rimM)
9384	transcriptional regulator
9388	ribosomal protein L20 (rplT)
9394	sugar-binding transcriptional repressor, LacI family (malR)
9396	proton/peptide symporter family protein
9398	amino acid permease
9400	exoribonuclease, VacB/Rnb family (vacB)
9402	multi-drug resistance efflux pump (pmrA)
9404	adhesion lipoprotein (psaA)
9406	iron-dependent transcriptional regulator (sirR)
9410	branched-chain amino acid ABC transporter, amino acid-binding protein (
9412	amino acid permease
9414	SpoU rRNA Methylase family protein
9416	sodium/dicarboxylate symporter (gltP-2)
9418	branched-chain amino acid transport system II carrier protein (brnQ)
9420	alcohol dehydrogenase, zinc-containing
9422	aminotransferase, class I (aspB)
9424	ribosomal protein S6 (rpsF)
9426	A/G-specific adenine glycosylase (mutY)
9428	acid phosphatase (olpA)
9430	ribosomal protein S12 (rpsL)
9434	microcin immunity protein MccF (mccF-1)
9436	undecaprenyl diphosphate synthase (uppS)
9438	preprotein translocase, YajC subunit (yajC)
9440	chaperonin, 10 kDa (groES)
9444	YitT family protein
9446	serine protease (htrA)
9448	ribose-phosphate pyrophosphokinase (prsA)
9450	aromatic amino acid aminotransferase (araT)
9452	Recombination protein O (recO)
9454	Abortive infection protein family
9456	fatty acid/phospholipid synthesis protein PlsX (plsX)
9458	acyl carrier protein (acpP)
9462	phosphoribosylaminoimidazole carboxylase, ATPase subunit (purK)
9464	alcohol dehydrogenase, iron-containing
9466	ribosomal protein L18 (rplR)
9468	preprotein translocase, SecY subunit
9470	transcriptional regulator ComX1 (comX1)
9472	deoxyuridine 5`-triphosphate nucleotidohydrolase (dut)
9478	sugar-binding transcriptional regulator, LacI family (rbsR)
9480	SPFH domain/Band 7 family
9488	zinc ABC transporter, permease protein (adcB)
9492	abortive infection protein
9494	hydrolase, haloacid dehalogenase-like family

9496	response regulator (lytT)
9500	transketolase, C-terminal subunit
9502	polyribonucleotide nucleotidyltransferase (pnp)
9504	serine O-acetyltransferase (cysE)
9508	ribosomal protein L13 (rplM)
9510	replication initiation protein
9518	amino acid ABC transporter, amino acid-binding protein
9522	glycyl-tRNA synthetase, alpha subunit (glyQ)
9524	NADH oxidase
9528	transketolase (tkt)
9534	penicillin-binding protein 1A (pbp1A)
9536	cell division protein DivIVA (divIVA)
9538	sensor histidine kinase
9540	serine/threonine protein kinase (pknB)
9542	transcriptional regulator
9544	PTS system, IIA component (lacF)
9546	glycerol dehydrogenase (gldA)
9548	aspartate kinase (thrA)
9550	enoyl-CoA hydratase/isomerase family protein
9552	acyl carrier protein (acpP)
9564	ABC transporter, ATP-binding protein
9566	N utilization substance protein A (nusA)
9568	ribosome-binding factor A (rbfA)
9570	Cof family protein
9572	CoA binding domain protein (b0965)
9574	transcriptional regulator, Fur family
9578	queuine tRNA-ribosyltransferase (tgt)
9580	ribonuclease P protein component (rnpA)
9582	serine protease, subtilase family
9584	glycosyl transferase domain protein
9586	transcriptional activator, AraC family
9588	transcriptional regulator, TetR family
9590	transcriptional regulator, AraC family
9594	surface protein Rib
9596	transposase, mutator family
9600	acetyltransferase, GNAT family
9602	Transposase, Mutator family
9606	UDP-sugar hydrolase
9610	anthranilate synthase component II (trpG)
9612	biotin synthetase (bioB)
9616	UDP-N-acetylmuramoylalanine--D-glutamate ligase (murD)
9618	ylmF protein (ylmF)
9620	amino acid ABC transporter, permease protein
9622	phosphoglucomutase (pgm)
9624	YjeF-related protein, C-terminus
9626	FemAB family protein (fibA)
9628	Cof family protein
9630	cell division ABC transporter, permease protein FtsX (ftsX)
9632	oxidoreductase, short-chain dehydrogenase/reductase family (fabG)
9634	aspartate aminotransferase (aspC)
9638	ribosomal protein L31 (rpmE)
9640	nrdI protein (nrdI)
9642	ribosomal protein L19 (rplS)
9644	bacteriophage L54a, repressor protein
9646	bacteriophage L54a, antirepressor
9652	single-strand binding protein (ssb)
9660	pneumococcal surface protein A
9666	DNA-binding response regulator (vncR)
9668	transposase OrfAB, subunit B

9670	cell division protein, FtsW/RodA/SpoVE family (rodA)
9672	DNA gyrase, B subunit (gyrB)
9674	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)
9676	RNA methyltransferase, TrmA family
9680	transcriptional regulator, AraC family
9682	ABC transporter, ATP-binding protein
9690	CylJ
9696	permease
9698	regulatory protein
9700	carbohydrate kinase, pfkB family
9702	beta-glucuronidase
9704	2-deydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldo
9706	3-oxoacyl-(acyl-carrier-protein) reductase
9708	catabolite control protein A (ccpA)
9712	ribonuclease III (rnc)
9714	SMC family, C-terminal domain family
9718	S1 RNA binding domain protein
9722	prolipoprotein diacylglyceryl transferase (lgt)
9724	riboflavin synthase, alpha subunit (ribE)
9726	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II (ri
9728	lysyl-tRNA synthetase (lysS)
9734	Transposase subfamily
9738	translation elongation factor Tu (tuf)
9740	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-a
9746	Glutathione S-transferases domain protein
9754	Ribonucleotide reductases
9756	biotin--acetyl-CoA-carboxylase ligase
9760	Uncharacterized protein family SNZ family
9762	methionine aminopeptidase, type I (map)
9764	DNA ligase, NAD-dependent (ligA)
9766	glucose-1-phosphate adenylyltransferase (glgC)
9768	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (murA)
9770	acetyltransferase, GNAT family
9772	exonuclease RexA (rexA)
9774	tRNA modification GTPase TrmE (trmE)
9776	ABC transporter, ATP-binding protein
9778	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase al
9782	Mur ligase family protein
9786	HD domain protein
9788	translation elongation factor G (fusA)
9796	pyruvate kinase (pyk)
9798	Signal peptidase I
9802	cytidine deaminase (cdd)
9804	sugar ABC transporter, ATP-binding protein
9806	sugar ABC transporter, permease protein
9808	acetyltransferase, GNAT family
9810	ABC transporter, permease protein
9812	SatD
9814	Helix-turn-helix domain, fis-type protein
9816	phosphate ABC transporter, ATP-binding protein (pstB-1)
9818	tRNA pseudouridine synthase B (truB)
9820	Acetyltransferase (GNAT) family
9822	DNA topoisomerase I (topA)
9824	ribonuclease HII (rnhB)
9830	orotidine 5'-phosphate decarboxylase (pyrF)
9832	aspartate-semialdehyde dehydrogenase (asd)
9836	pantothenate metabolism flavoprotein (dfp)
9840	Sua5/YciO/YrdC/YwlC family protein
9844	thiamine biosynthesis protein ApbE

9846	Domain of unknown function
9848	DNA repair protein RadC (radC)
9850	glycosyl hydrolase, family 1 (bglA)
9852	Cof family protein (b0844)
9854	spermidine/putrescine ABC transporter, permease protein (potH)
9856	folylpolyglutamate synthase (folC)
9858	homoserine dehydrogenase (hom)
9860	succinate-semialdehyde dehydrogenase (gabD-1)
9862	membrane protein
9864	ATP-dependent DNA helicase PcrA (pcrA)
9866	uracil permease (uraA)
9868	sodiumalanine symporter family protein
9878	capsular polysaccharide biosynthesis protein Cps4B (cps4B)
9880	transcriptional regulator, LysR family
9882	CpslaS
9884	chloride channel protein
9886	tributyrin esterase (estA)
9888	ABC transporter, ATP-binding protein (potA)
9890	alpha-acetolactate decarboxylase (budA)
9892	TPR domain protein
9896	metallo-beta-lactamase superfamily protein
9898	tRNA delta(2)-isopentenylpyrophosphate transferase (miaA)
9902	glycerophosphoryl diester phosphodiesterase
9904	transposase OrfAB, subunit B
9906	IS3-Spn1, transposase
9908	transposase OrfAB, subunit B (orfB)
9910	reverse transcriptase
9916	transposase OrfAB, subunit B
9918	integrase, phage family (int)
9920	transcription regulator
9922	TnpA
9926	structural gene for ultraviolet resistance (uvra)
9930	Helicases conserved C-terminal domain protein
9932	abortive infection bacteriophage resistance protein (abiEi)
9944	ribosomal protein L7/L12 (rplL)
9948	ATP-dependent Clp protease, ATP-binding subunit ClpX (clpX)
9950	dihydrofolate reductase (folA)
9952	hemolysin
9954	transcriptional regulator, MarR family
9958	polyA polymerase family protein
9960	PTS system, fructose specific IIABC components (fruA-1)
9962	lactose phosphotransferase system repressor (lacR)
9964	choline binding protein D (cbpD)
9968	pyrimidine operon regulatory protein (pyrR)
9970	ribosomal large subunit pseudouridine synthase D (rluD)
9972	thiamine biosynthesis protein ThiI (thiI)
9974	3-dehydroquinate dehydratase, type I (aroD)
9976	iron compound ABC transporter, ATP-binding protein (fepC)
9980	transcriptional regulator
9982	glycosyl transferase domain protein
9984	Cps9H
9988	4-diphosphocytidyl-2C-methyl-D-erythritol synthase (ispD)
9990	licD1 protein (licD1)
9996	large conductance mechanosensitive channel protein (mscL)
10000	maltose ABC transporter, maltose-binding protein
10004	nucleotide sugar synthetase-like protein
10006	transcriptional regulator
10008	oxidoreductase, aldo/keto reductase family
10010	NAD(P)H-flavin oxidoreductase

10016	transcriptional regulator MutR
10018	GTP-binding protein Era (era)
10022	peptide methionine sulfoxide reductase (msrA)
10026	peptide ABC transporter, ATP-binding protein
10028	peptide ABC transporter, ATP-binding protein (amiE)
10030	peptide ABC transporter, peptide-binding protein
10032	transposase, IS30 family
10034	transcriptional regulator, LysR family
10036	spoE family protein (ftsK)
10044	methionyl-tRNA synthetase (metG)
10046	D-isomer specific 2-hydroxyacid dehydrogenase family protein (serA)
10048	acetyltransferase, GNAT family
10050	phosphoserine aminotransferase (serC)
10054	thymidylate kinase (tmk)
10060	branched-chain amino acid ABC transporter, permease protein (livH)
10062	ATP-dependent Clp protease, proteolytic subunit ClpP (clpP)
10064	uracil phosphoribosyltransferase (upp)
10066	potassium uptake protein, Trk family (trkH)
10068	glutamate racemase (murI)
10070	membrane protein
10072	HD domain protein
10074	Acylphosphatase
10076	spoIIIJ family protein
10078	acetyltransferase, GNAT family
10080	glucose-inhibited division protein B (gidB)
10082	potassium uptake protein, Trk family
10084	ABC transporter, permease protein
10088	isochorismatase family protein
10092	haloacid dehalogenase-like hydrolase superfamily
10094	membrane protein
10096	glutamyl-tRNA(Gln) amidotransferase, B subunit (gatB)
10098	CBS domain protein protein
10100	transcriptional regulator (codY)
10102	universal stress protein family
10104	L-asparaginase (ansA)
10106	oxidoreductase, aldo/keto reductase 2 family
10108	preprotein translocase, SecA subunit (secA)
10112	excinuclease ABC, A subunit (uvrA)
10114	magnesium transporter, CorA family (corA)
10116	thioredoxin (trx)
10118	MutS2 family protein (mutS2)
10122	DNA-damage inducible protein P (dinP)
10124	formate acetyltransferase (pfl)
10126	transcriptional regulator, Crp family
10128	transport ATP-binding protein CydC
10138	ribosomal-protein-alanine acetyltransferase (rimI)
10140	hydrolase
10144	D-alanine-activating enzyme (dltA)
10148	carbohydrate kinase, FGGY family
10150	transaldolase
10160	Helix-turn-helix domain protein
10164	single-strand binding protein (ssb)
10166	type II DNA modification methyltransferase Spn5252IP (spn5252IMP)
10174	integrase, phage family
10178	Cyclic nucleotide-binding domain protein
10180	transcriptional regulator, MarR family
10182	prolyl-tRNA synthetase (proS)
10184	leucine-rich protein
10186	lacX protein, truncation (lacX)

10188	tagatose-6-phosphate kinase (lacC)
10190	galactose-6-phosphate isomerase, LacB subunit (lacB)
10192	neuraminidase
10198	Histidine kinase-, DNA gyrase B-, phytochrome-like ATPase domain protei
10200	ABC transporter, ATP-binding protein
10202	PTS system, IIABC components (ptsG)
10204	phosphate regulon response regulator PhoB (phoB)
10212	Uncharacterized ACR, COG2161 subfamily
10216	abortive phage resistance protein
10222	TnpA
10226	acetyltransferase, GNAT family
10230	ABC transporter domain protein
10234	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (
10236	branched-chain amino acid transport protein AzlC (azlC)
10240	DNA-binding response regulator (srrA)
10242	leucyl-tRNA synthetase (leuS)
10246	NupC family protein
10248	transcriptional regulator, GntR family
10252	glyoxalase family protein
10254	anaerobic ribonucleoside-triphosphate reductase (nrdD)
10256	competence-induced protein Ccs4
10262	competence/damage-inducible protein CinA (cinA)
10264	DNA-3-methyladenine glycosylase I (tag)
10268	DNA mismatch repair protein HexB (hexB)
10270	arginine repressor (argR)
10272	arginyl-tRNA synthetase (argS)
10274	aspartyl-tRNA synthetase (aspS)
10276	histidyl-tRNA synthetase (hisS)
10280	AGR_pAT_51p
10286	hydrolase, alpha/beta hydrolase fold family
10288	phage infection protein
10290	Glucose inhibited division protein A (gidA)
10292	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (trmU)
10296	arginine/ornithine antiporter (arcD)
10298	chromosomal replication initiator protein DnaA (dnaA)
10302	peptidyl-tRNA hydrolase (pth)
10310	phosphotyrosine protein phosphatase
10316	ribosomal protein L36 (rpmJ)
10318	ribosomal protein S13/S18 (rpsM)
10328	L-lactate dehydrogenase (ldh)
10330	ribosomal protein L28 (rpmB)
10362	RNA polymerase sigma-70 factor, ECF subfamily
10384	BioY family protein
10386	AtsA/ElaC family protein
10388	cytidine/deoxycytidylate deaminase family protein
10394	phosphorylase, Pnp/Udp family
10396	transcriptional regulator, MerR family
10402	methyltransferase (ubiE)
10412	type IV prepilin peptidase
10416	ylmG protein (ylmG)
10444	transposase OrfAB, subunit B
10446	IS150-like transposase
10452	Bacterial regulatory proteins, tetR family domain protein
10454	cell wall surface anchor family protein, authentic frameshift (clfB)
10456	transposase OrfAB, subunit A (orfA)
10460	chaperonin, 33 kDa (hslO)
10472	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase (fabZ)
10482	sprT protein
10490	transcriptional regulator, MarR family

10498	transcriptional regulator
10504	glycogen biosynthesis protein GlgD (glgD)
10536	ribonucleoside-diphosphate reductase, alpha subunit, truncation (nrdD)
10538	LPXTG-motif cell wall anchor domain
10550	membrane protein
10554	arsenate reductase (arsC)
10564	transposase, authentic frameshift
10570	transposase OrfAB, subunit A (orfA)
10574	Tn5252, Orf 9 protein
10580	IS3-Spn1, transposase
10584	transcriptional regulator, ArsR family
10628	ribosomal protein L35 (rpmI)
10630	cytidylate kinase (cmk)
10636	MutT/nudix family protein
10644	preprotein translocase, SecG subunit
10680	ribosomal protein S18 (rpsR)
10682	single-strand binding protein (ssb)
10692	glyceraldehyde 3-phosphate dehydrogenase (gap)
10694	translation elongation factor G (fusA)
10696	ribosomal protein S7 (rpsG)
10704	phosphinothricin N-acetyltransferase (pat)
10730	nrdI protein (nrdI)
10732	accessory gene regulator protein C (blpH)
10744	rhodanese family protein (pspE)
10746	cAMP factor
10758	competence/damage-inducible protein CinA (cinA)
10770	transcriptional regulator, ArgR family (argR)
10772	FliP family family
10794	peptide ABC transporter, peptide-binding protein
10800	ribosomal protein S21 (rpsU)
10802	transposase, IS30 family
10816	mucin 2 precursor, intestinal
10854	SV40-transformed marker protein pG1-related protein
10856	SV40-transformed marker protein pG1-related protein
10858	SV40-transformed marker protein pG1-related protein
10860	SV40-transformed marker protein pG1-related protein
10862	SV40-transformed marker protein pG1-related protein
10864	SV40-transformed marker protein pG1-related protein
10866	SV40-transformed marker protein pG1-related protein
10910	transcriptional regulator
10920	ribosomal protein S11 (rpsK)
10922	elaA protein
10926	5-formyltetrahydrofolate cyclo-ligase family protein
10938	inositol monophosphatase family protein
10940	amino acid ABC transporter, amino acid-binding protein (artI)
10944	Holliday junction DNA helicase RuvB (ruvB)
10946	D-alanyl-D-alanine carboxypeptidase (dacA)
10948	lipoprotein (bmpD)
10950	peptidase, U32 family family
10952	protease maturation protein
10954	glutamyl-tRNA synthetase (gltX)
10956	GTP-binding protein LepA (lepA)
10960	translation initiation factor if-2
10962	phosphoenolpyruvate carboxylase (ppc)
10964	calcium E1-E2-type ATPase
10966	serine protease, subtilase family

CLAIMS

1. A protein comprising an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1014, 1016, 1018, 1020, 1022, 1024, 1026, 1028, 1030, 1032, 1034, 1036, 1038, 1040, 1042, 1044, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1068, 1070, 1072, 1074, 1076, 1078, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1134, 1136, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408, 1410, 1412, 1414, 1416, 1418, 1420, 1422, 1424, 1426, 1428, 1430, 1432, 1434, 1436, 1438, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1454, 1456, 1458, 1460, 1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490, 1492, 1494, 1496, 1498, 1500, 1502, 1504, 1506, 1508, 1510, 1512, 1514, 1516, 1518, 1520, 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550, 1552, 1554, 1556, 1558, 1560, 1562, 1564, 1566, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1586, 1588, 1590, 1592, 1594, 1596, 1598, 1600, 1602, 1604, 1606, 1608, 1610, 1612, 1614, 1616, 1618, 1620, 1622, 1624, 1626, 1628, 1630, 1632, 1634, 1636, 1638, 1640, 1642, 1644, 1646, 1648, 1650, 1652, 1654, 1656, 1658, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1678, 1680, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1706, 1708, 1710, 1712, 1714, 1716, 1718, 1720,

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2. A protein having 50% or greater sequence identity to a protein according to claim 1.

3. A protein comprising a fragment of 7 or more consecutive amino acids from an amino acid sequence selected from the group consisting of SEQ IDs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1014, 1016, 1018, 1020, 1022, 1024, 1026, 1028, 1030, 1032, 1034, 1036, 1038, 1040, 1042, 1044, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1068, 1070, 1072, 1074, 1076, 1078, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1134, 1136, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408, 1410, 1412, 1414, 1416, 1418, 1420, 1422, 1424, 1426, 1428, 1430, 1432, 1434, 1436, 1438, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1454, 1456, 1458, 1460, 1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490, 1492, 1494, 1496, 1498, 1500, 1502, 1504, 1506, 1508, 1510, 1512, 1514, 1516, 1518, 1520, 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550, 1552, 1554, 1556, 1558, 1560, 1562, 1564, 1566, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1586, 1588, 1590,

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4. An antibody which binds to a protein according to any one of claims 1 to 3.

5. The antibody of claim 4, wherein said antibody is a monoclonal antibody, a chimeric antibody, a humanised antibody, or a fully human antibody.

6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.

7. A nucleic acid molecule according to claim 6, comprising a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, 687, 689, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729, 731, 733, 735, 737, 739, 741, 743, 745, 747, 749, 751, 753, 755, 757, 759, 761, 763, 765, 767, 769, 771, 773, 775, 777, 779, 781, 783, 785, 787, 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859, 861, 863, 865, 867, 869, 871, 873, 875, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 899, 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 965, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1015, 1017, 1019, 1021, 1023, 1025, 1027, 1029, 1031, 1033, 1035, 1037, 1039, 1041, 1043, 1045, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1069, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1115, 1117, 1119, 1121, 1123, 1125, 1127, 1129, 1131, 1133, 1135, 1137, 1139, 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1161, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1211, 1213, 1215, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329,

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8. A nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ IDs 10967, 10968, 10969, 10970, 10971, 10972, 10973, 10974, 10975, 10976, 10977, 10978, 10979, 10980, 10981, 10982, 10983, 10984, 10985, 10986, 10987, 10988, 10989, 10990, 10991, 10992, 10993, 10994, 10995, 10996, 10997, 10998, 10999, 11000, 11001, 11002, 11003, 11004, 11005, 11006, 11007, 11008, 11009, 11010, 11011, 11012, 11013, 11014, 11015, 11016, 11017, 11018, 11019, 11020, 11021, 11022, 11023, 11024, 11025, 11026, 11027, 11028, 11029, 11030, 11031, 11032, 11033, 11034, 11035, 11036, 11037, 11038, 11039, 11040, 11041, 11042, 11043, 11044, 11045, 11046, 11047, 11048, 11049, 11050, 11051, 11052, 11053, 11054, 11055, 11056, 11057, 11058, 11059, 11060, 11061, 11062, 11063, 11064, 11065, 11066, 11067, 11068, 11069, 11070, 11071, 11072, 11073, 11074, 11075, 11076, 11077, 11078, 11079, 11080, 11081, 11082, 11083, 11084, 11085, 11086, 11087, 11088, 11089, 11090, 11091, 11092, 11093, 11094, 11095, 11096, 11097, 11098, 11099, 11100, 11101, 11102, 11103, 11104, 11105, 11106, 11107, 11108, 11109, 11110, 11111, 11112, 11113, 11114, 11115, 11116, 11117, 11118, 11119, 11120, 11121, 11122, 11123, 11124, 11125, 11126, 11127, 11128, 11129, 11130, 11131, 11132, 11133, 11134, 11135, 11136, 11137, 11138, 11139, 11140, 11141, 11142, 11143, 11144, 11145, 11146, 11147, 11148, 11149, 11150, 11151, 11152, 11153, 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161, 11162, 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170, 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178, 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186, 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195, 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203, 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211, 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219, 11220, 11221, 11222, 11223, 11224, 11225, 11226, 11227, 11228, 11229, 11230, 11231, 11232, 11233, 11234, 11235, 11236, 11237, 11238, 11239, 11240, 11241, 11242, 11243, 11244, 11245, 11246, 11247, 11248, 11249, 11250, 11251, 11252, 11253, 11254, 11255, 11256, 11257, 11258, 11259, 11260, 11261, 11262, 11263, 11264, 11265, 11266, 11267, 11268, 11269, 11270, 11271, 11272, 11273, 11274, 11275, 11276, 11277, 11278, 11279, 11280, 11281, 11282, 11283, 11284, 11285, 11286, 11287, 11288, 11289, 11290, 11291, 11292, 11293, 11294, 11295, 11296, 11297, 11298, 11299, 11300, 11301, 11302, 11303, 11304, 11305, 11306, 11307, 11308, 11309, 11310, 11311, 11312, 11313, 11314, 11315, 11316, 11317, 11318, 11319, 11320, 11321, 11322, 11323, 11324, 11325, 11326, 11327, 11328, 11329, 11330, 11331, 11332, 11333, 11334, 11335, 11336, 11337, 11338, 11339, 11340, 11341, 11342, 11343, 11344, 11345, 11346, 11347, 11348, 11349, 11350, 11351, 11352, 11353, 11354, 11355, 11356, 11357, 11358, 11359, 11360, 11361, 11362, 11363, 11364, 11365, 11366, 11367, 11368, 11369, 11370, 11371, 11372, 11373, 11374, 11375, 11376, 11377, 11378, 11379, 11380, 11381, 11382, 11383, 11384,

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12009, 12010, 12011, 12012, 12013, 12014, 12015, 12016, 12017, 12018, 12019, 12020, 12021, 12022, 12023 and 12024.

9. A nucleic acid molecule comprising a fragment of 10 or more consecutive nucleotides from a nucleotide sequence selected from the group consisting of SEQ IDs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 675, 677, 679, 681, 683, 685, 687, 689, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729, 731, 733, 735, 737, 739, 741, 743, 745, 747, 749, 751, 753, 755, 757, 759, 761, 763, 765, 767, 769, 771, 773, 775, 777, 779, 781, 783, 785, 787, 789, 791, 793, 795, 797, 799, 801, 803, 805, 807, 809, 811, 813, 815, 817, 819, 821, 823, 825, 827, 829, 831, 833, 835, 837, 839, 841, 843, 845, 847, 849, 851, 853, 855, 857, 859, 861, 863, 865, 867, 869, 871, 873, 875, 877, 879, 881, 883, 885, 887, 889, 891, 893, 895, 897, 899, 901, 903, 905, 907, 909, 911, 913, 915, 917, 919, 921, 923, 925, 927, 929, 931, 933, 935, 937, 939, 941, 943, 945, 947, 949, 951, 953, 955, 957, 959, 961, 963, 965, 967, 969, 971, 973, 975, 977, 979, 981, 983, 985, 987, 989, 991, 993, 995, 997, 999, 1001, 1003, 1005, 1007, 1009, 1011, 1013, 1015, 1017, 1019, 1021, 1023, 1025, 1027, 1029, 1031, 1033, 1035, 1037, 1039, 1041, 1043, 1045, 1047, 1049, 1051, 1053, 1055, 1057, 1059, 1061, 1063, 1065, 1067, 1069, 1071, 1073, 1075, 1077, 1079, 1081, 1083, 1085, 1087, 1089, 1091, 1093, 1095, 1097, 1099, 1101, 1103, 1105, 1107, 1109, 1111, 1113, 1115, 1117, 1119, 1121, 1123, 1125, 1127, 1129, 1131, 1133, 1135, 1137, 1139, 1141, 1143, 1145, 1147, 1149, 1151, 1153, 1155, 1157, 1159, 1161, 1163, 1165, 1167, 1169, 1171, 1173, 1175, 1177, 1179, 1181, 1183, 1185, 1187, 1189, 1191, 1193, 1195, 1197, 1199, 1201, 1203, 1205, 1207, 1209, 1211, 1213, 1215, 1217, 1219, 1221, 1223, 1225, 1227, 1229, 1231, 1233, 1235, 1237, 1239, 1241, 1243, 1245, 1247, 1249, 1251, 1253, 1255, 1257, 1259, 1261, 1263, 1265, 1267, 1269, 1271, 1273, 1275, 1277, 1279, 1281, 1283, 1285, 1287, 1289, 1291, 1293, 1295, 1297, 1299, 1301, 1303, 1305, 1307, 1309, 1311, 1313, 1315, 1317, 1319, 1321, 1323, 1325, 1327, 1329, 1331, 1333, 1335, 1337, 1339, 1341, 1343, 1345, 1347, 1349, 1351, 1353, 1355, 1357, 1359, 1361, 1363, 1365, 1367, 1369, 1371, 1373, 1375, 1377, 1379, 1381, 1383, 1385, 1387, 1389, 1391, 1393, 1395, 1397, 1399, 1401, 1403, 1405, 1407, 1409, 1411, 1413, 1415, 1417, 1419, 1421, 1423, 1425, 1427, 1429, 1431, 1433, 1435, 1437, 1439, 1441, 1443, 1445, 1447, 1449, 1451, 1453, 1455, 1457, 1459, 1461, 1463, 1465, 1467, 1469, 1471, 1473, 1475, 1477, 1479, 1481, 1483, 1485, 1487, 1489, 1491, 1493, 1495, 1497, 1499, 1501, 1503, 1505, 1507, 1509, 1511, 1513, 1515, 1517, 1519, 1521, 1523, 1525, 1527, 1529, 1531, 1533, 1535, 1537, 1539, 1541, 1543, 1545, 1547, 1549, 1551, 1553, 1555, 1557, 1559, 1561, 1563, 1565, 1567, 1569, 1571, 1573, 1575, 1577, 1579, 1581, 1583, 1585, 1587, 1589, 1591, 1593, 1595, 1597, 1599, 1601, 1603, 1605, 1607, 1609, 1611, 1613, 1615, 1617, 1619, 1621, 1623,

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10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to any one of claims 6 to 9.

11. A nucleic acid molecule comprising a nucleotide sequences having 50% or greater sequence identity to a nucleic acid molecule according to any one of claims 6 to 10.

12. A nucleic acid molecule which can hybridise to a nucleic acid molecule according to any one of claims 6 to 11 under high stringency conditions.

13. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.

14. A composition according to claim 13, being an immunogenic composition, a vaccine composition or a diagnostic composition.

15. A composition according to claim 13 or claim 14 for use as a pharmaceutical.

16. The use of a composition according to claim 13 in the manufacture of a medicament for the treatment or prevention of infection or disease caused by streptococcus bacteria, particularly *S.agalactiae* and *S.pyogenes*.

17. A method of treating a patient, comprising administering to the patient a therapeutically effective amount of the composition of claim 13.

18. A hybrid protein represented by the formula NH_2-A-[-X-L-]$_n$-B-COOH, wherein X is an amino acid sequence as defined in claim 1, L is an optional linker amino acid sequence, A is an optional N-terminal amino acid sequence, B is an optional C-terminal amino acid sequence, and n is an integer greater than 1.

19. A kit comprising primers for amplifying a template sequence contained within a *Streptococcus* nucleic acid sequence, the kit comprising a first primer and a second primer, wherein the first primer is substantially complementary to said template sequence and the second primer is substantially complementary to a complement of said template sequence, wherein the parts of said primers which have substantial complementarity define the termini of the template sequence to be amplified.

20. A kit comprising first and second single-stranded oligonucleotides which allow amplification of a Streptococcus template nucleic acid sequence contained in a single- or double-stranded nucleic acid (or mixture thereof), wherein: (a) the first oligonucleotide comprises a primer sequence which is substantially complementary to said template nucleic acid sequence; (b) the second oligonucleotide comprises a primer sequence which is substantially complementary to the complement of said template nucleic acid sequence; (c) the first oligonucleotide and/or the second oligonucleotide comprise(s) sequence which is not compementary to said template nucleic acid; and (d) said primer sequences define the termini of the template sequence to be amplified.

21. The kit of claim 20, wherein the non-complementary sequence(s) of (c) comprise a restriction site and/or a promoter sequence.

22. A computer-readable medium containing one or more of SEQ IDs 1 to 12024.

23. A process for detecting Streptococcus in a biological sample, comprising the step of contacting nucleic acid according to any of claims 6 to 12 with the biological sample under hybridising conditions.

24. The process of claim 23, wherein the process involves nucleic acid amplification.

25. A process for determining whether a compound binds to a protein according to claim 1, claim 2 or claim 3, comprising the step of contacting a test compound with a protein according to claim 1, claim 2 or claim 3 and determining whether the test compound binds to said protein.

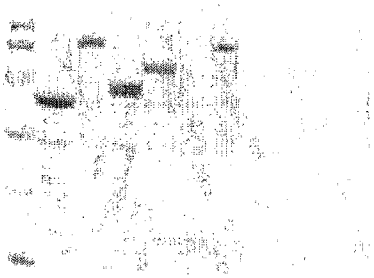
26. A compound identified by the process of claim 25.

27. A composition comprising a protein according to claim 1, claim 2 or claim 3 and one or more of the following antigens:

- a protein antigen from *Helicobacter pylori*;
- a protein antigen from *N.meningitidis* serogroup B;
- an outer-membrane vesicle (OMV) preparation from *N.meningitidis* serogroup B;
- a saccharide antigen from N.meningitidis serogroup A, C, W135 and/or Y;
- a saccharide antigen from *Streptococcus pneumoniae*;
- an antigen from hepatitis A virus;
- an antigen from hepatitis B virus;
- an antigen from hepatitis C virus;
- an antigen from *Bordetella pertussis*;
- a diphtheria antigen;
- a tetanus antigen;
- a saccharide antigen from *Haemophilus influenzae* B.
- an antigen from N.gonorrhoeae;
- an antigen from *Chlamydia pneumoniae*;
- an antigen from *Chlamydia trachomatis*;
- an antigen from *Porphyromonas gingivalis*;
- polio antigen(s);
- rabies antigen(s);
- measles, mumps and/or rubella antigens;
- influenza antigen(s);
- an antigen from *Moraxella catarrhalis*; and/or
- an antigen from *Staphylococcus aureus*.

28. A composition comprising two or more proteins, wherein each protein is a protein according to claim 1, claim 2 or claim 3.

FIGURE 1



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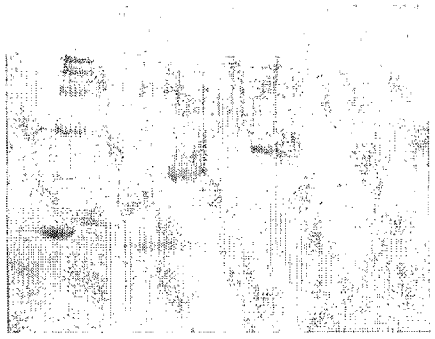

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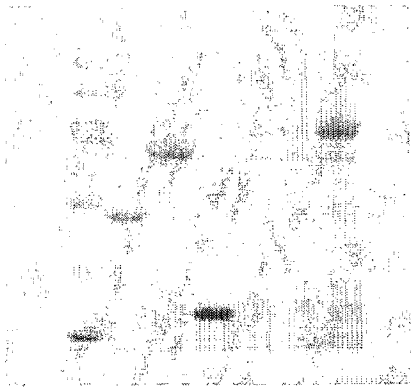

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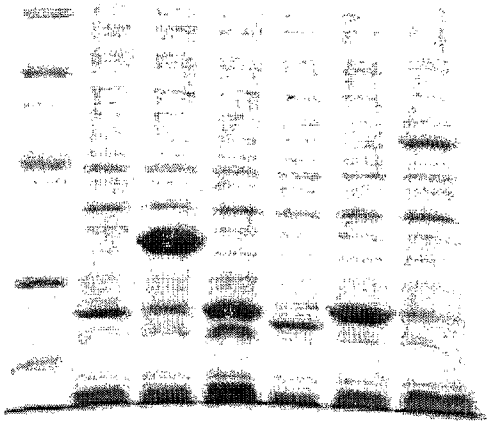

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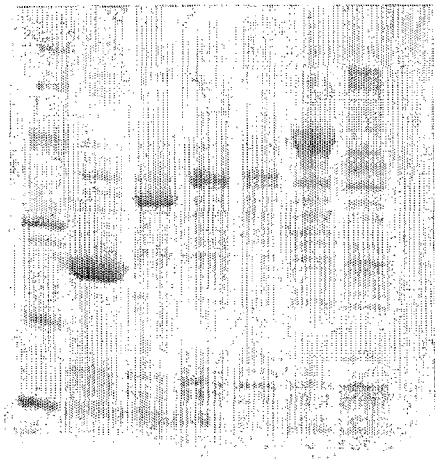

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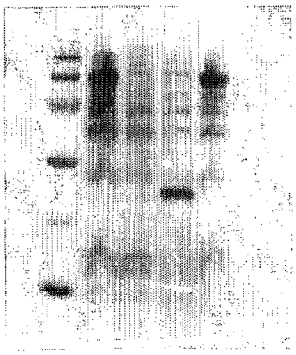

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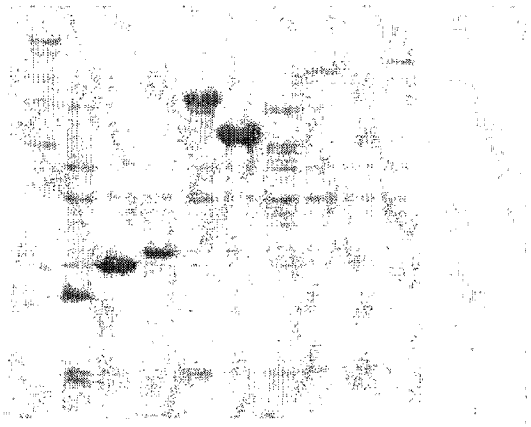
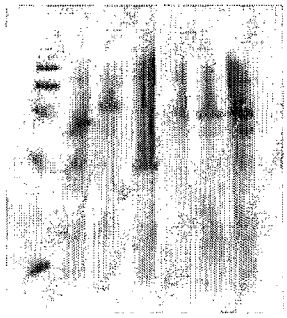


FIGURE 8

FIGURE 9



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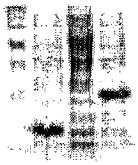

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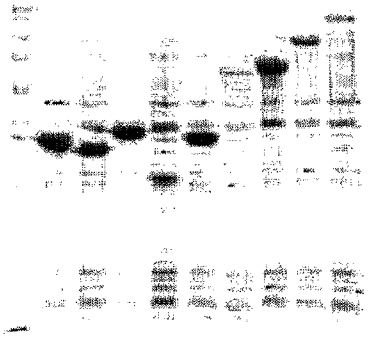

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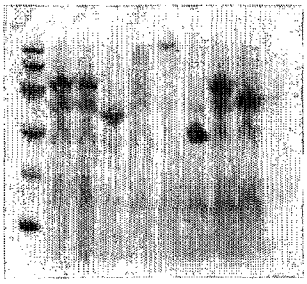

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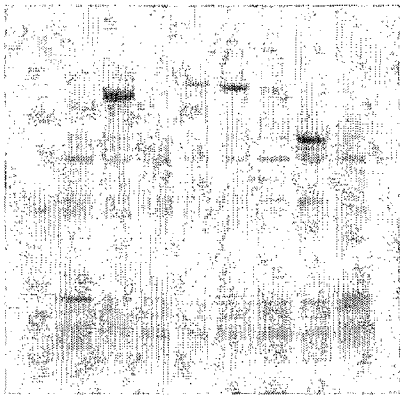

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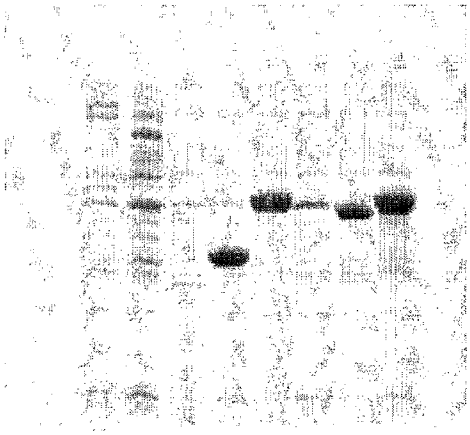

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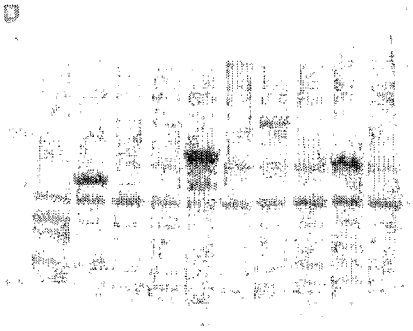

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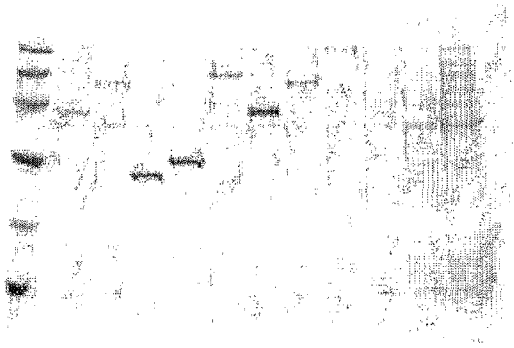

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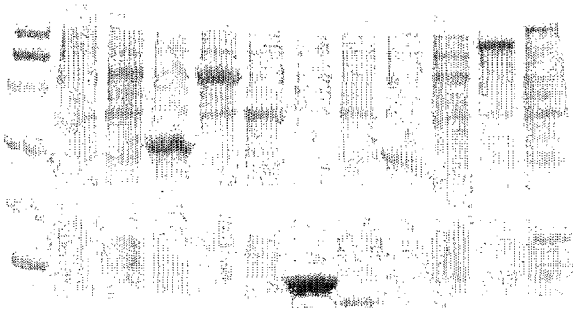

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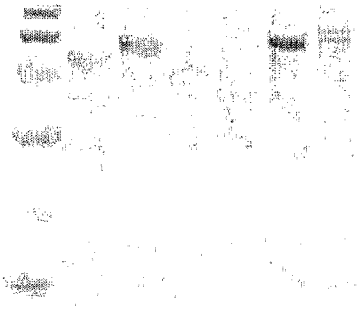

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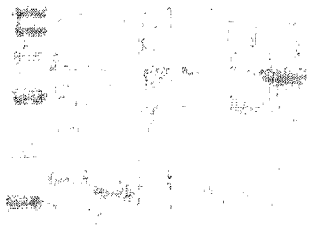

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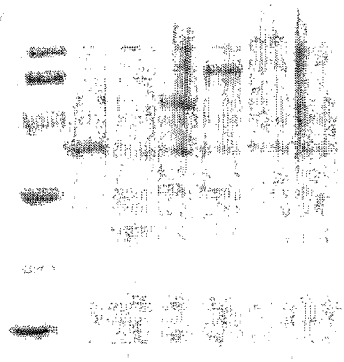

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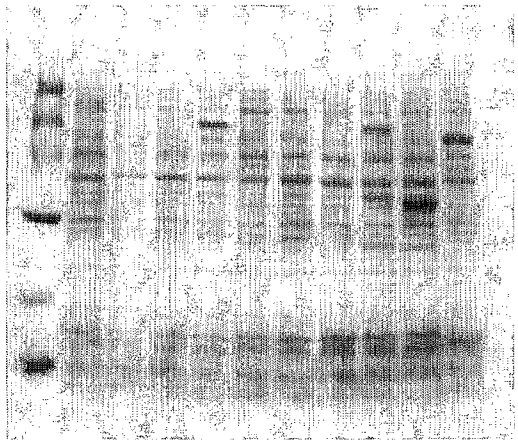

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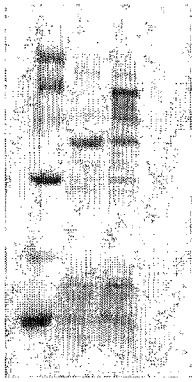

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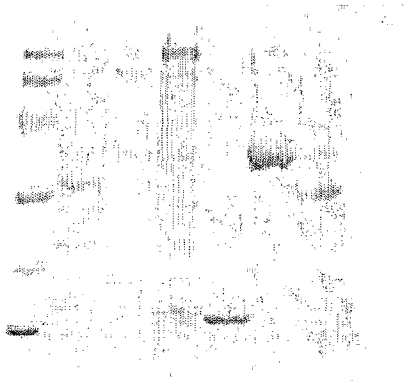

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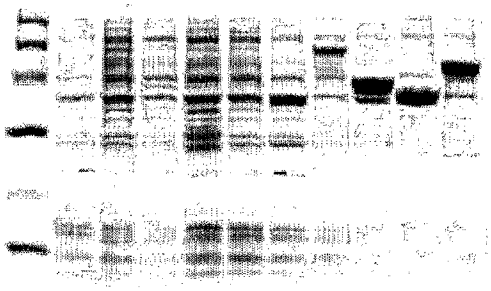

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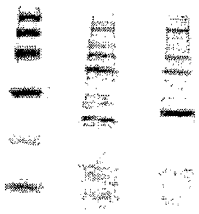

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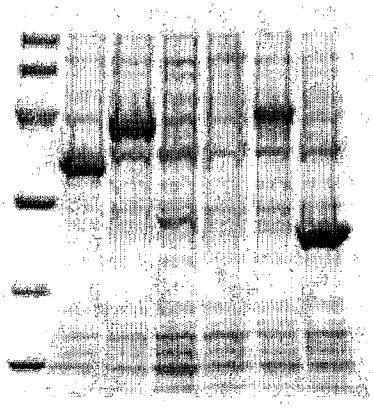

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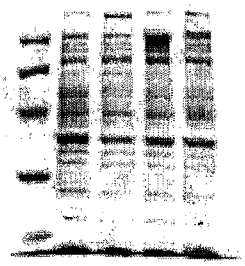

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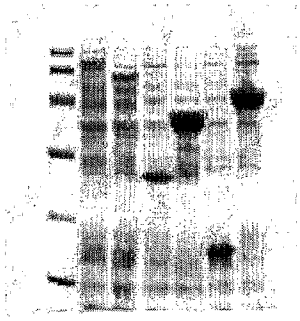

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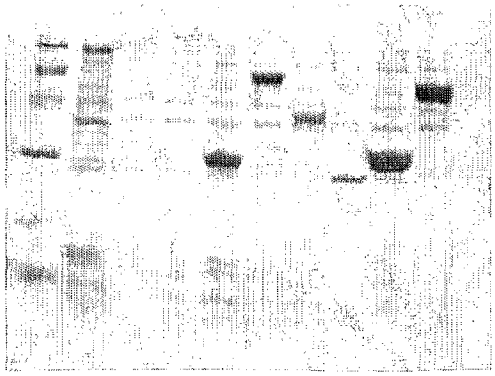

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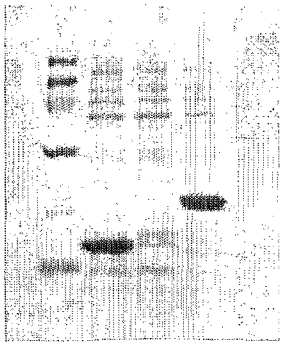

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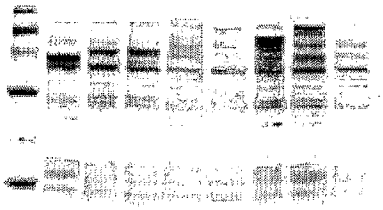

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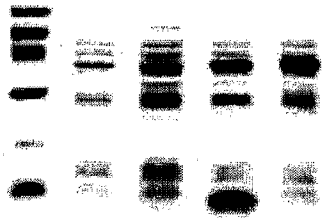

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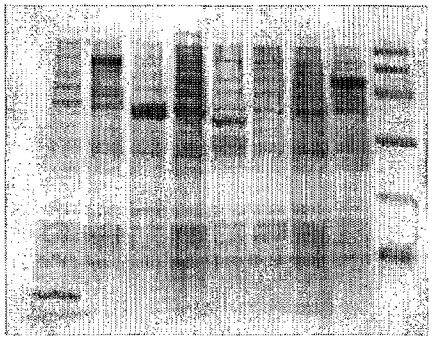

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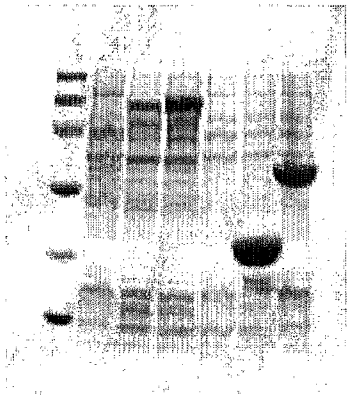

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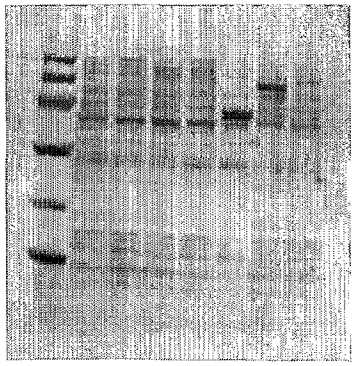

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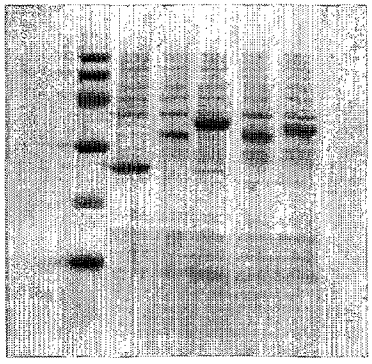

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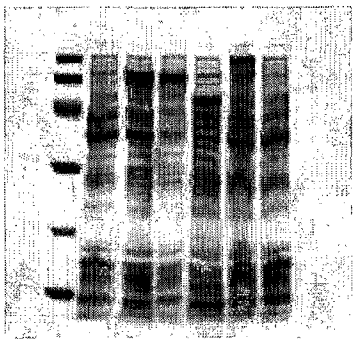

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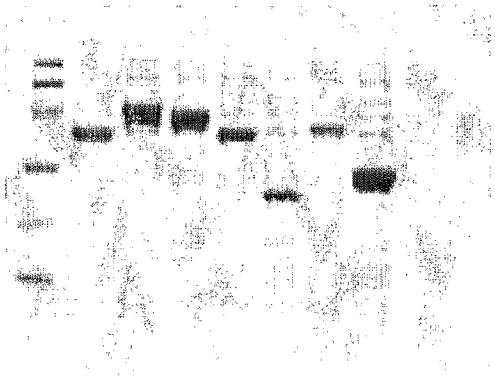

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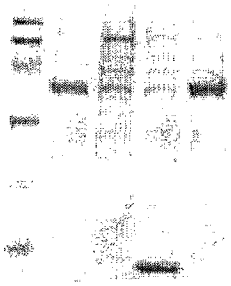

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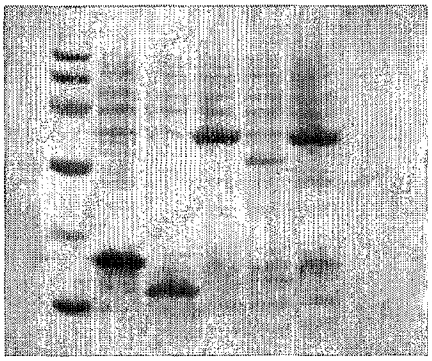

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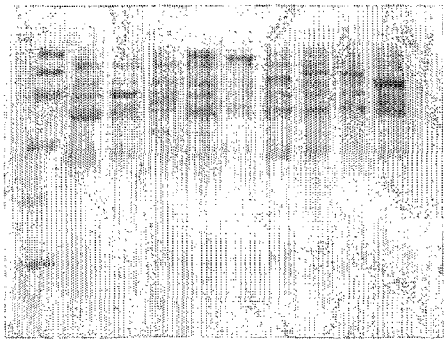
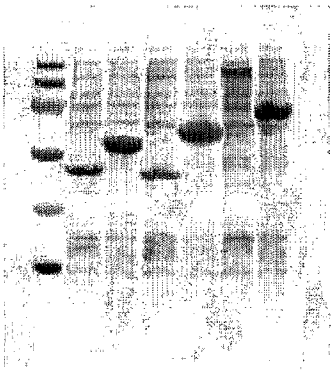


FIGURE 42

FIGURE 43



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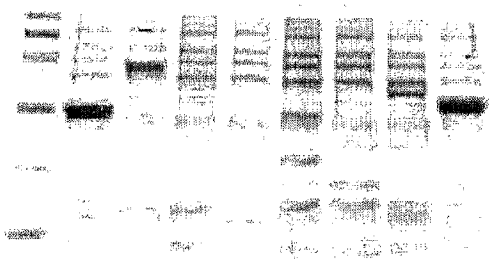

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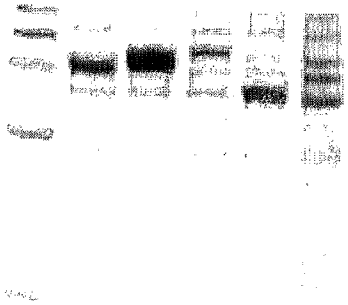

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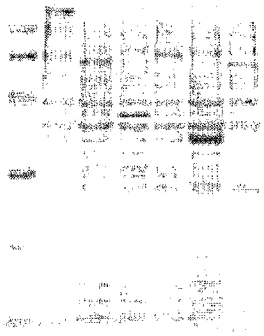

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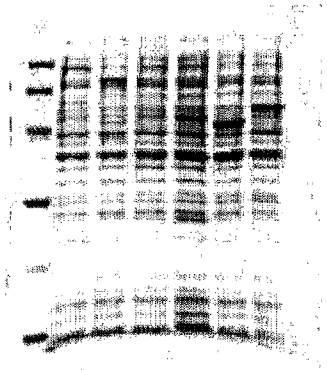

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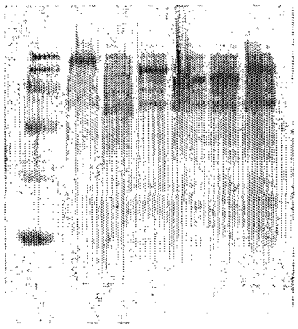

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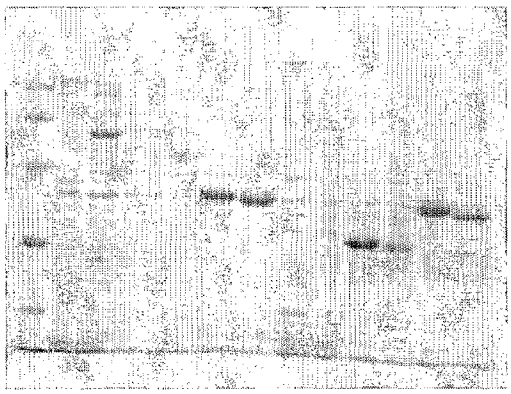

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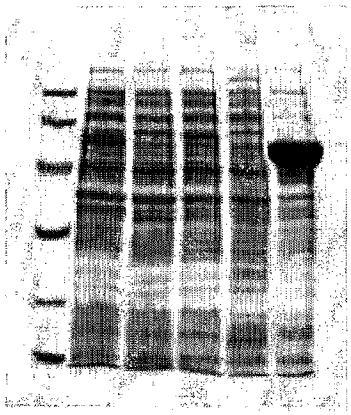

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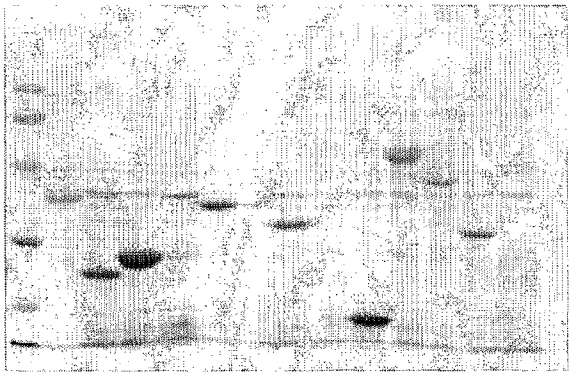

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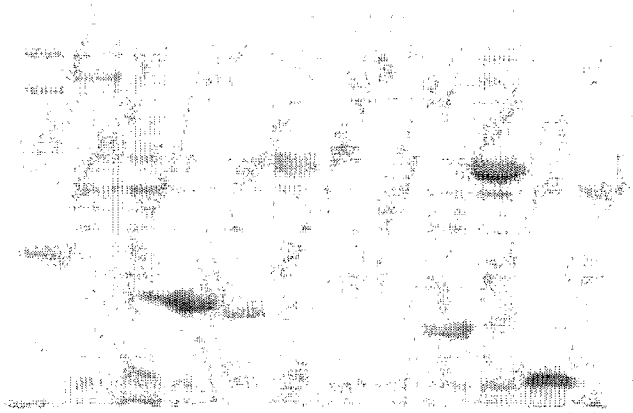
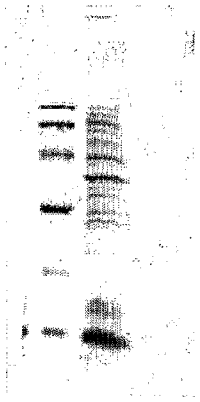


FIGURE 53



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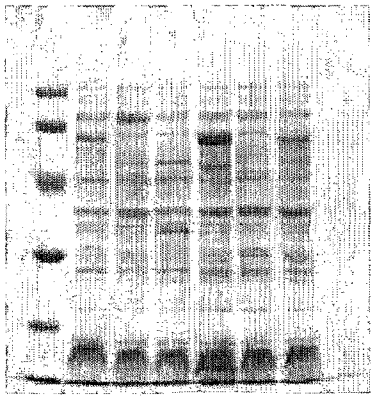

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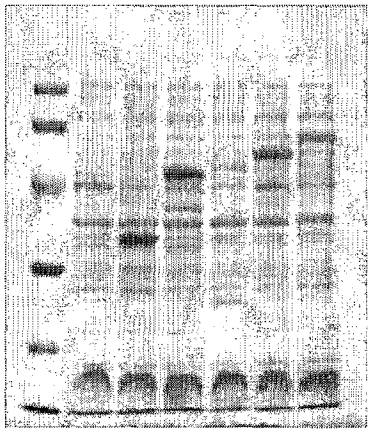

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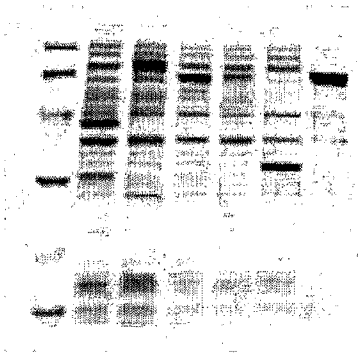

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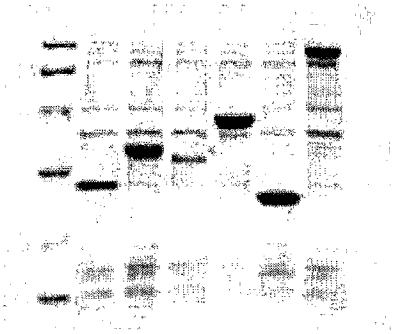

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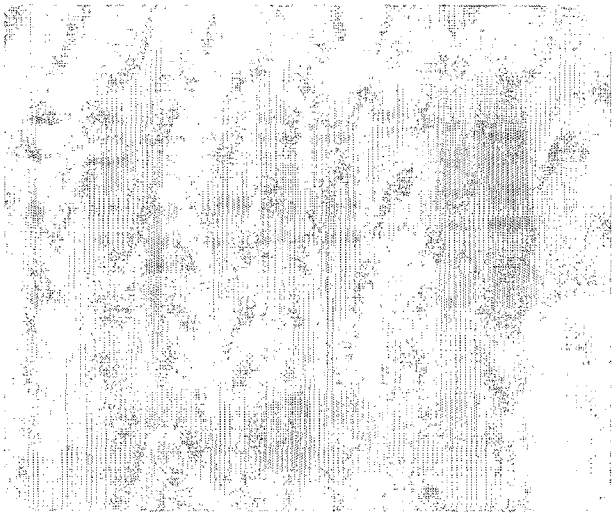

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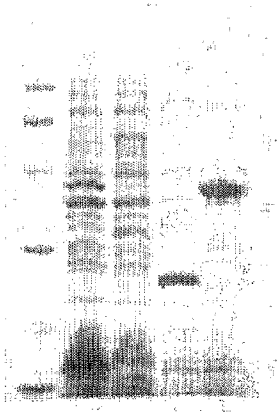

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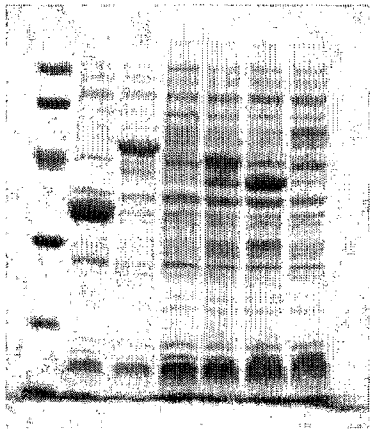

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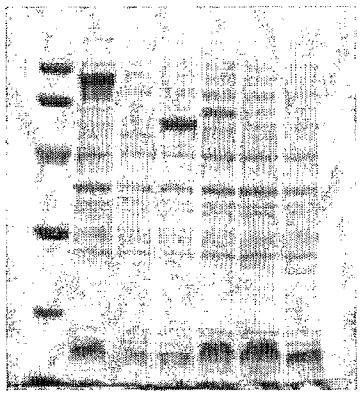

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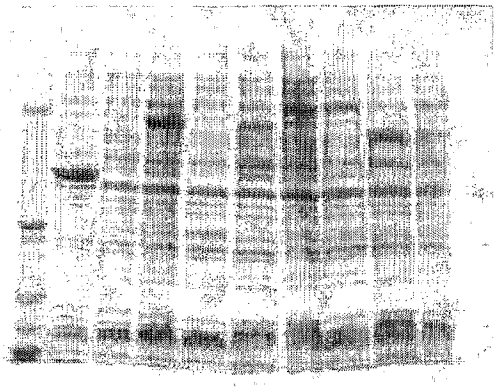

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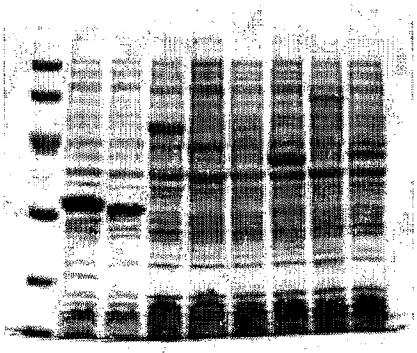

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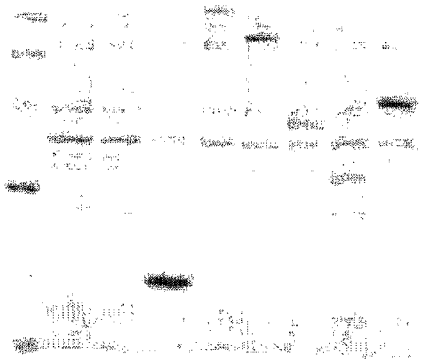

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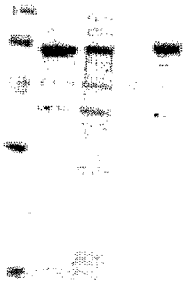

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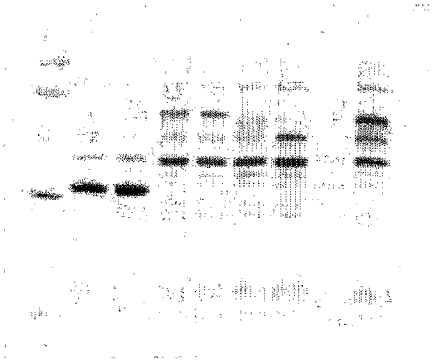

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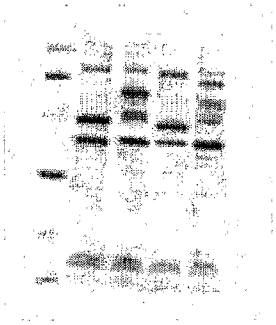

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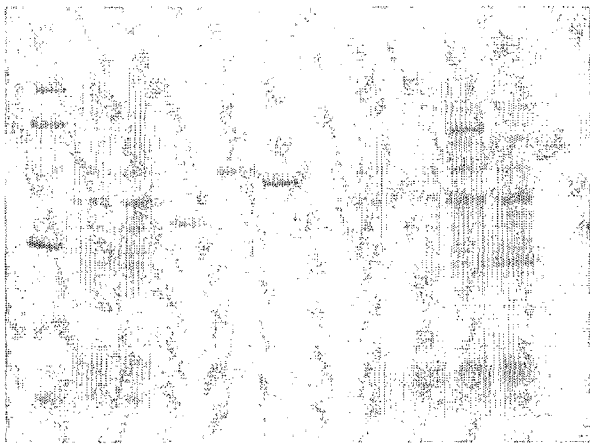

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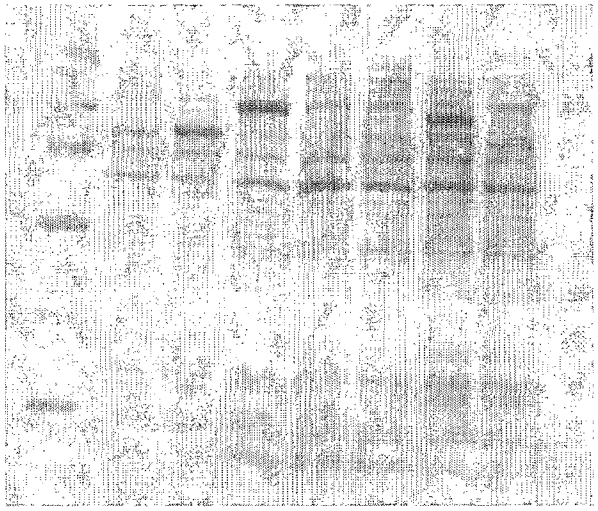

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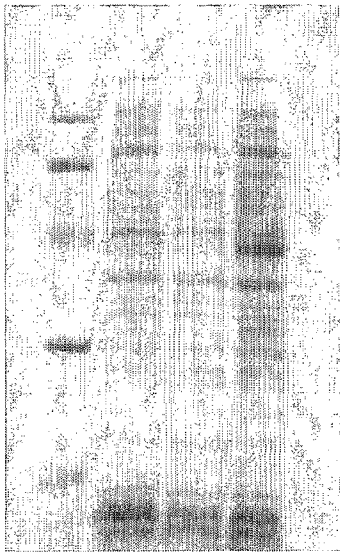

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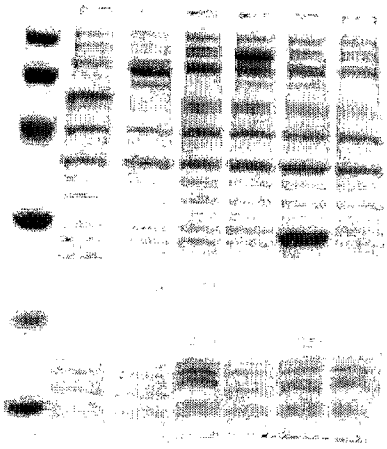

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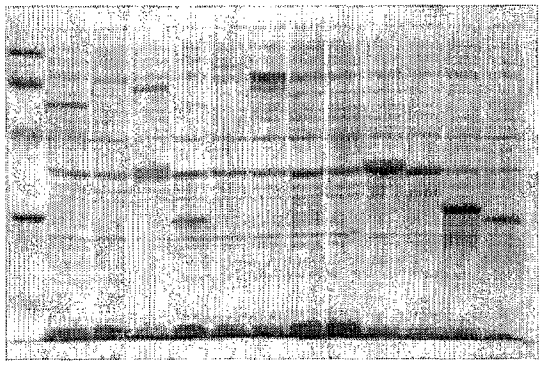

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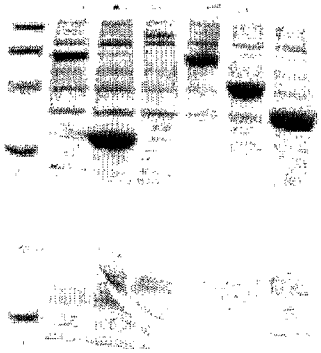

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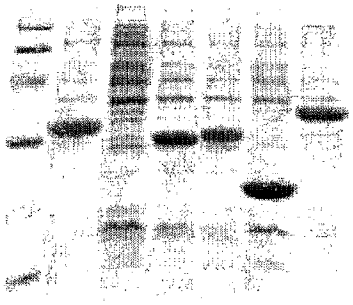

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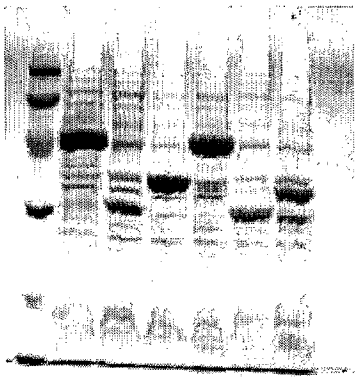

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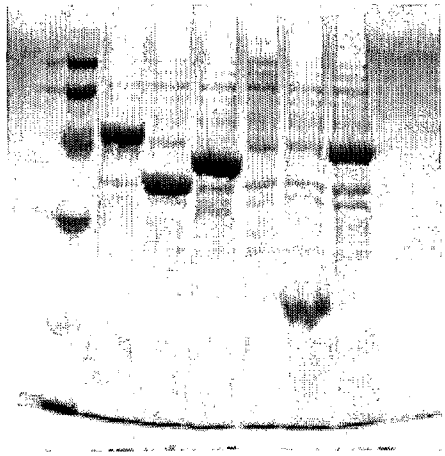

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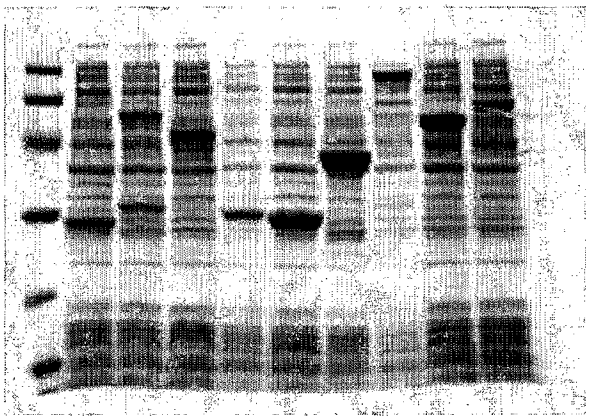

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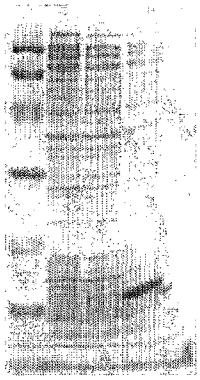

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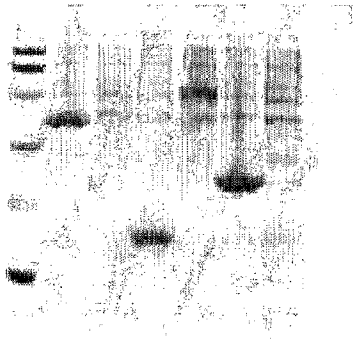

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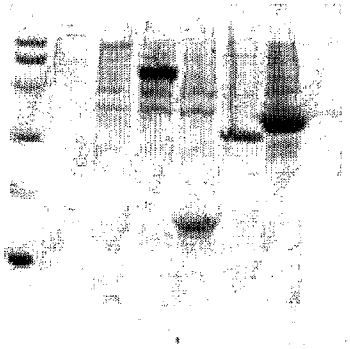

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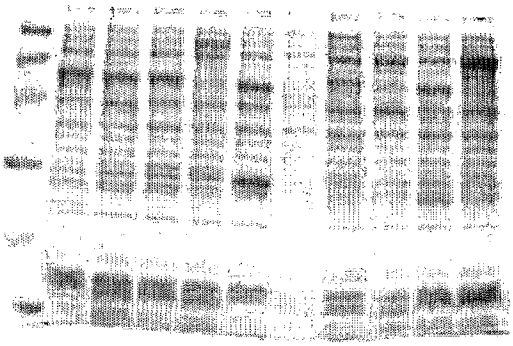

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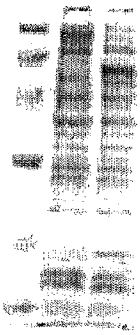

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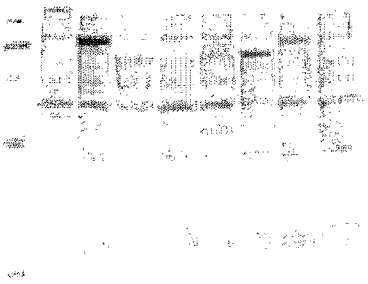

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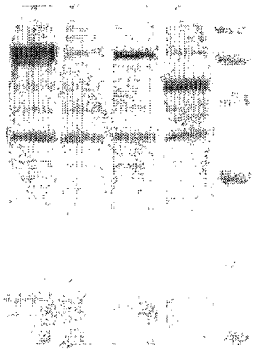

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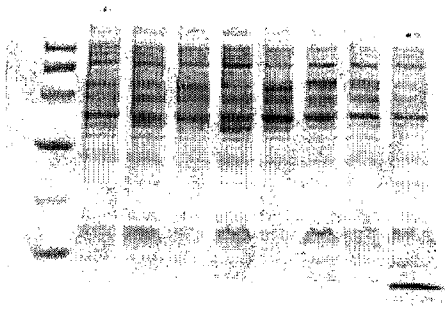

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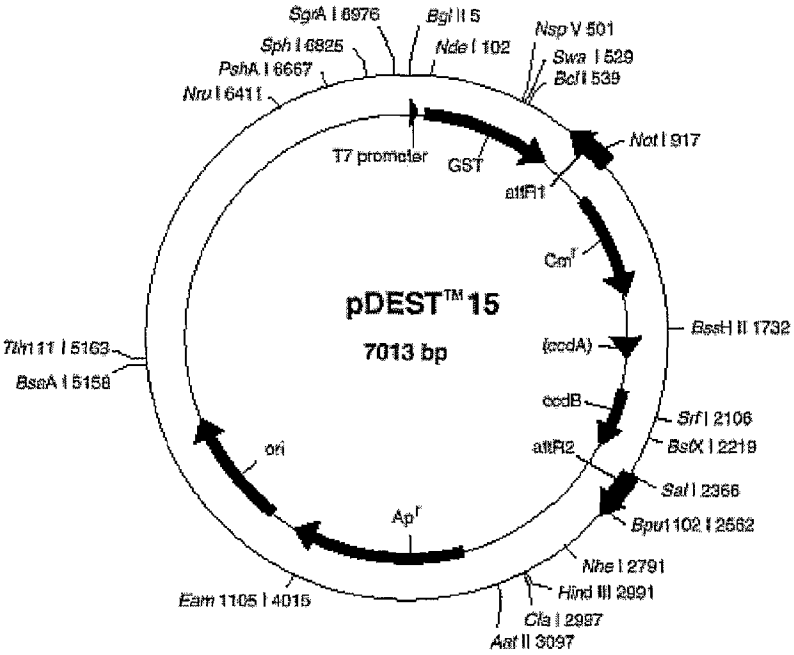

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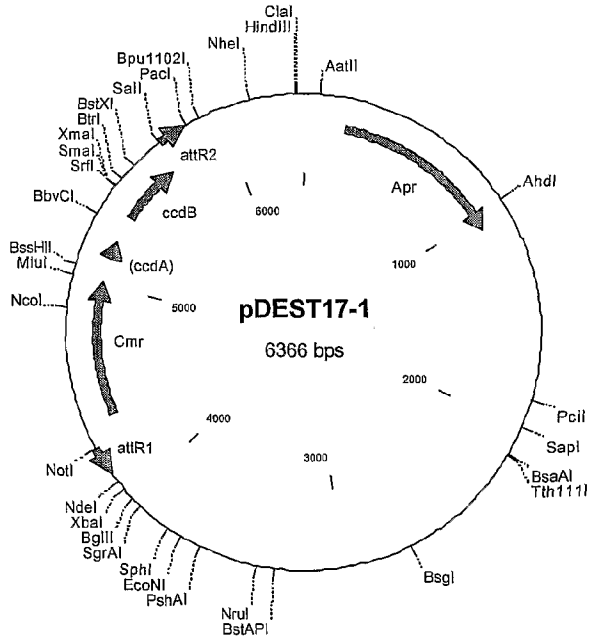


FIGURE 87

FIGURE 87A

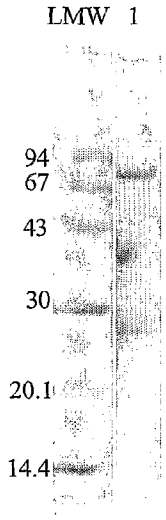


FIGURE 87B

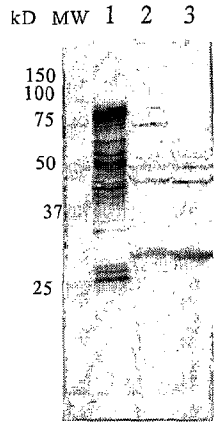
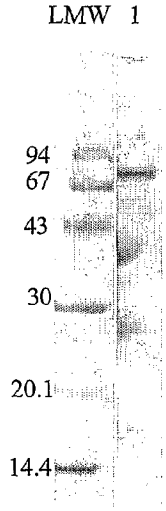


FIGURE 88

FIGURE 88A



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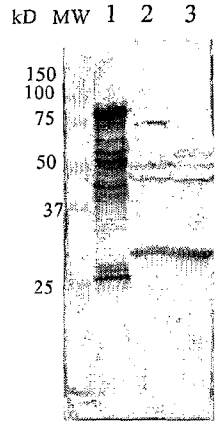


FIGURE 89

FIGURE 89A

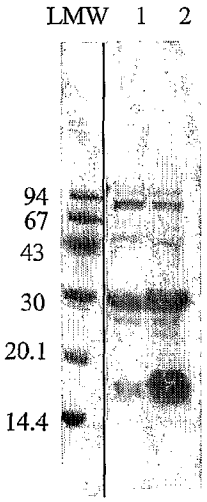


FIGURE 89B

FIGURE 90

FIGURE 90A

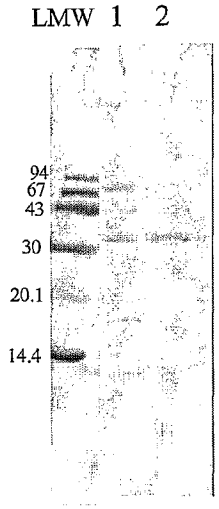


FIGURE 90B

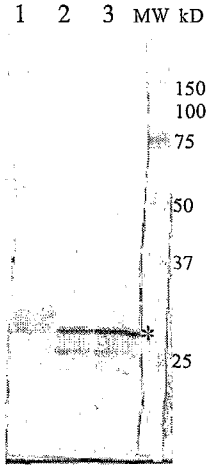


FIGURE 90C

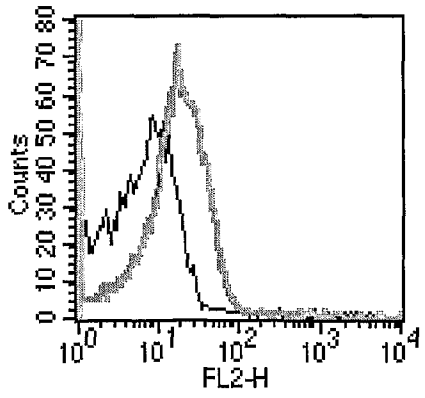
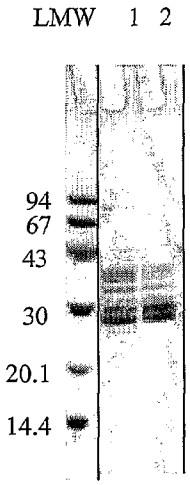


FIGURE 91

FIGURE 91A



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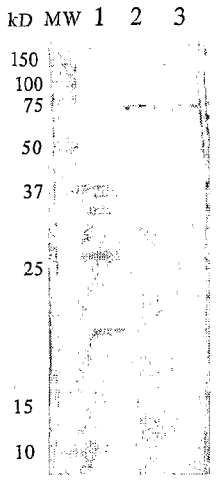


FIGURE 91C

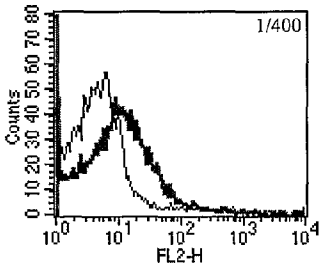


FIGURE 92

FIGURE 92A

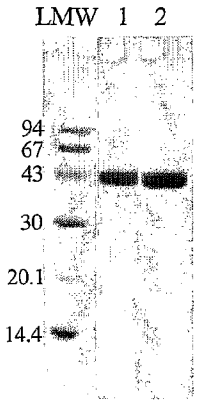


FIGURE 92B

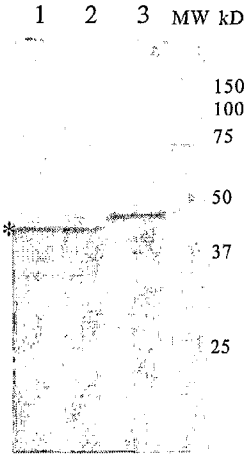


FIGURE 92C

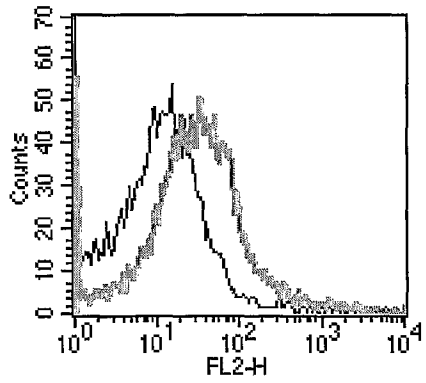


FIGURE 93

FIGURE 93A

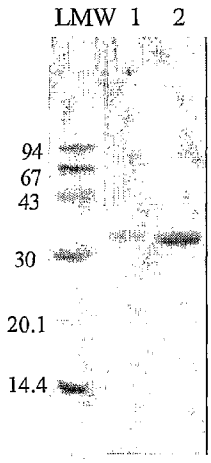


FIGURE 93B

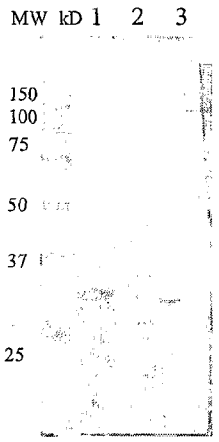


FIGURE 93C

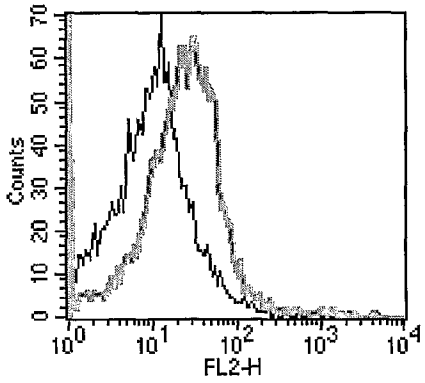


FIGURE 94

FIGURE 94A

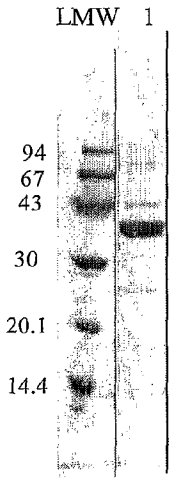
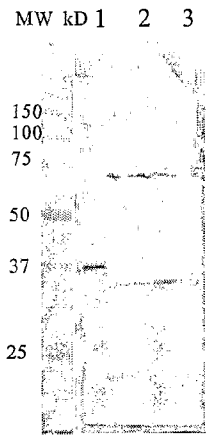


FIGURE 94B



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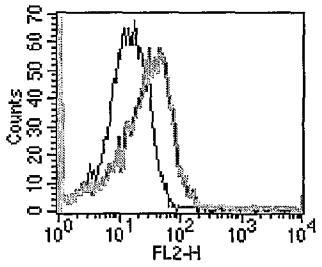


FIGURE 95

FIGURE 95A

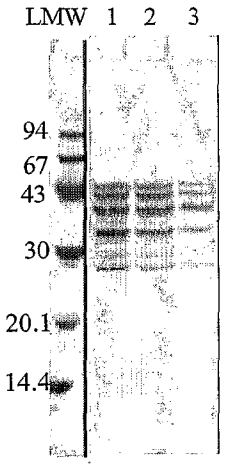


FIGURE 95B

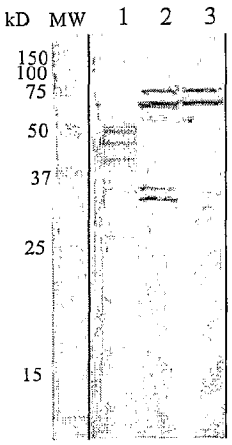


FIGURE 95C

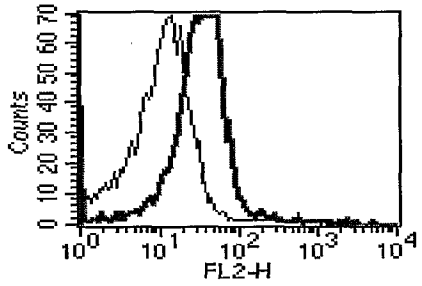


FIGURE 96

FIGURE 96A

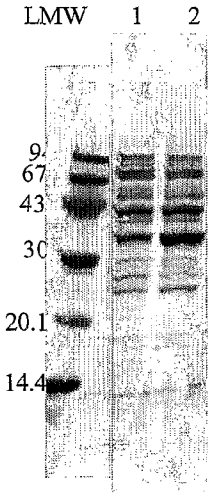


FIGURE 96B

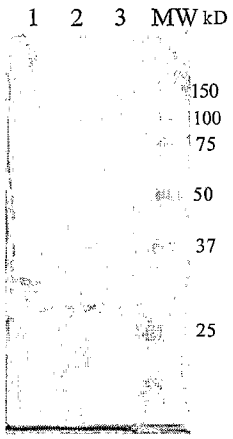


FIGURE 96C

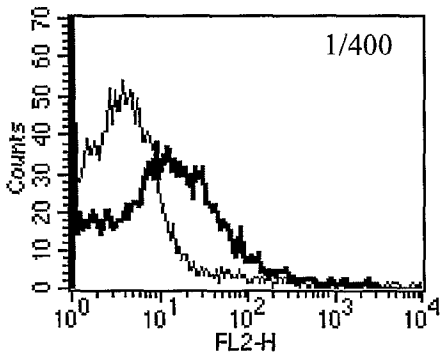


FIGURE 97

FIGURE 97A

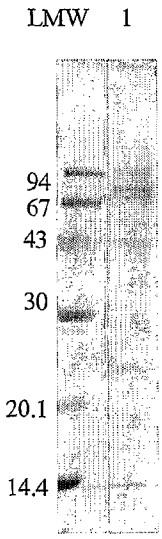
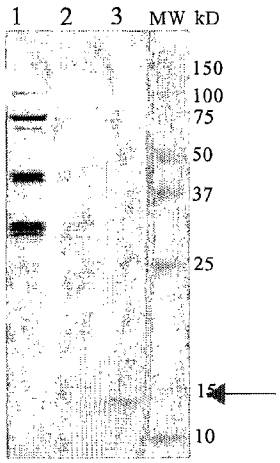


FIGURE 97B



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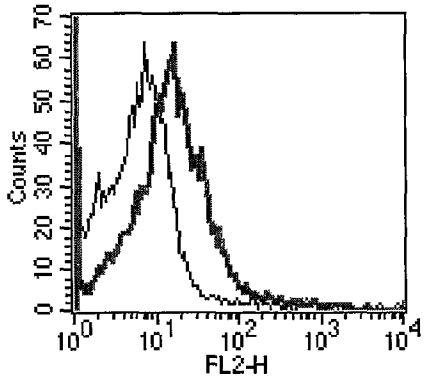
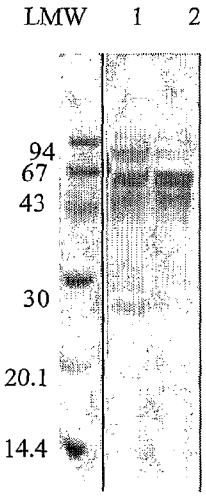


FIGURE 98

FIGURE 98A



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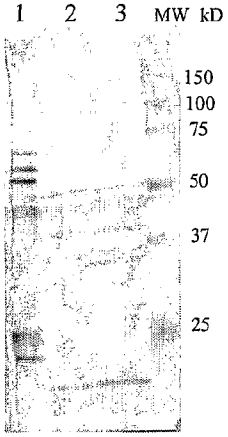


FIGURE 98C

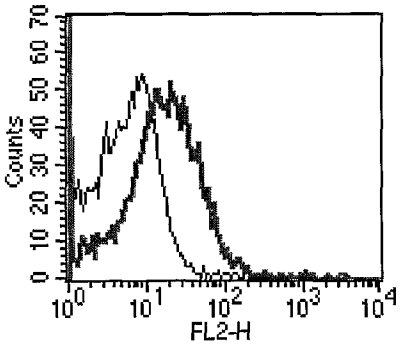
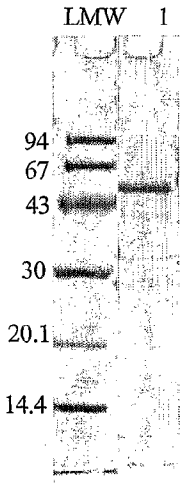


FIGURE 99

FIGURE 99A



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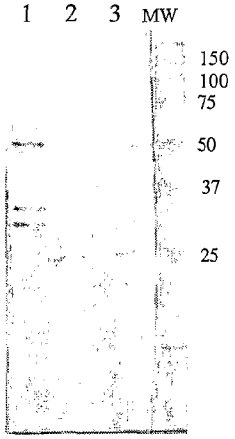


FIGURE 99C

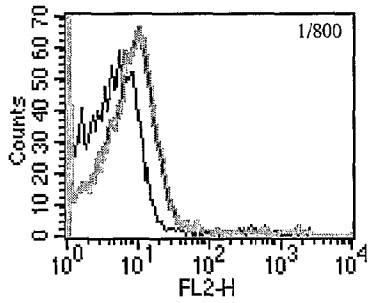


FIGURE 100

FIGURE 100A

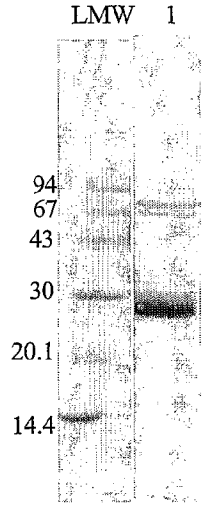


FIGURE 100B

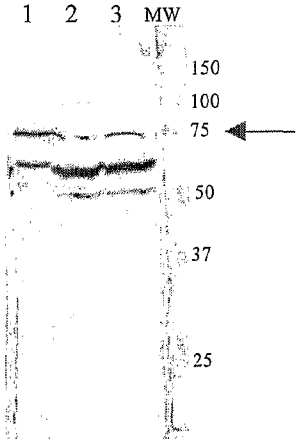


FIGURE 100C

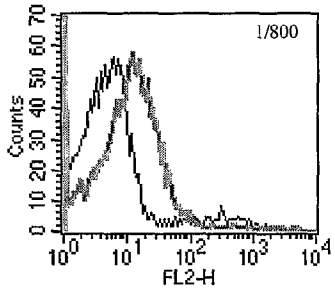
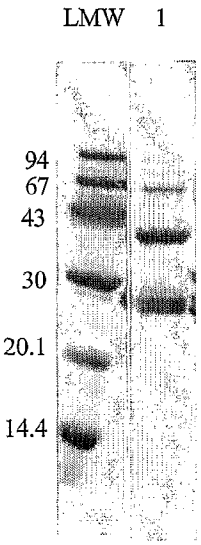


FIGURE 101

FIGURE 101A



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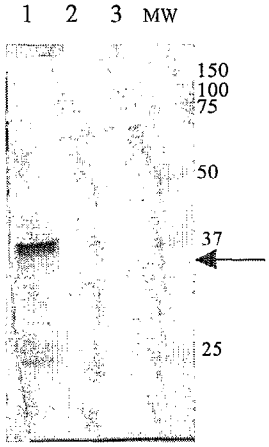


FIGURE 101C

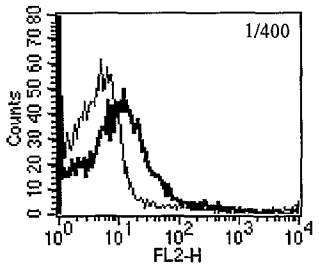


FIGURE 102

FIGURE 102A

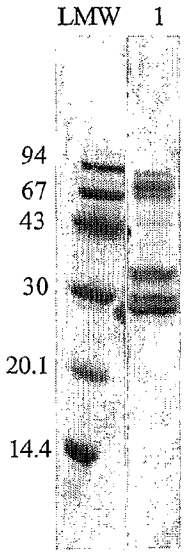


FIGURE 102B

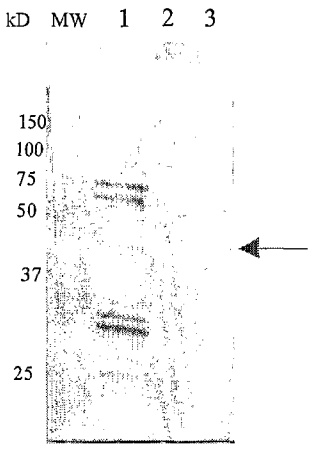
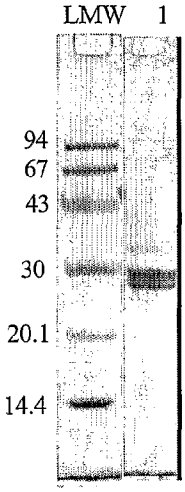


FIGURE 103

FIGURE 103A



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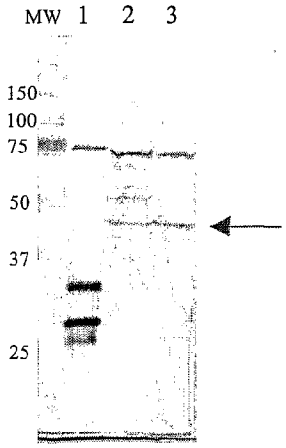


FIGURE 103C

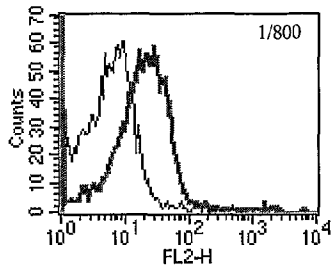


FIGURE 104

FIGURE 104A

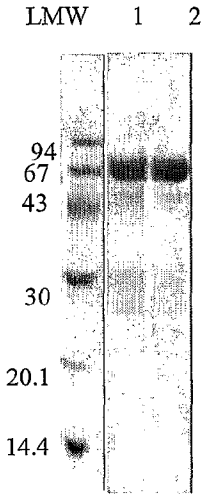


FIGURE 104B

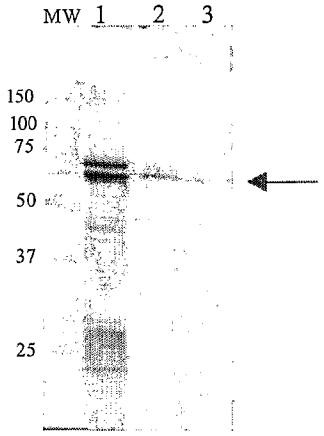


FIGURE 104C

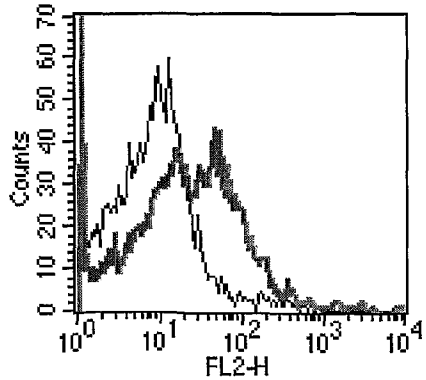


FIGURE 105

FIGURE 105A

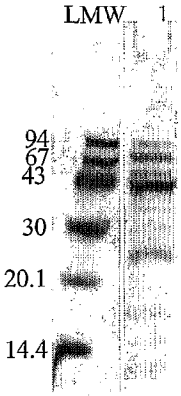


FIGURE 105B

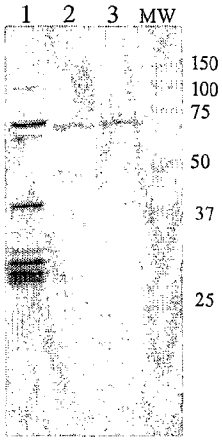


FIGURE 105C

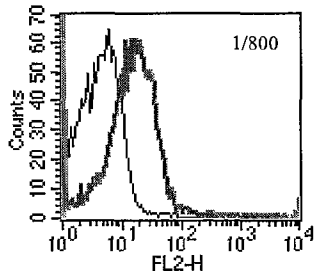


FIGURE 106

FIGURE 106A

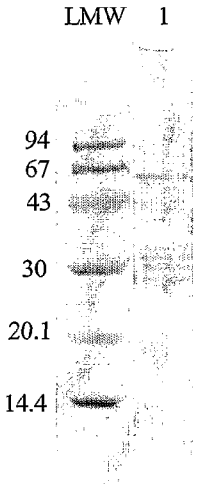


FIGURE 106B

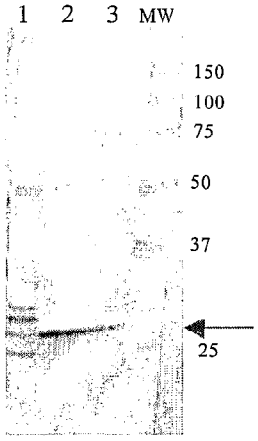


FIGURE 106C

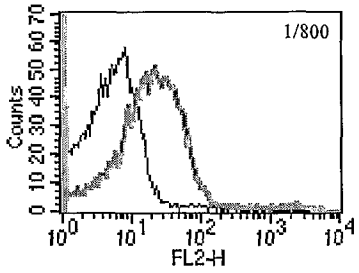


FIGURE 107

FIGURE 107A

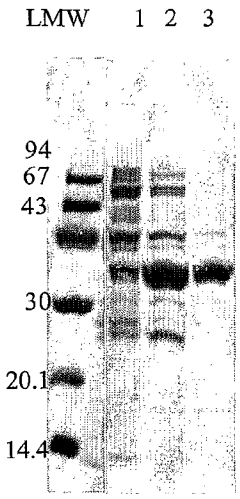


FIGURE 107B

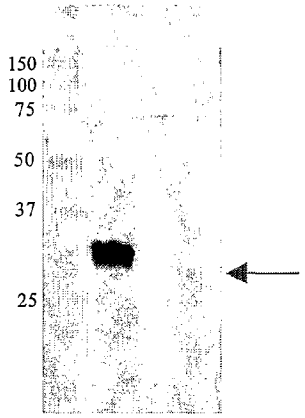


FIGURE 107C

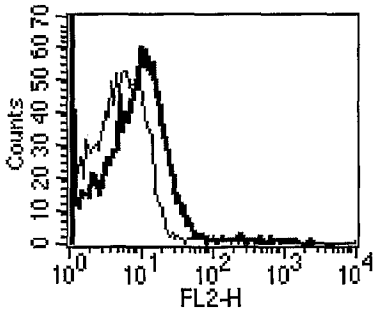


FIGURE 108

FIGURE 108A

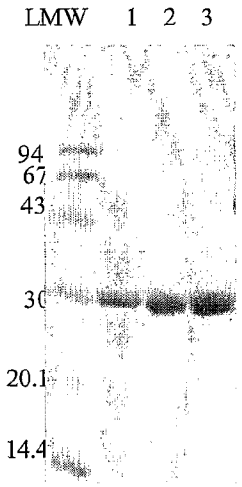


FIGURE 108B

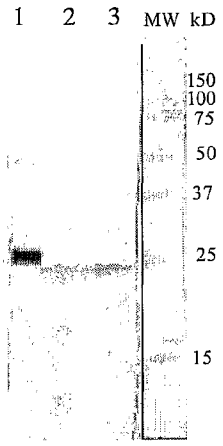


FIGURE 108C

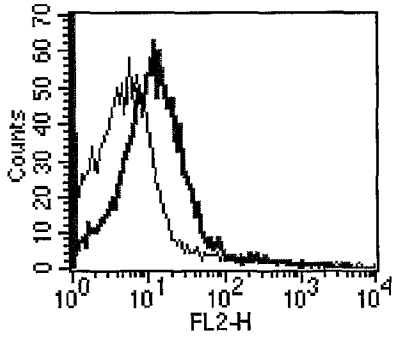


FIGURE 109

FIGURE 109A

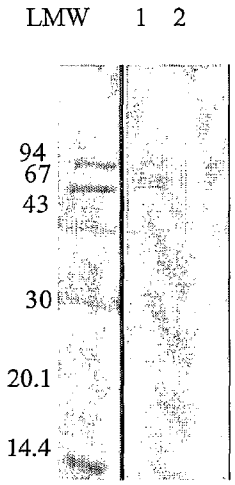


FIGURE 109B

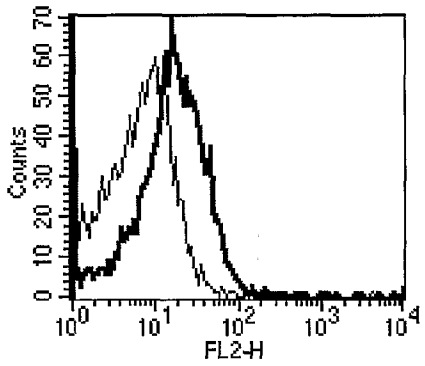


FIGURE 110

FIGURE 110A

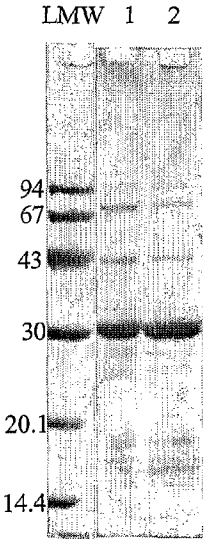


FIGURE 110B

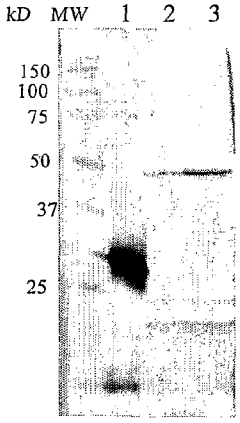
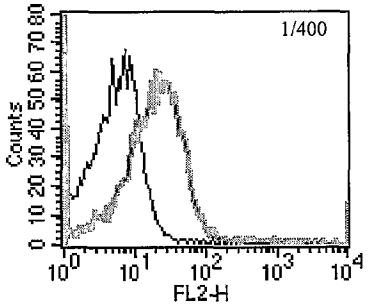


FIGURE 110C



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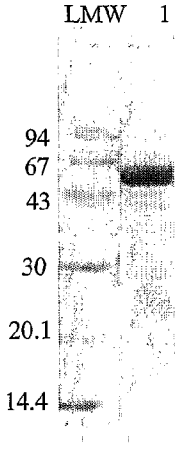

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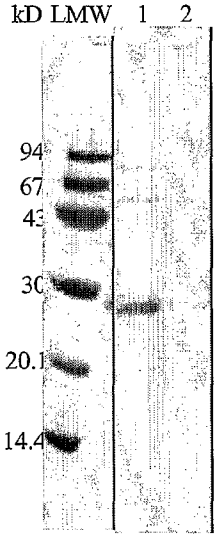


FIGURE 112

FIGURE 112A

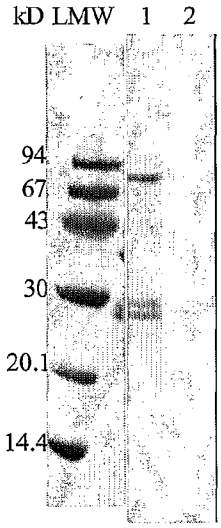


FIGURE 112B

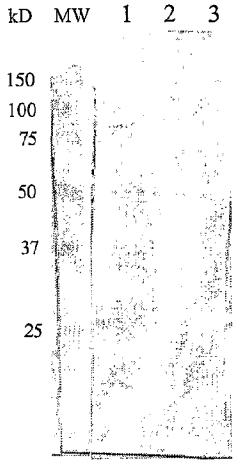


FIGURE 114

FIGURE 114A

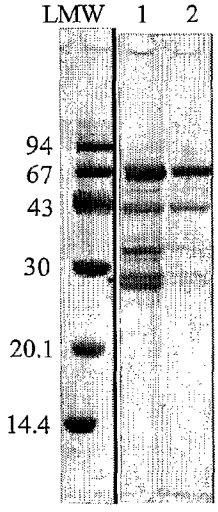


FIGURE 114B

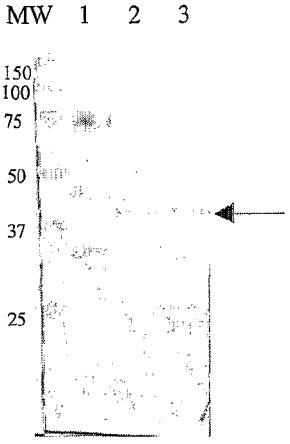
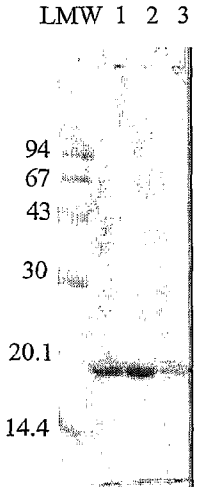


FIGURE 115

FIGURE 115A



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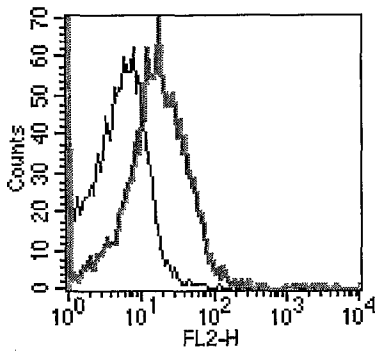


FIGURE 116

FIGURE 116A

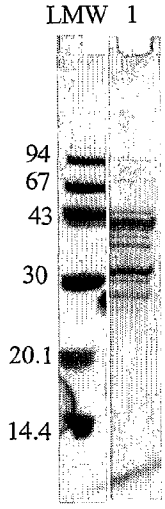


FIGURE 117

FIGURE 117A

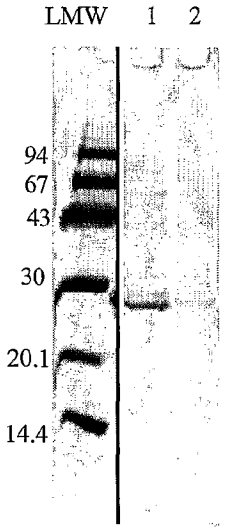


FIGURE 117B

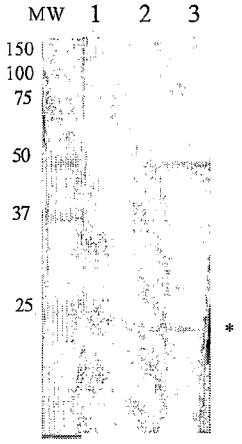
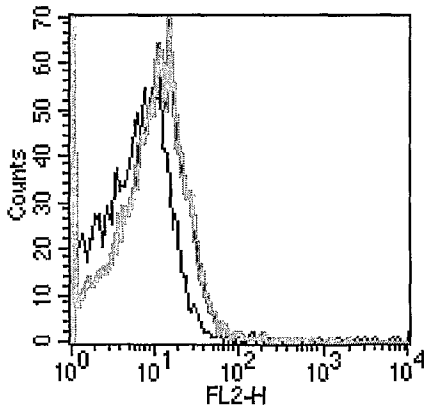


FIGURE 117C



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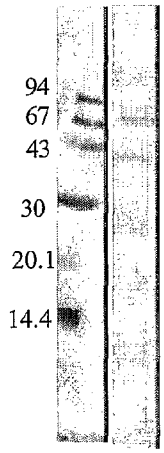

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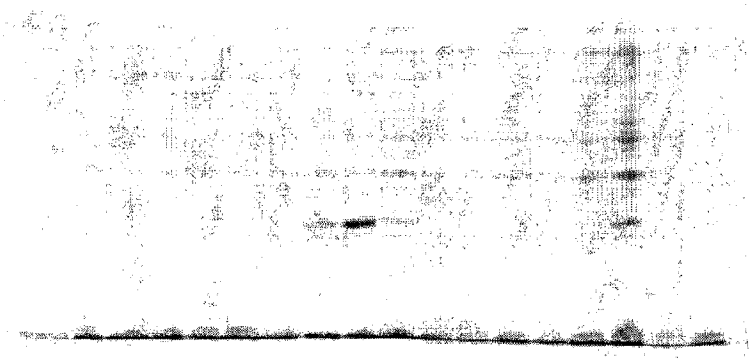

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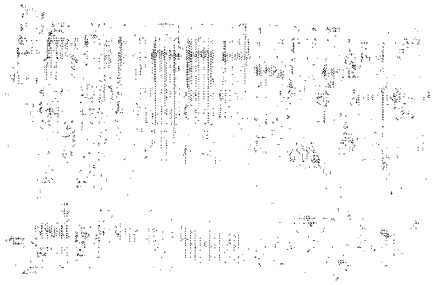

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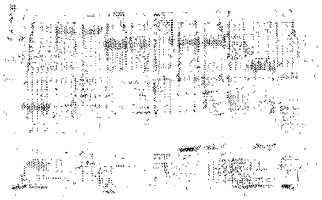

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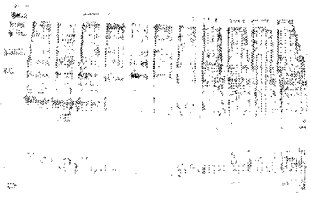

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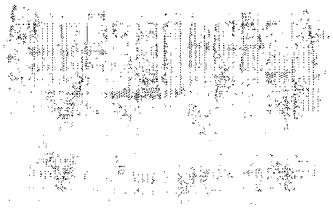

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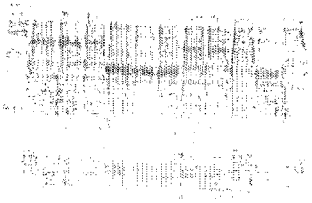

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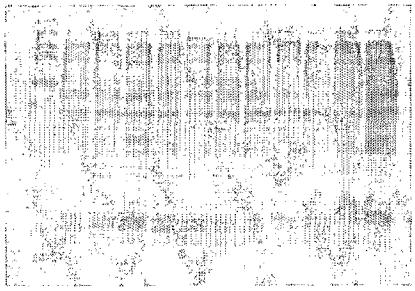

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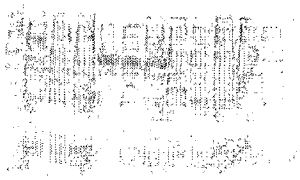

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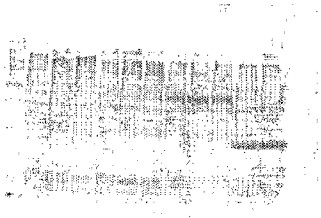

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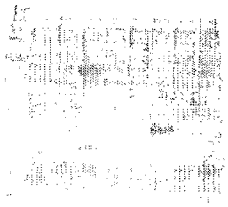

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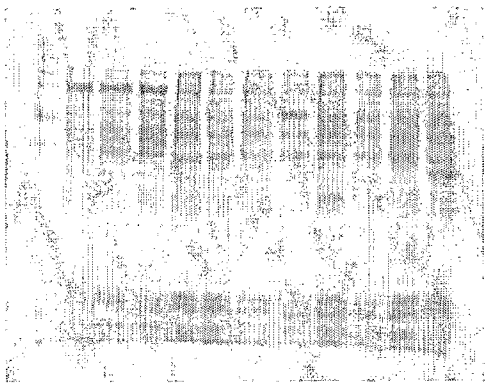

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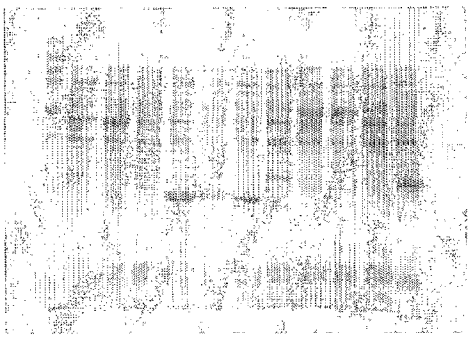

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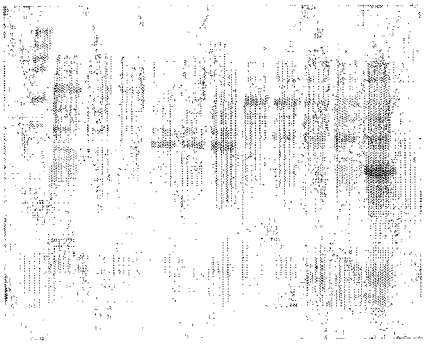

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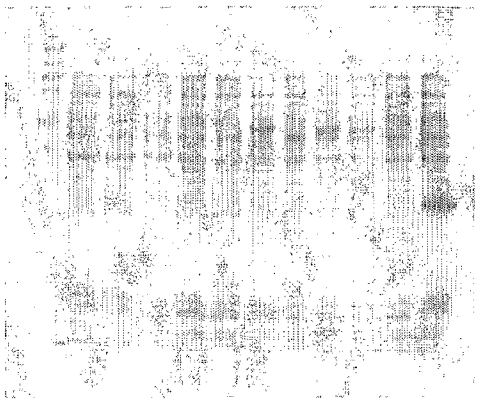

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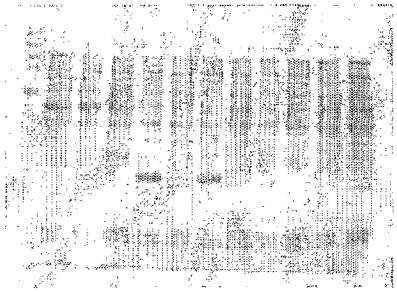

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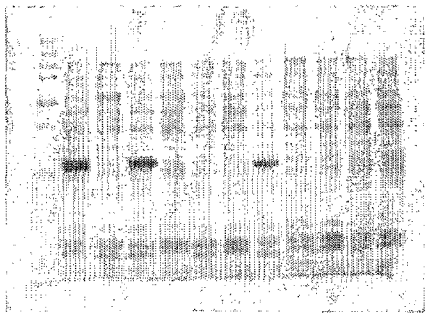

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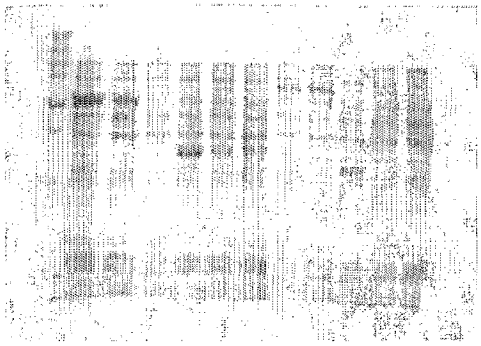

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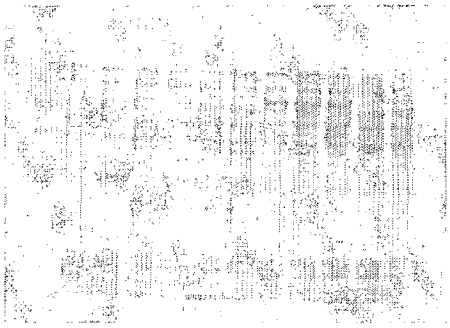

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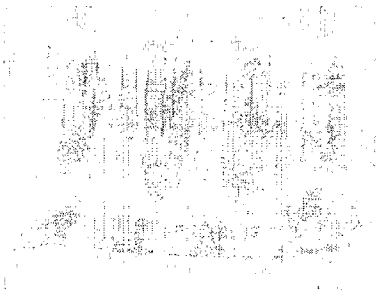

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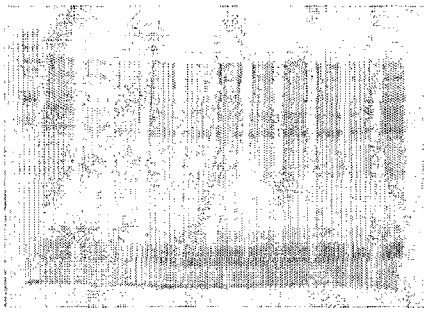

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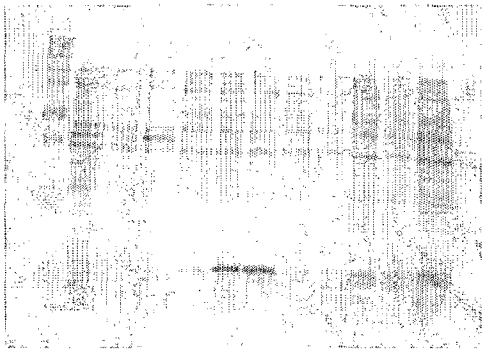

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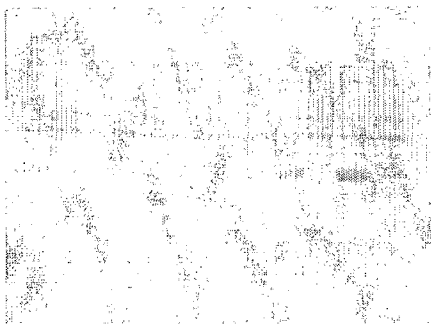
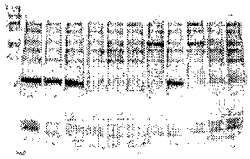


FIGURE 141

FIGURE 142



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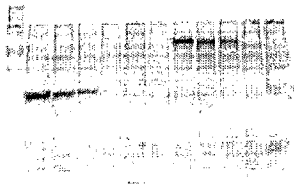

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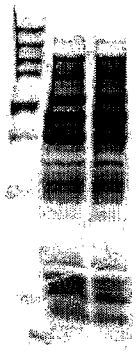

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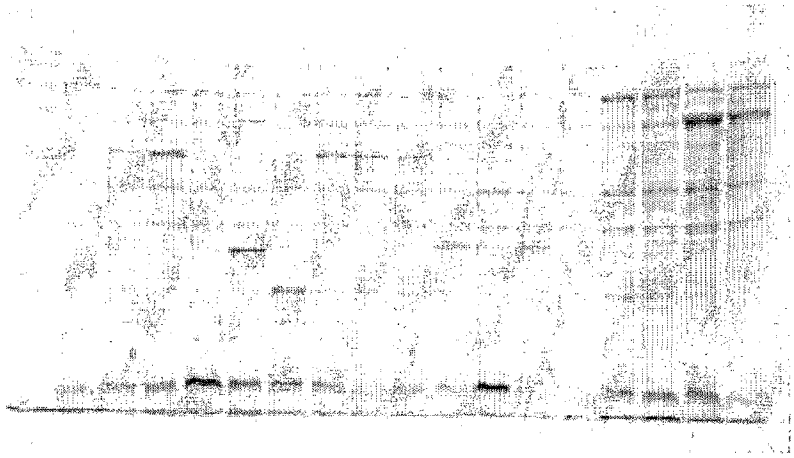

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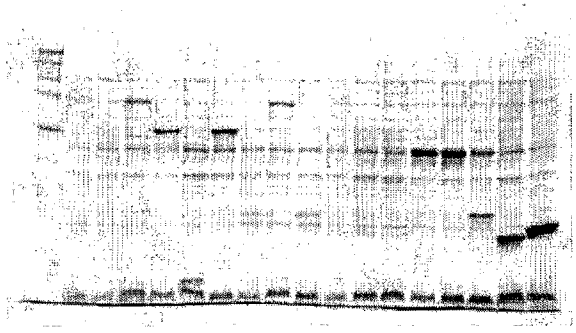

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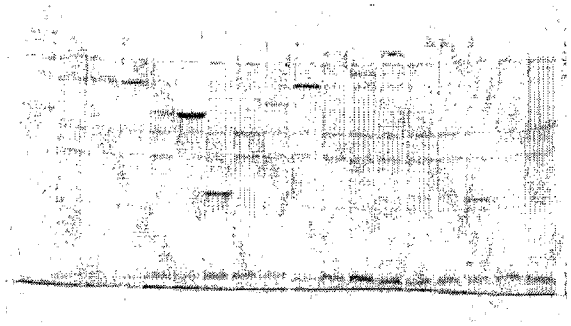

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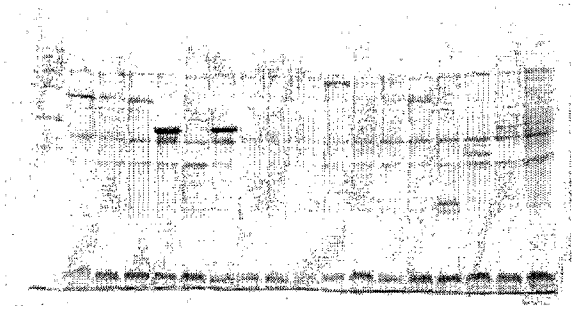

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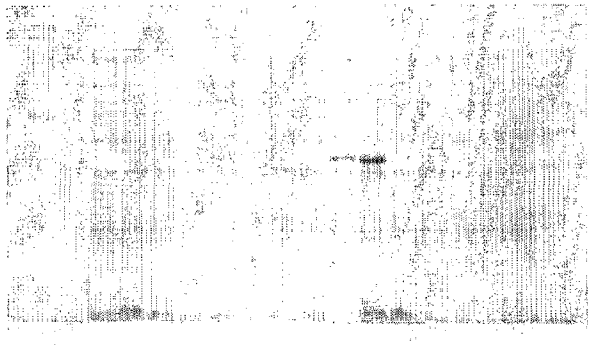

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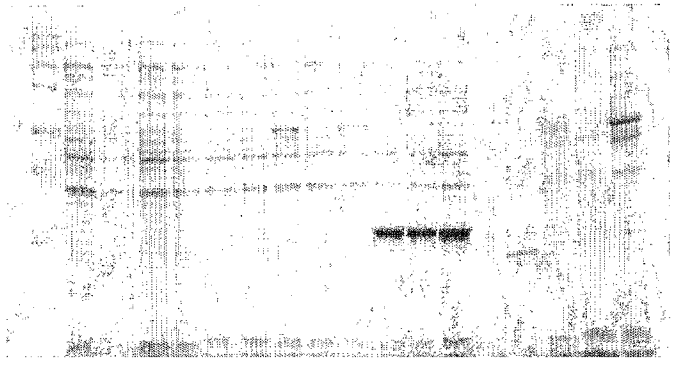

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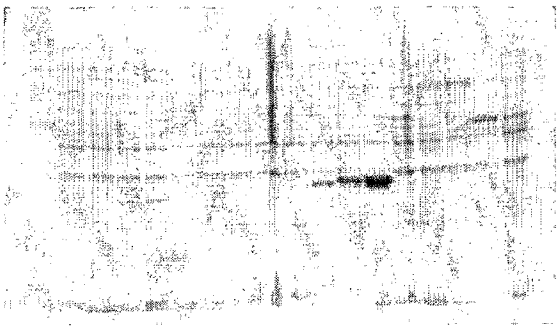

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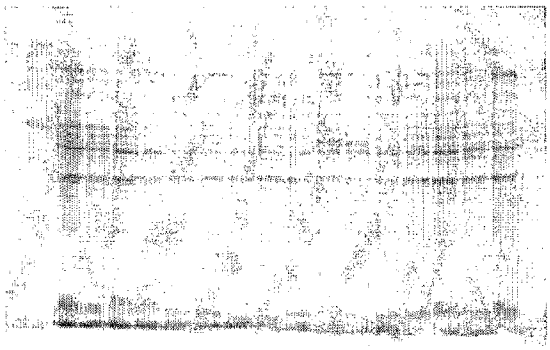

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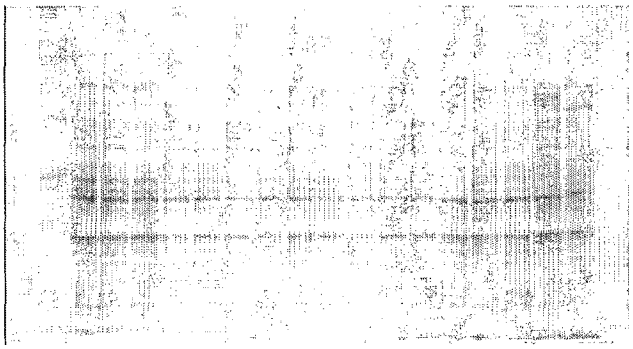

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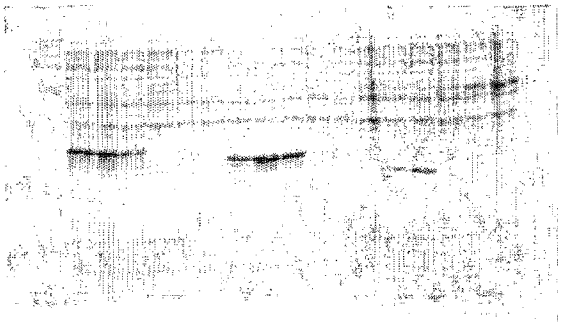

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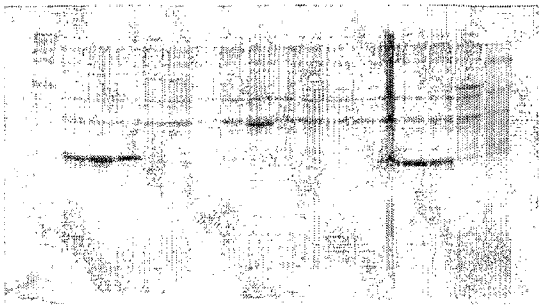

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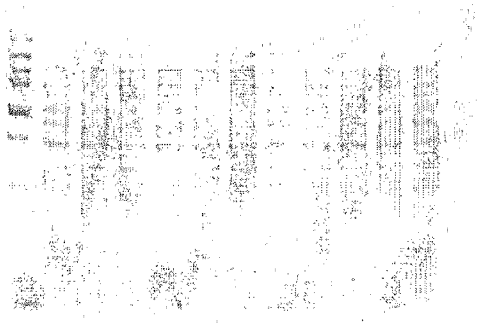

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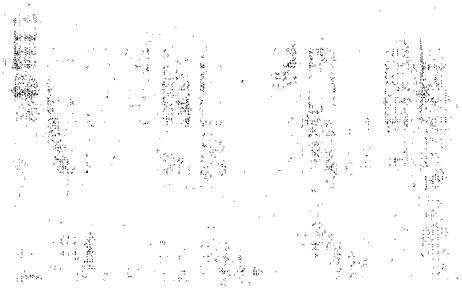

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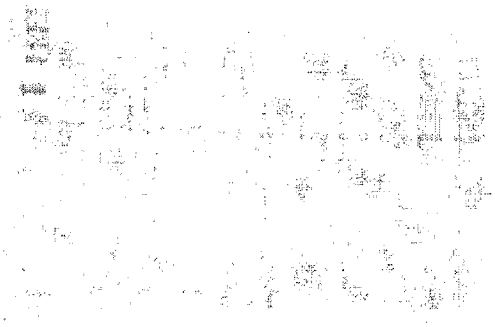

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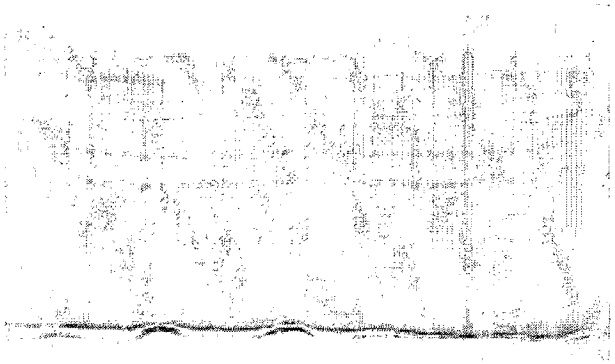

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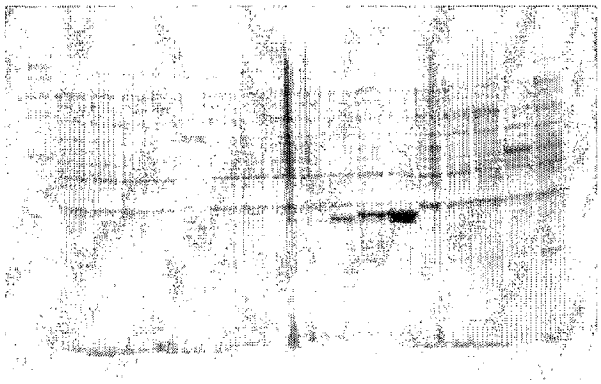

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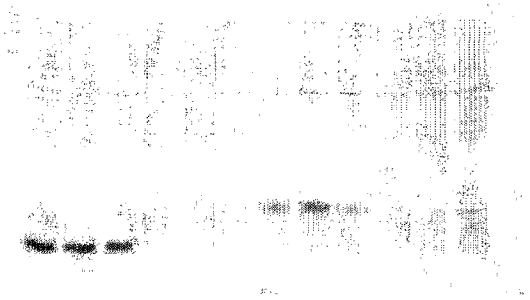

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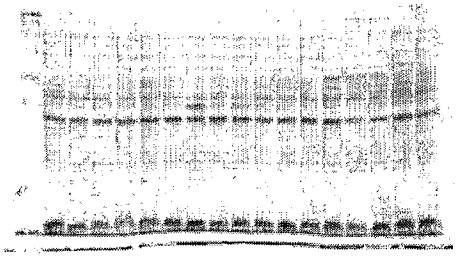

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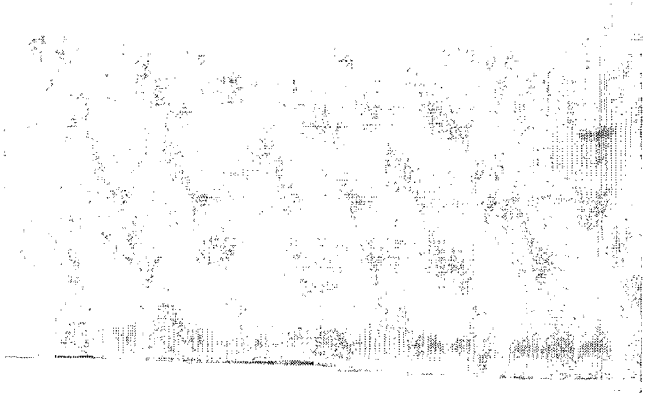

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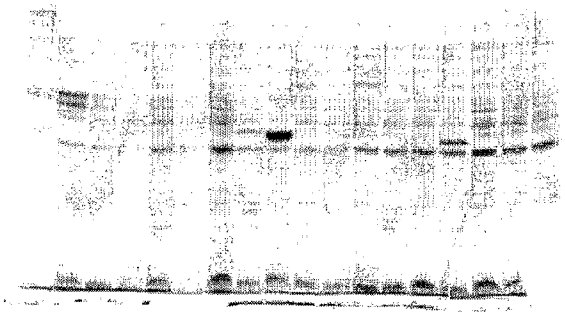

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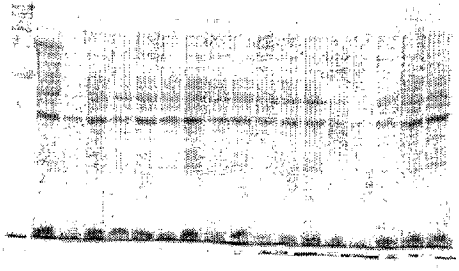

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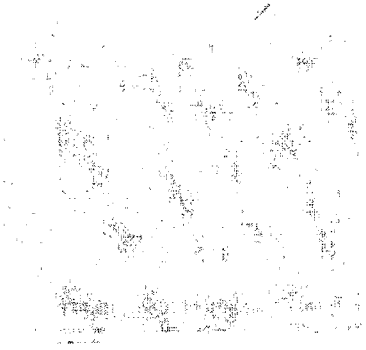

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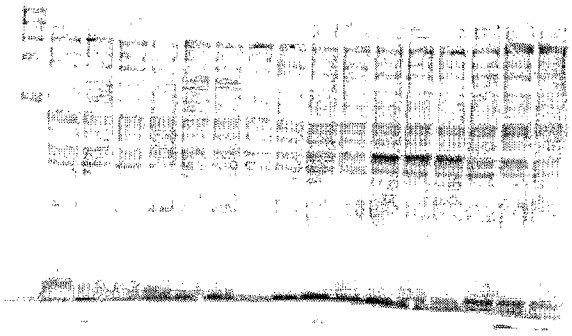

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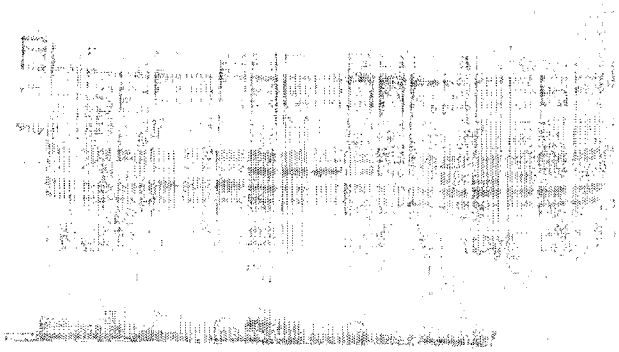

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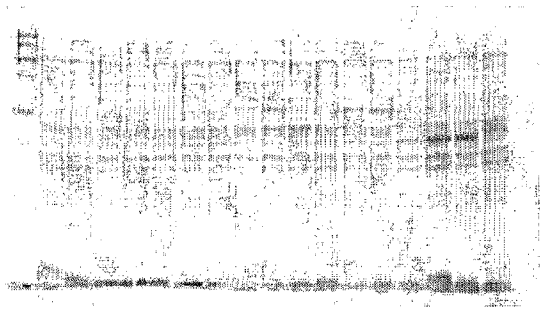

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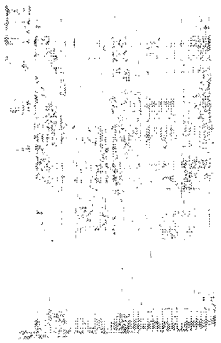

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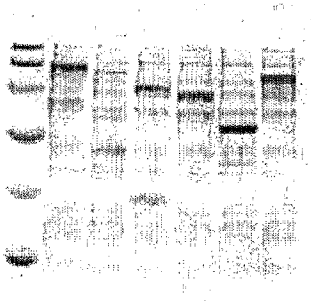

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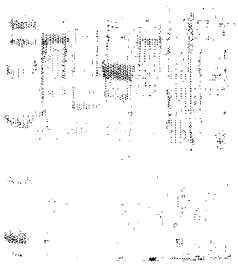

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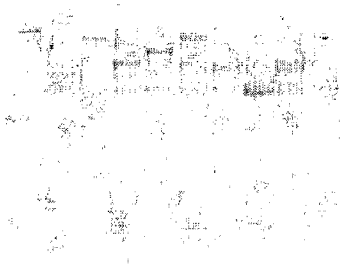


FIGURE 174

FIGURE 175

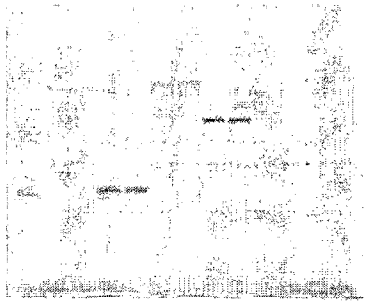
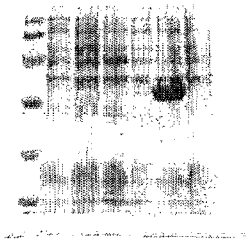


FIGURE 176



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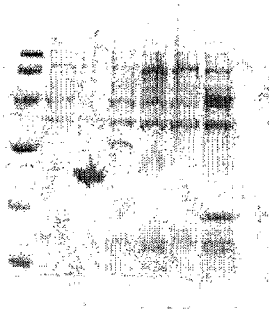

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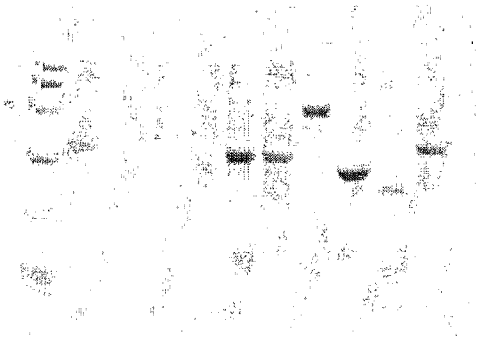

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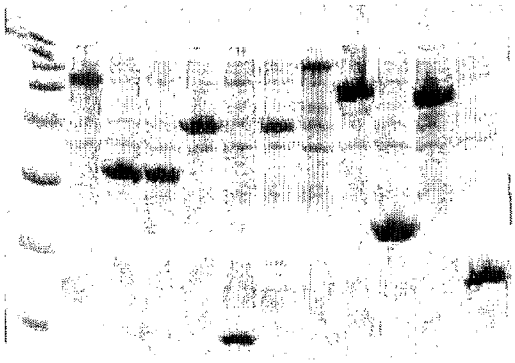

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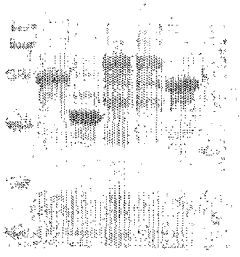

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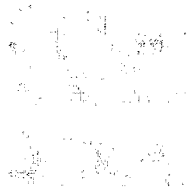

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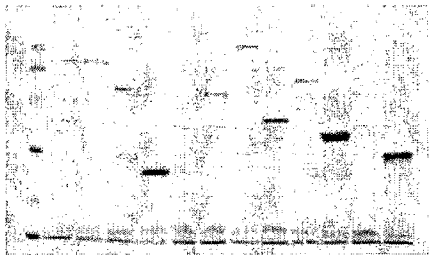

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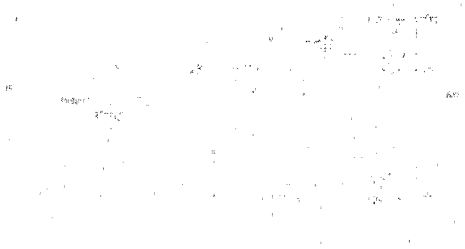

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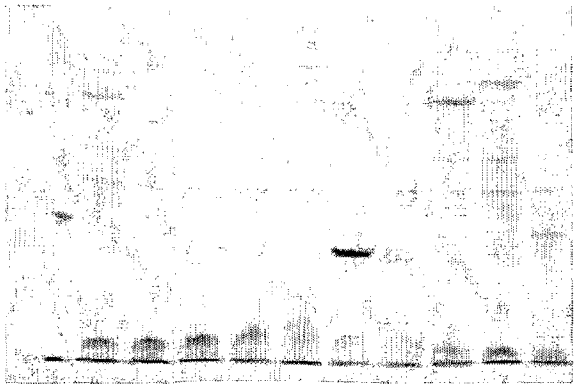

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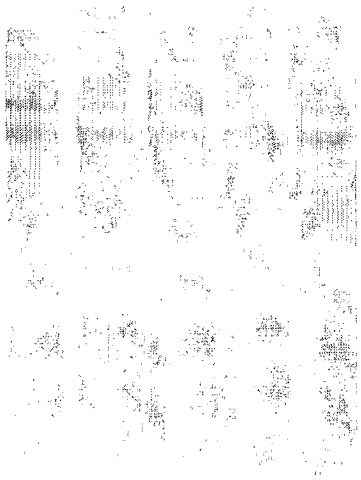

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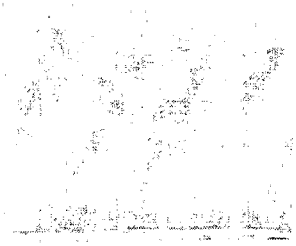

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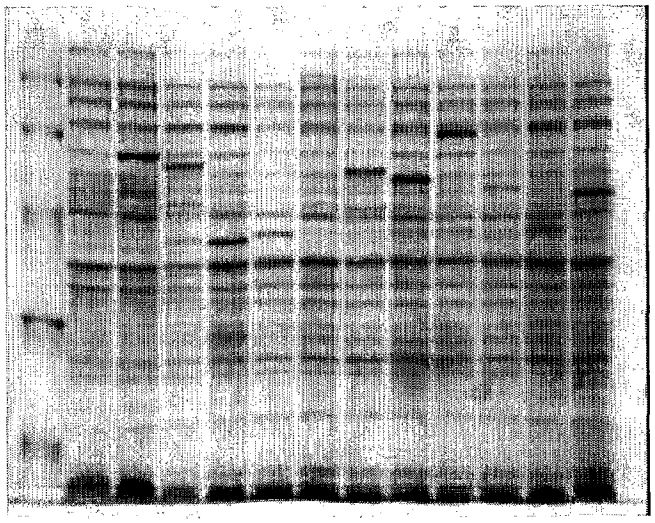

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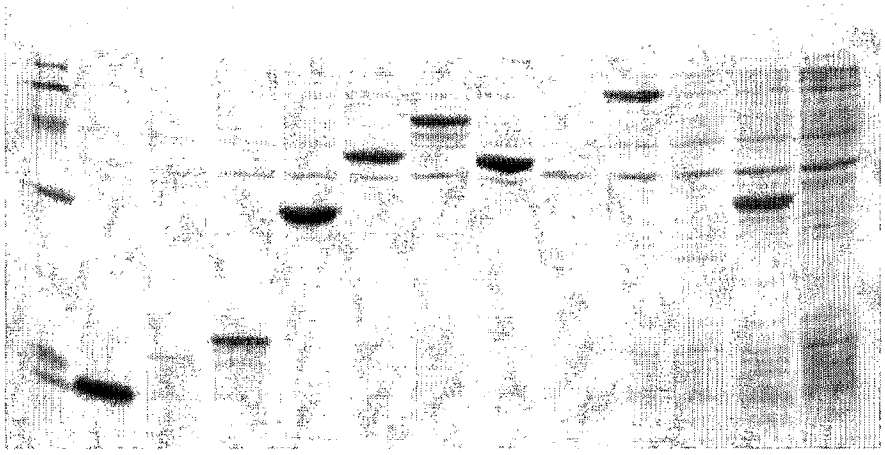

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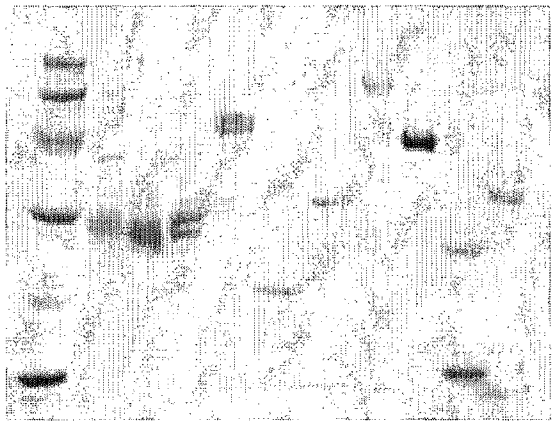

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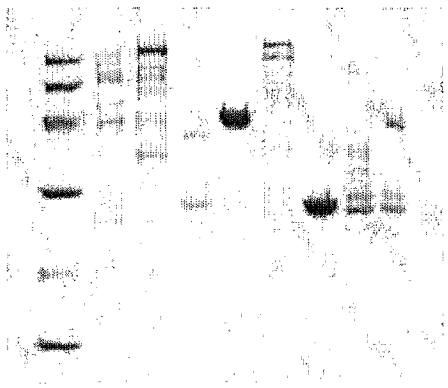

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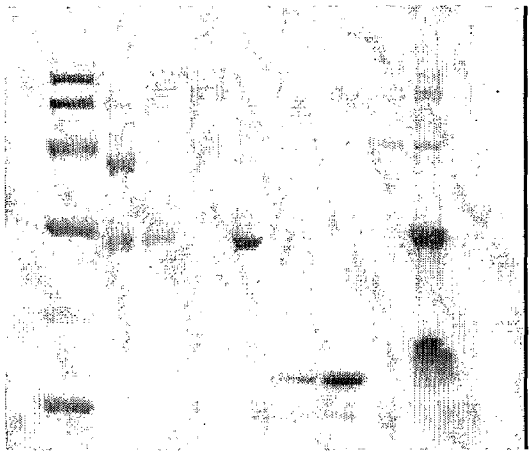

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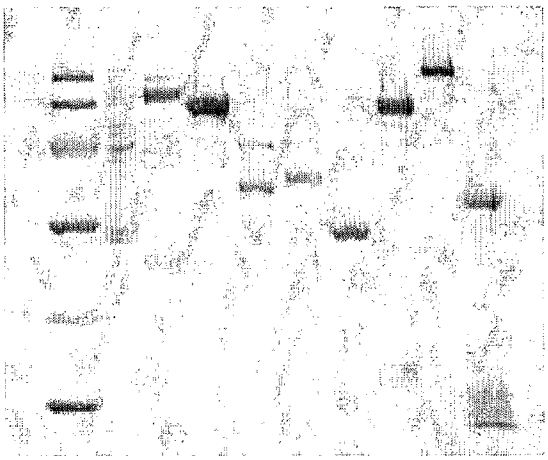

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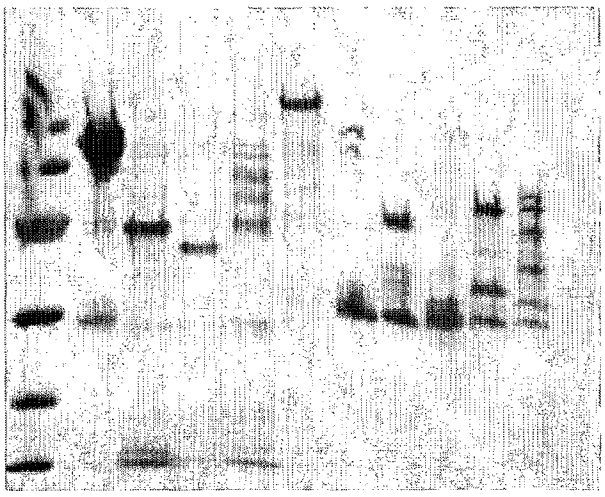

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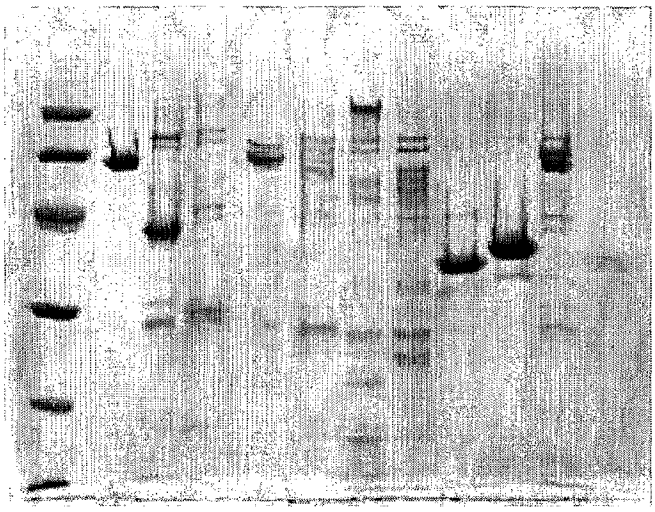

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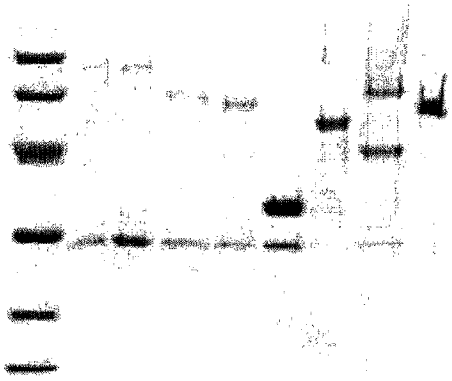

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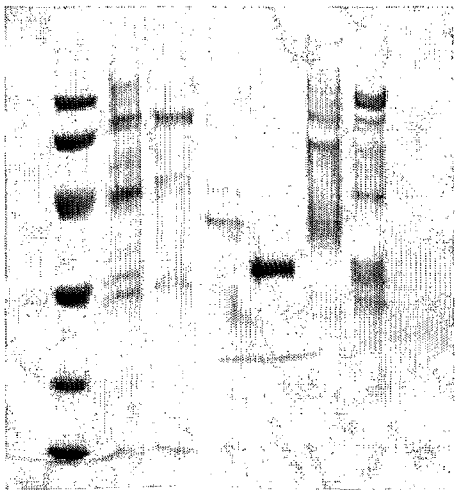

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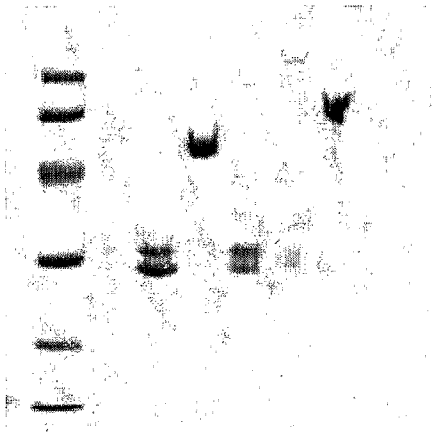

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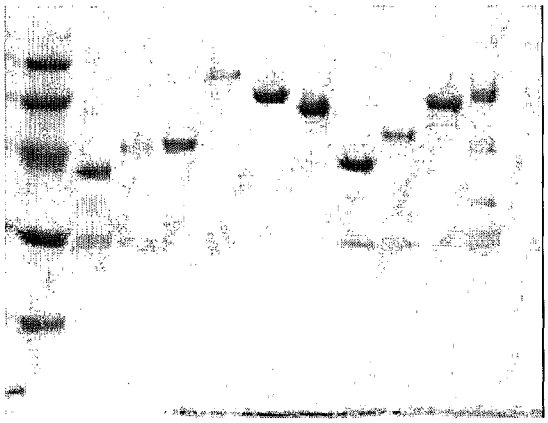

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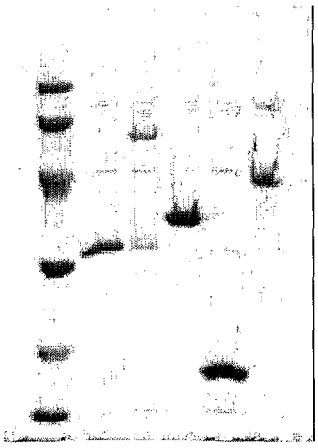

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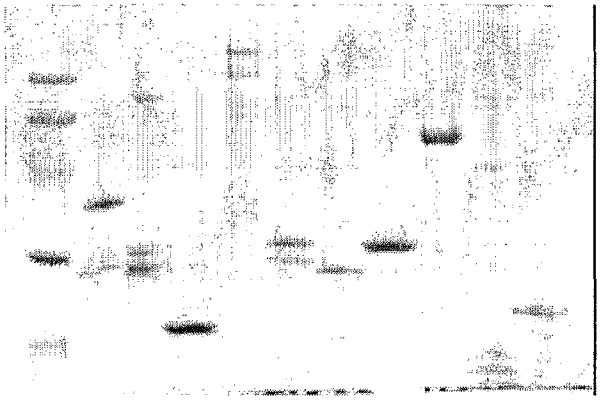

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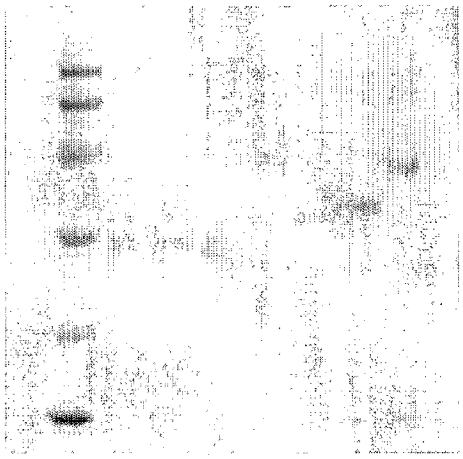

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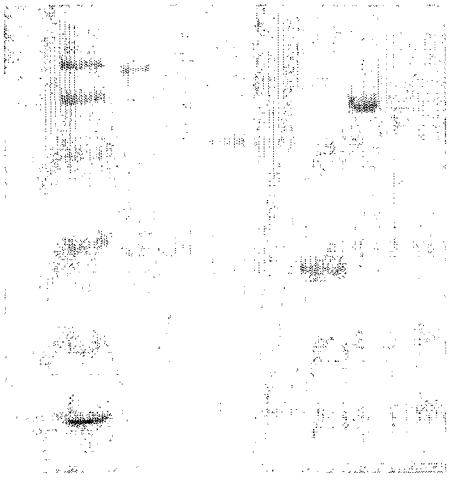

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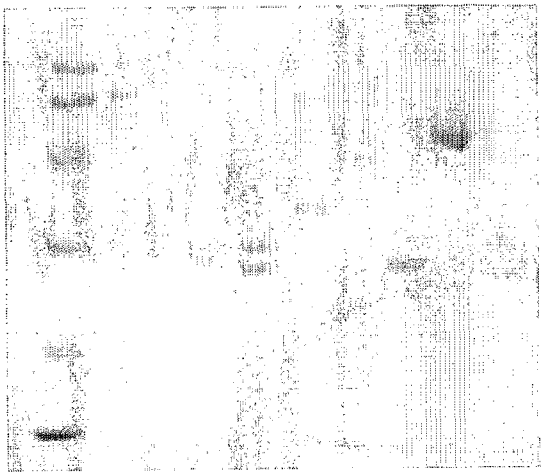

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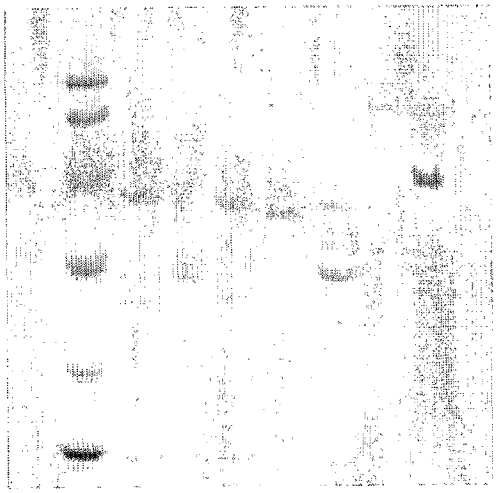

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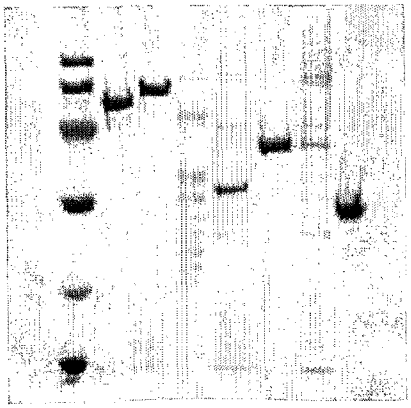

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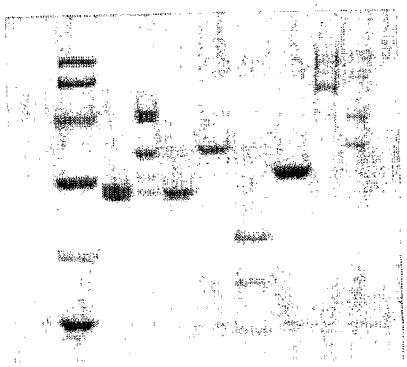

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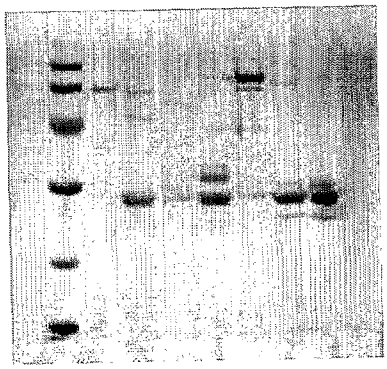

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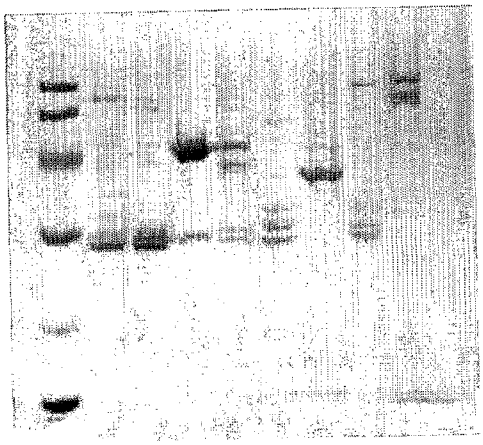

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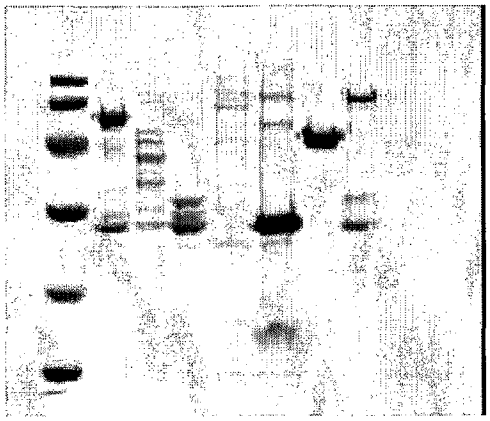

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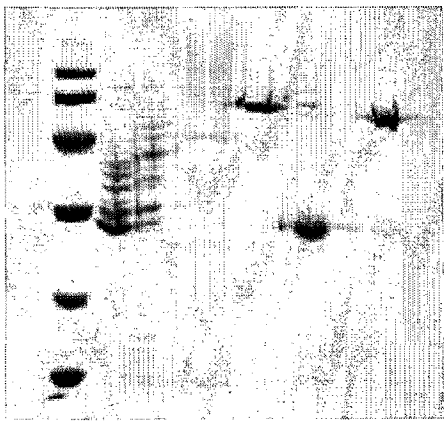

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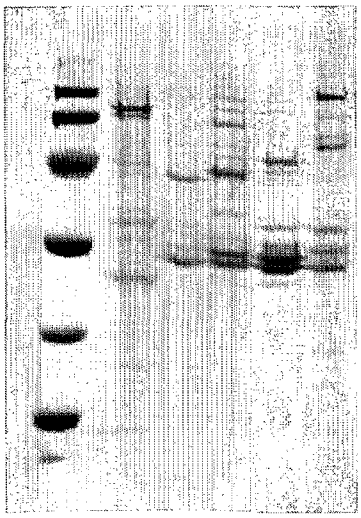

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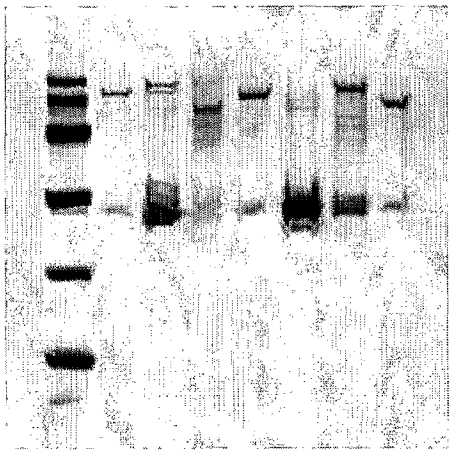

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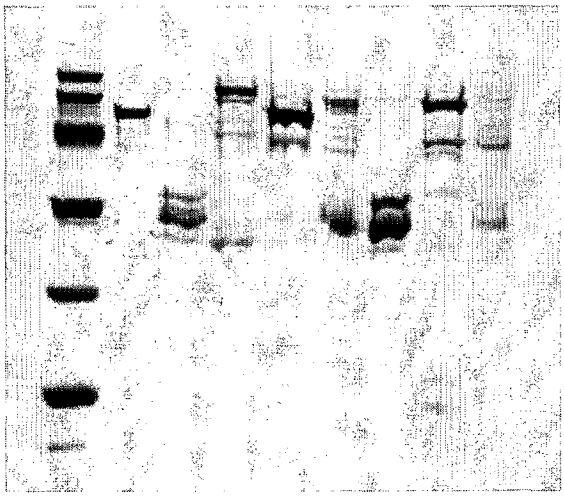

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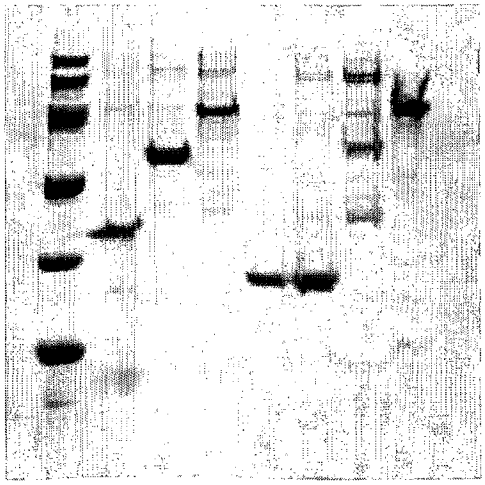

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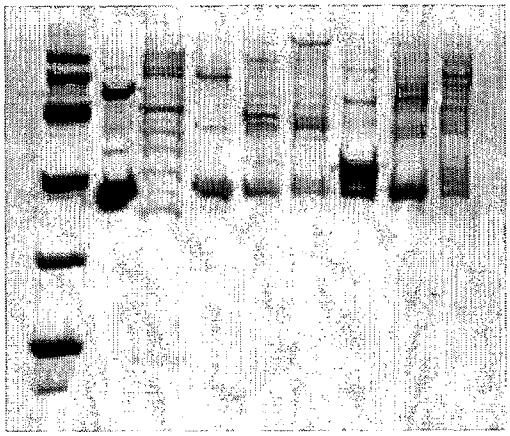

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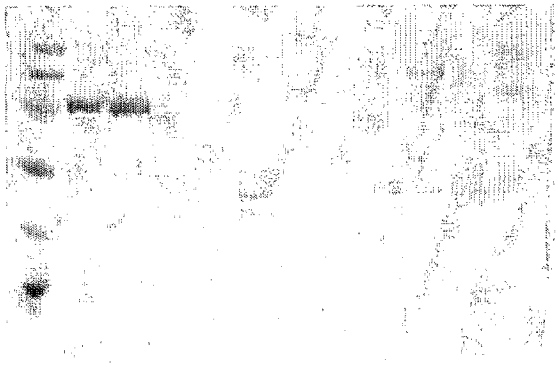

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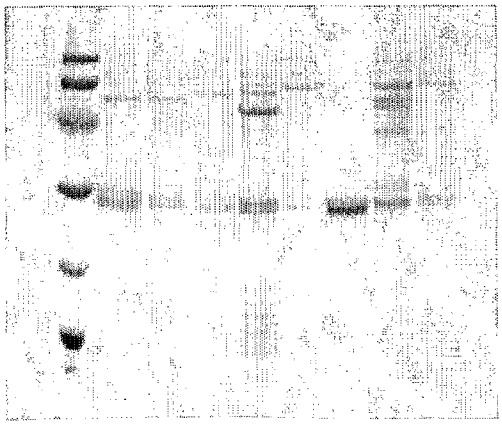

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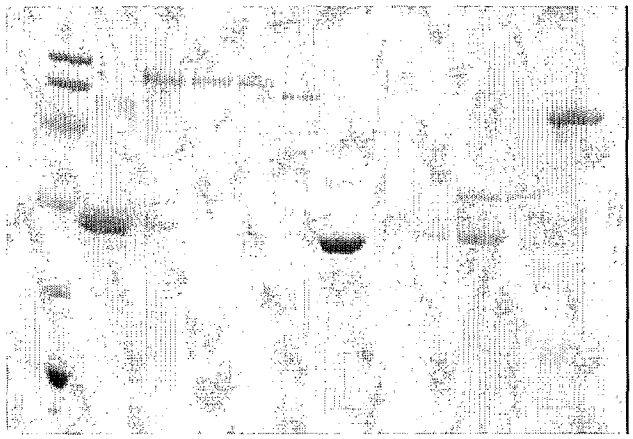

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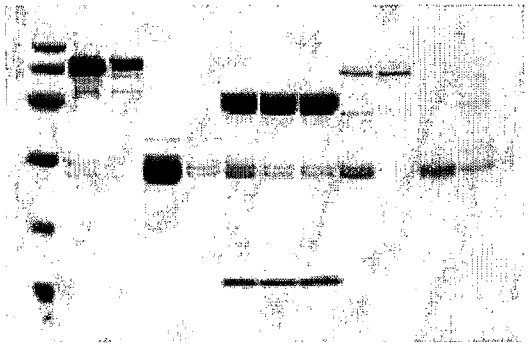

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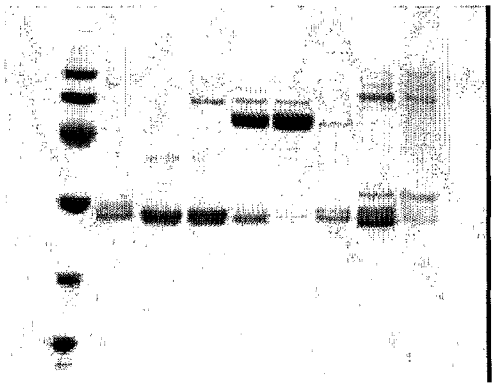

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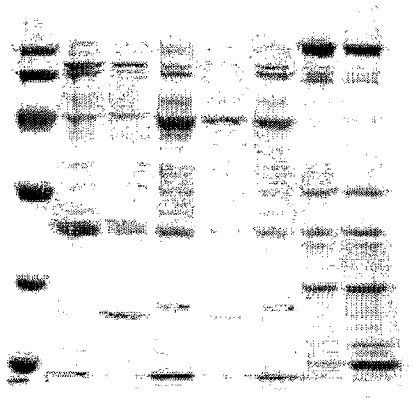

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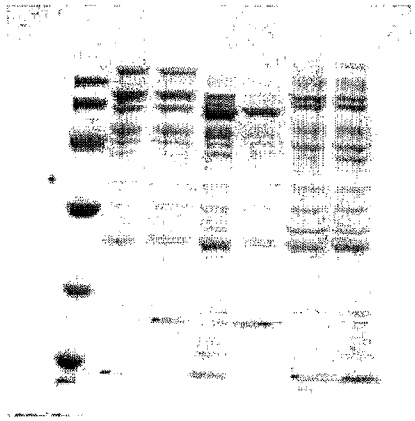

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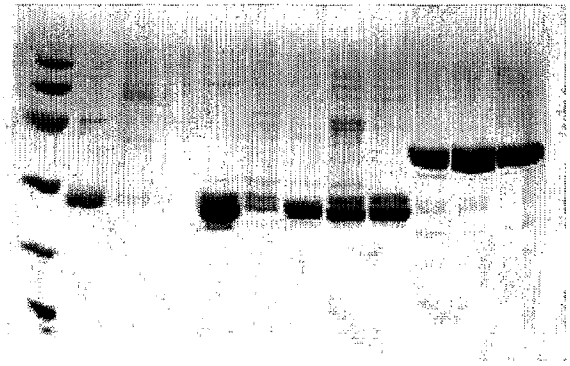

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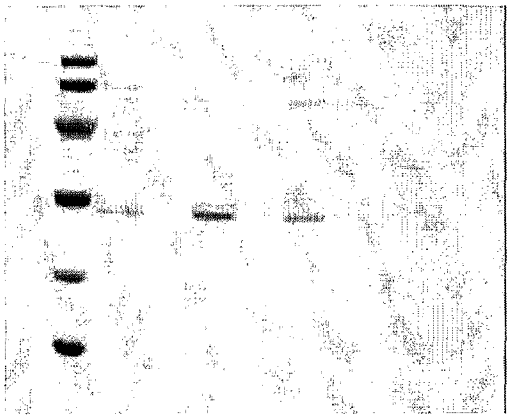

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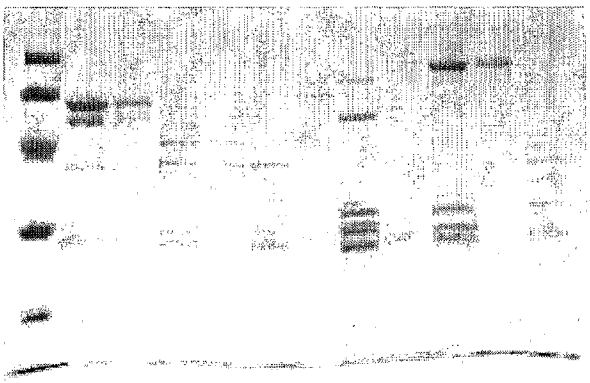

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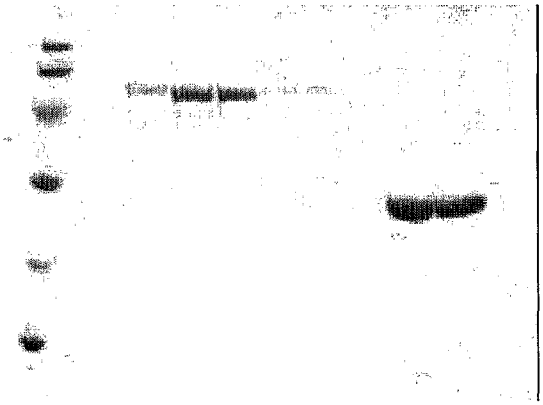

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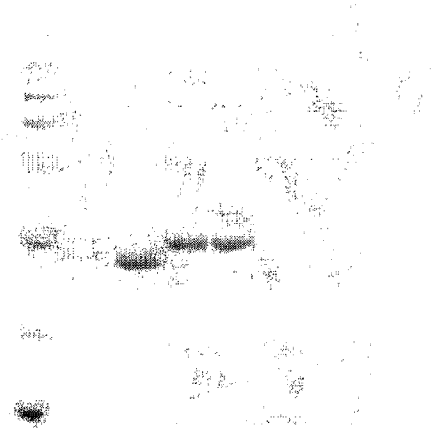

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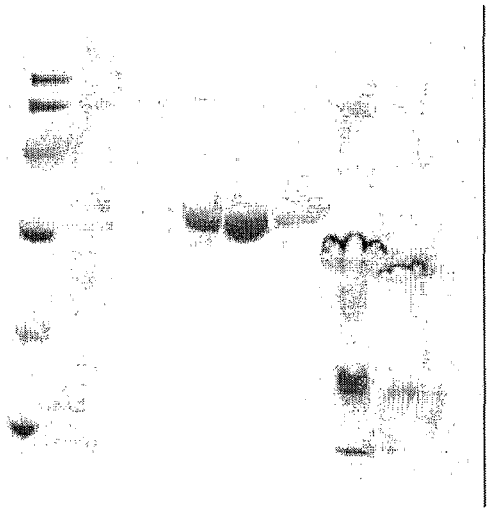

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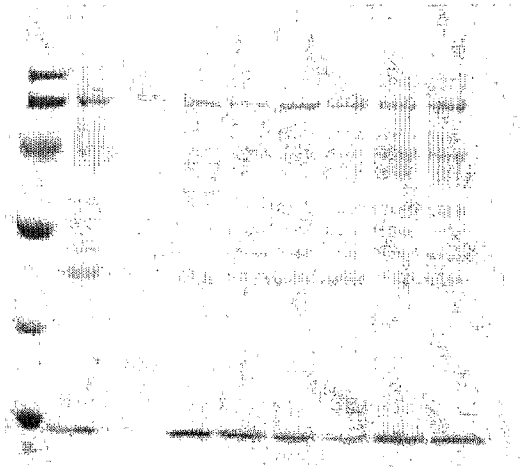

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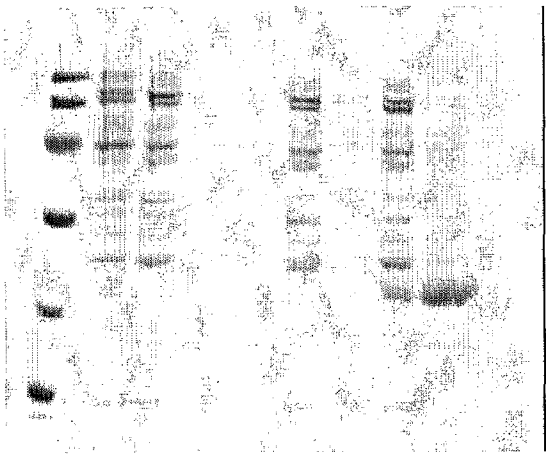

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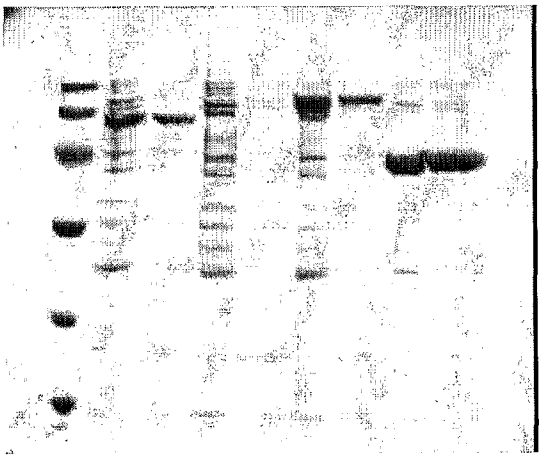

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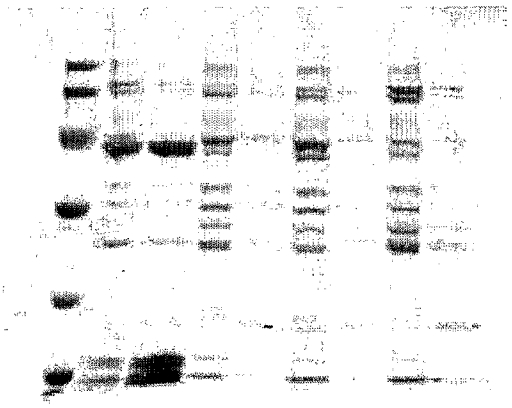
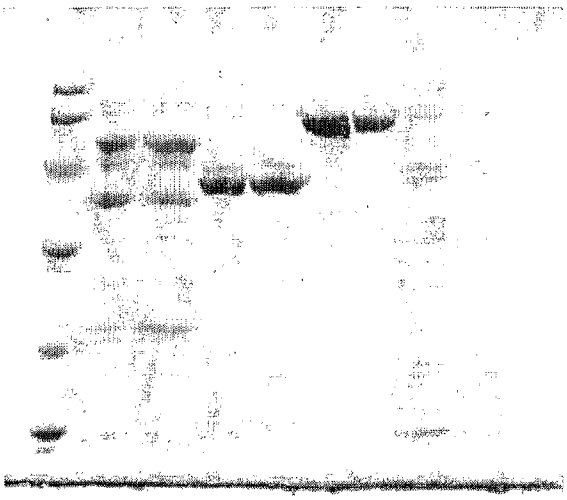


FIGURE 233



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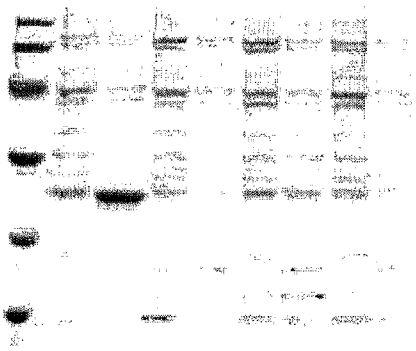

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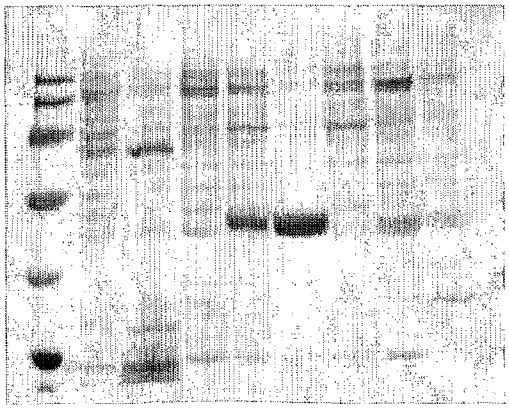

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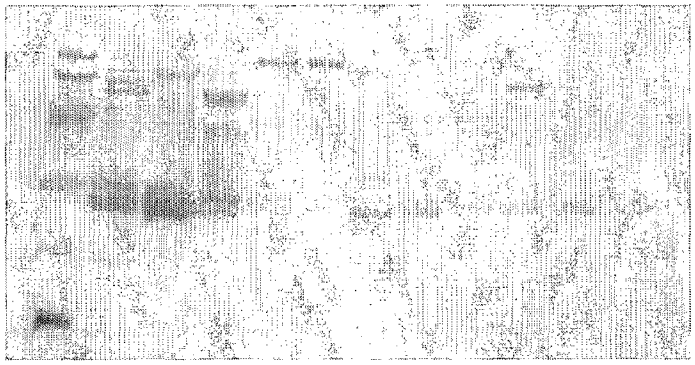

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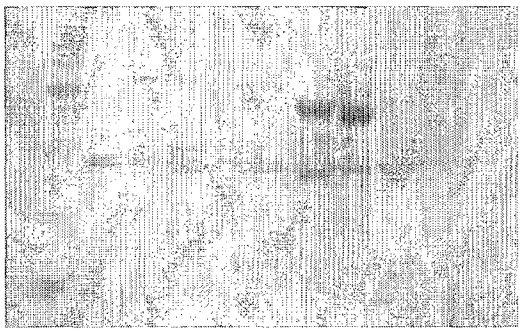

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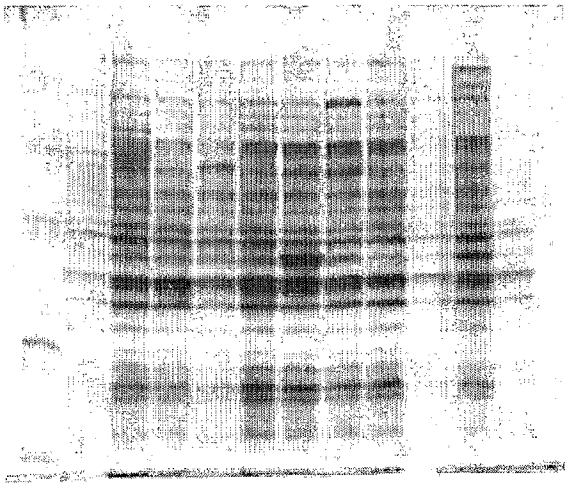

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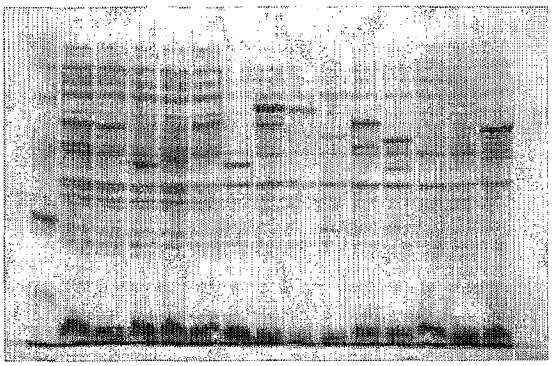

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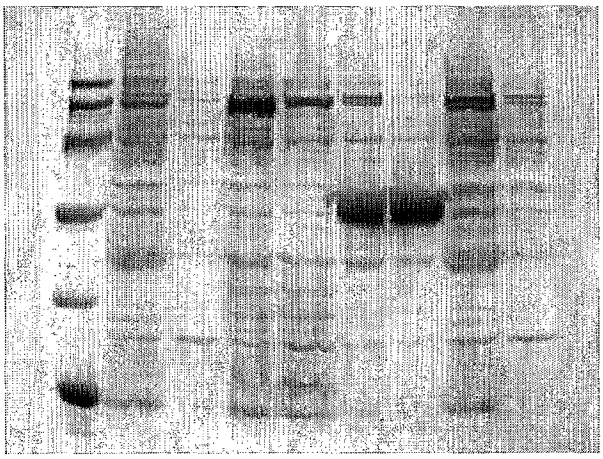

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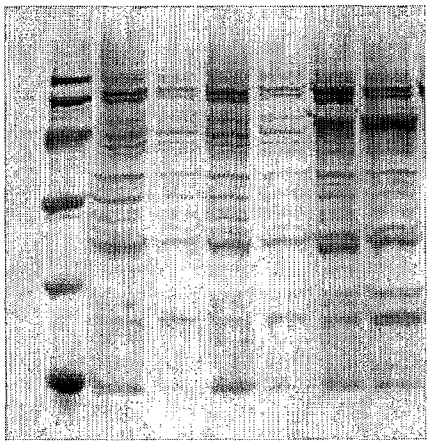

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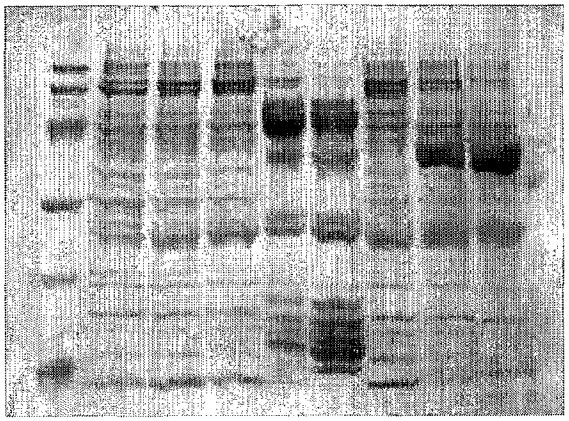

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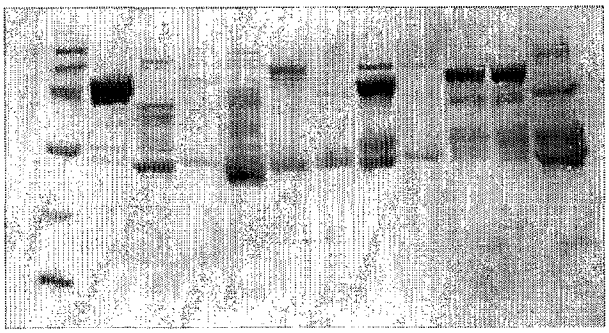

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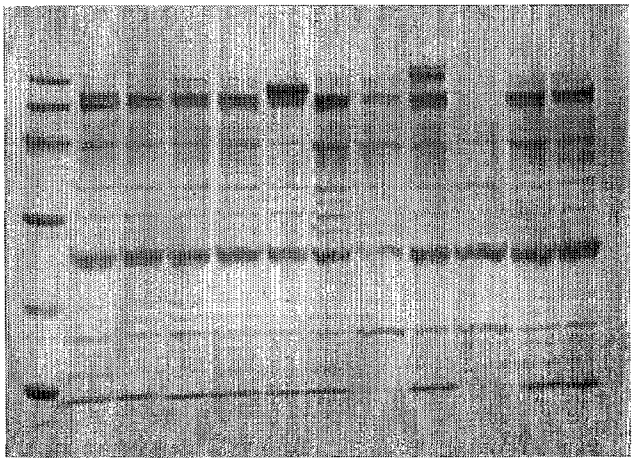
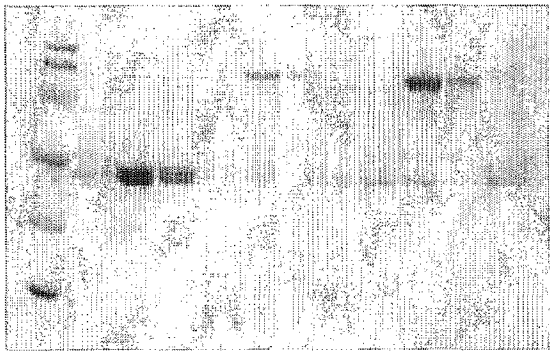


FIGURE 245

FIGURE 246



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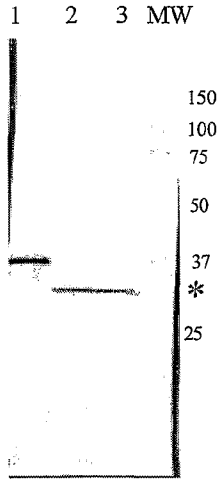


FIGURE 248

FIGURE 248A

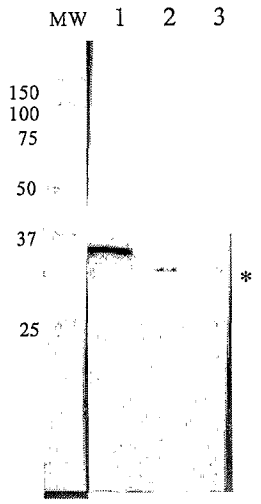
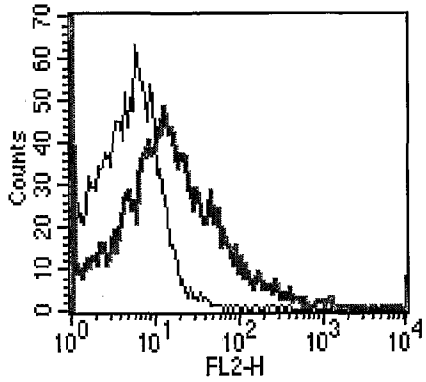


FIGURE 248B



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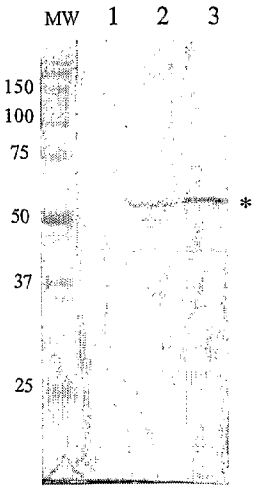

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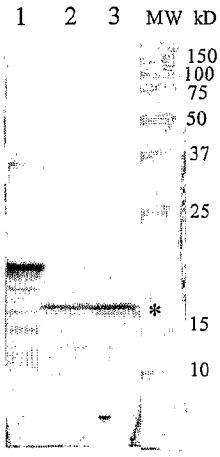

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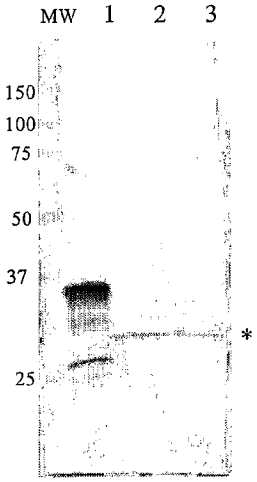
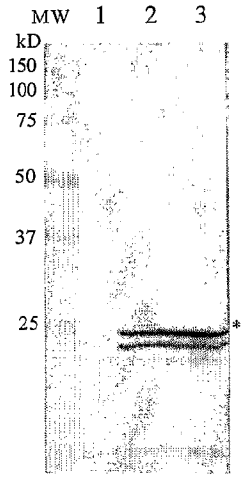


FIGURE 252

FIGURE 252A



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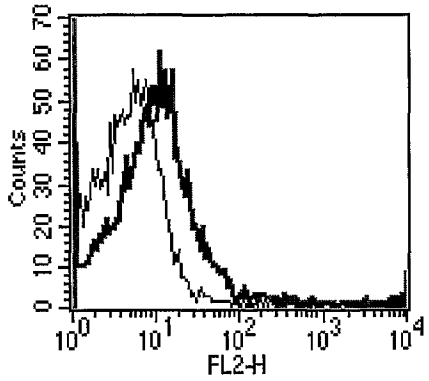

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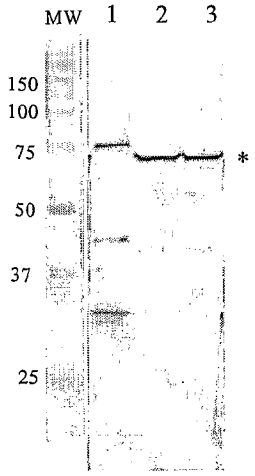

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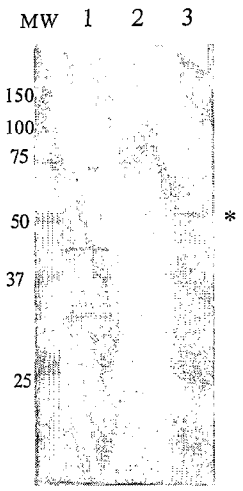
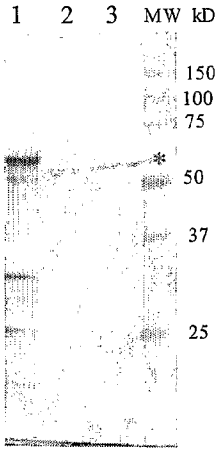


FIGURE 255

FIGURE 255A



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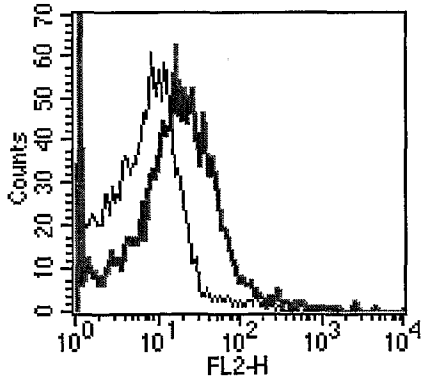
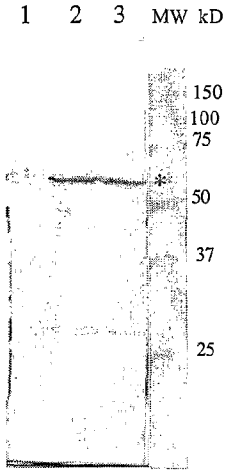


FIGURE 256

FIGURE 256A



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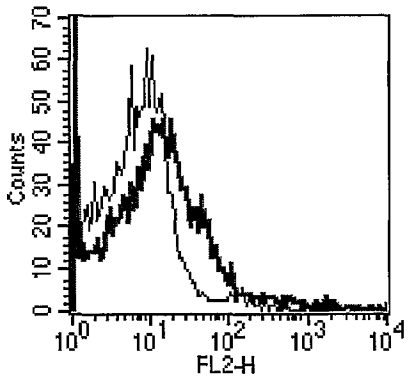

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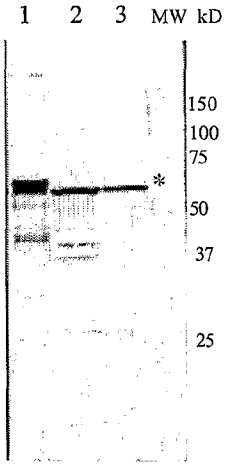

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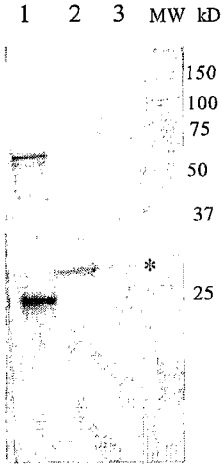

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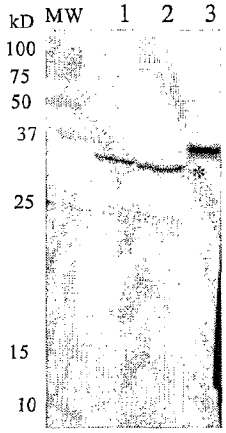

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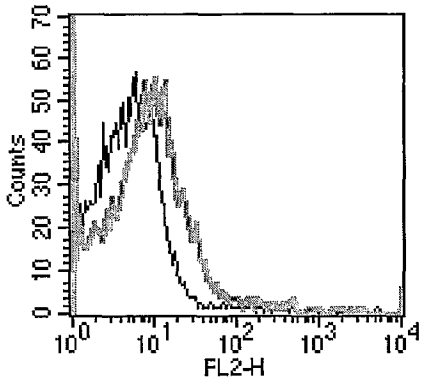

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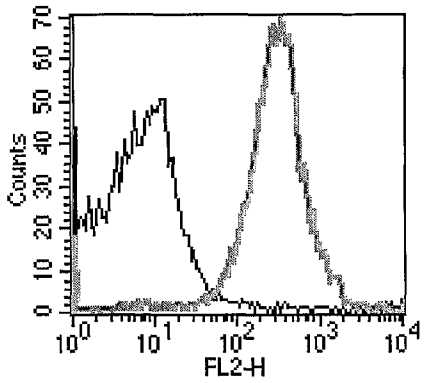

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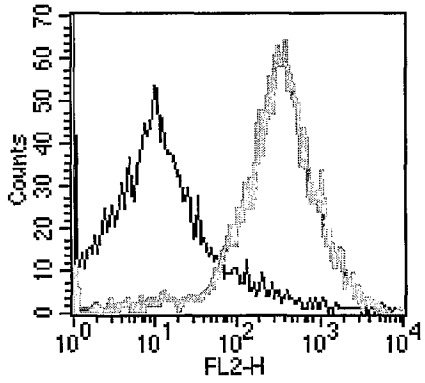

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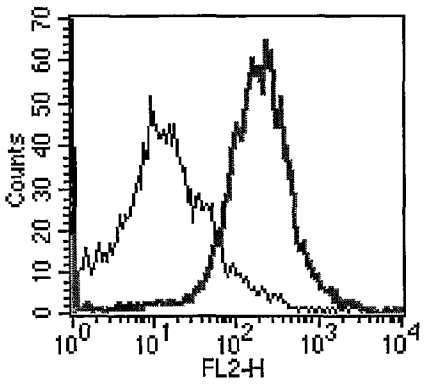

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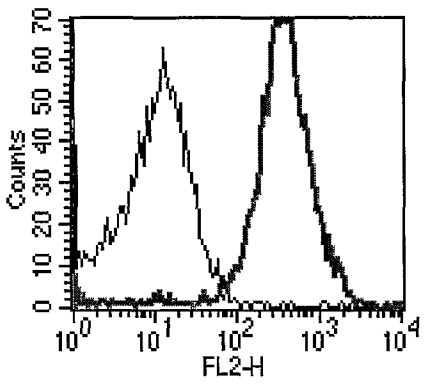

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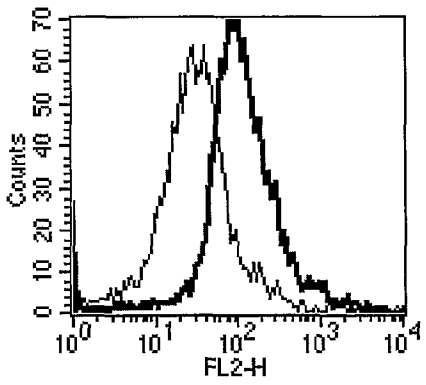

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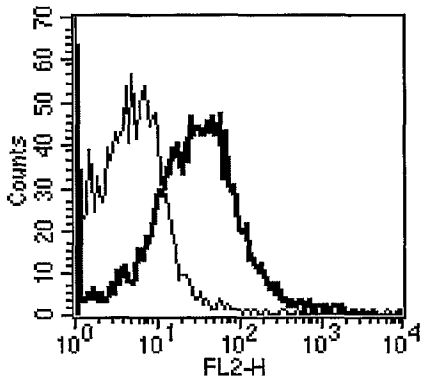

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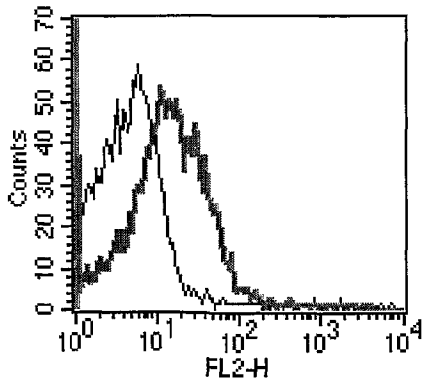

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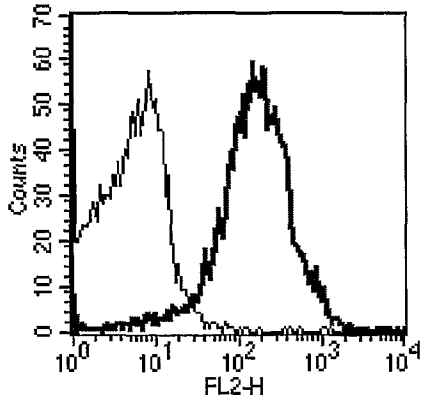

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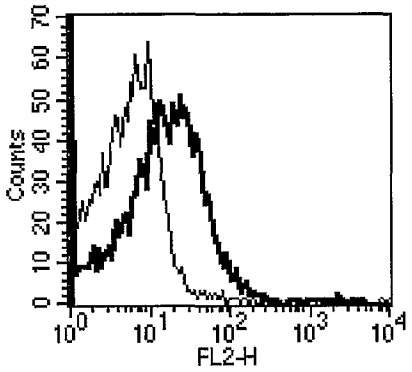

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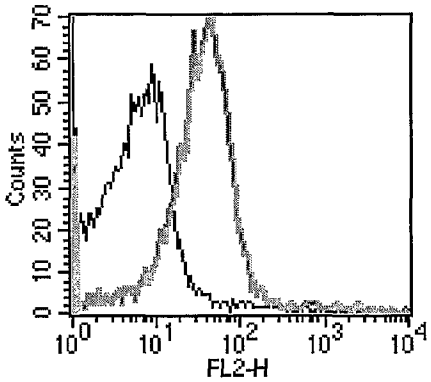

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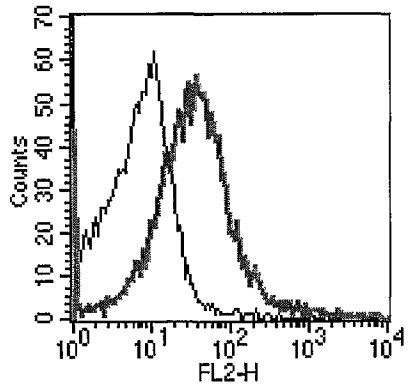

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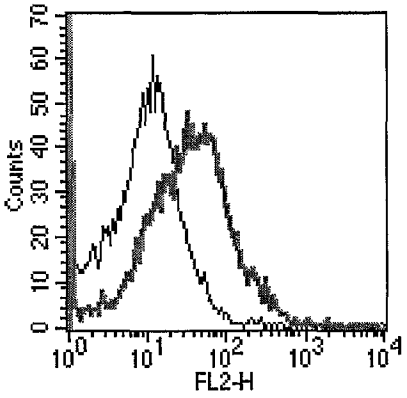

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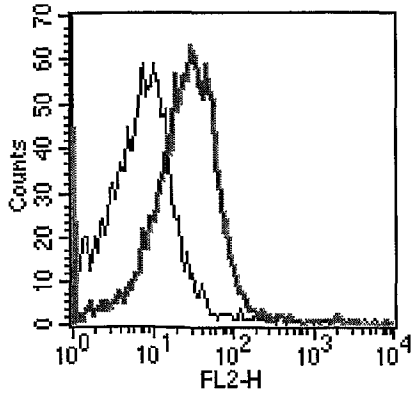

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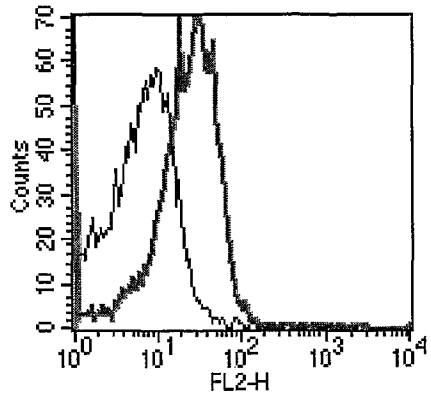

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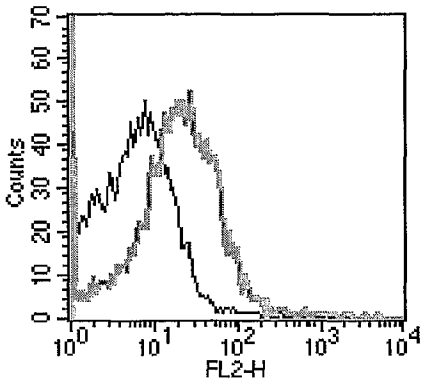

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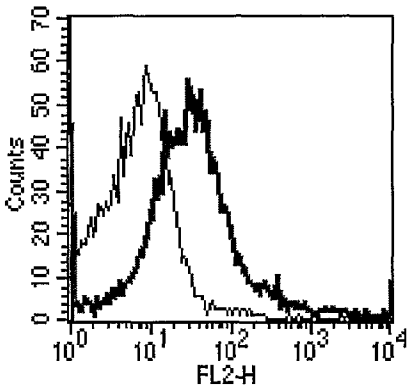

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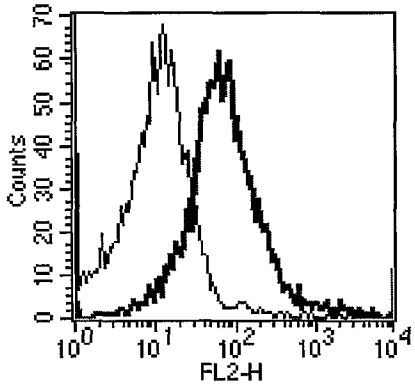

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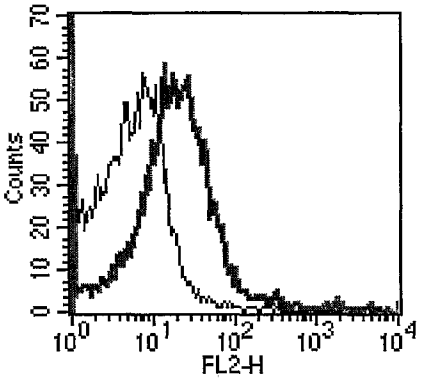

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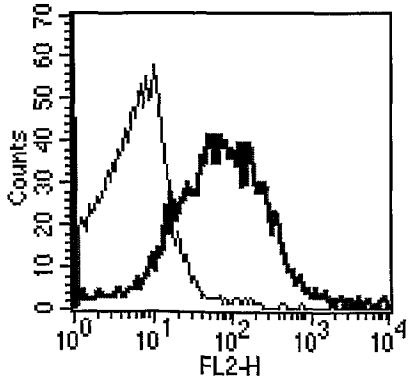

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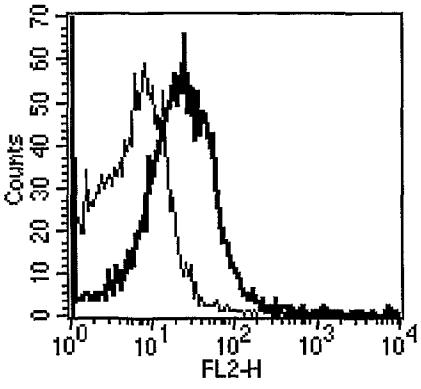

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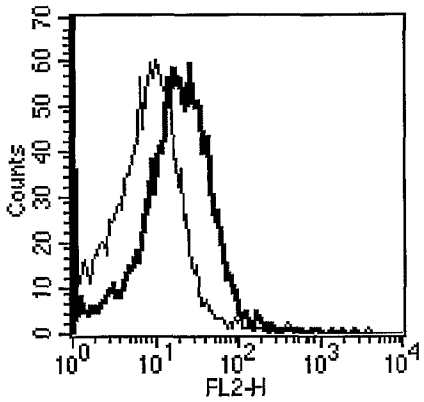

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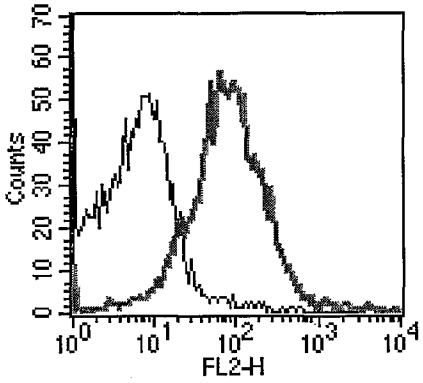

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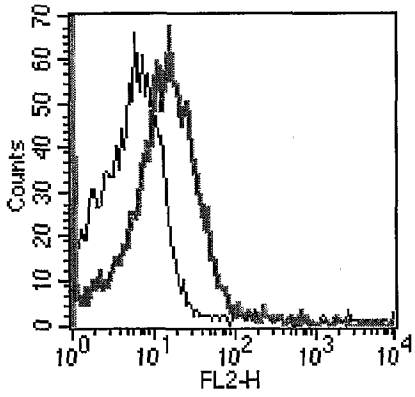

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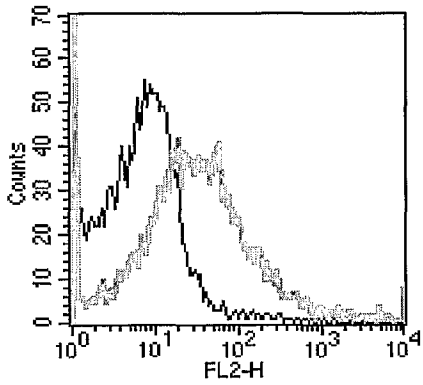

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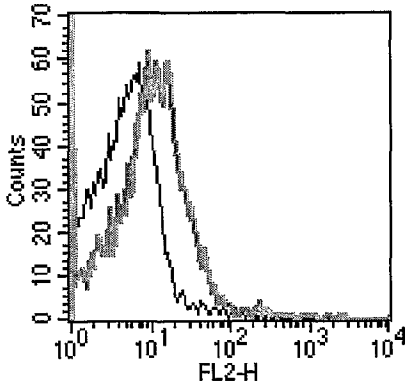
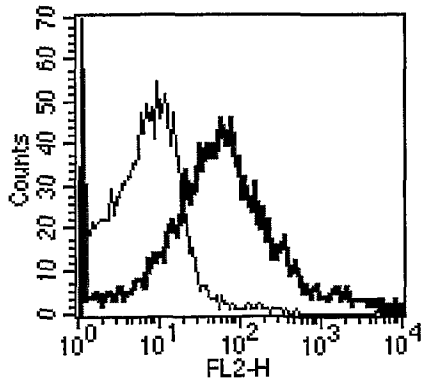


FIGURE 285



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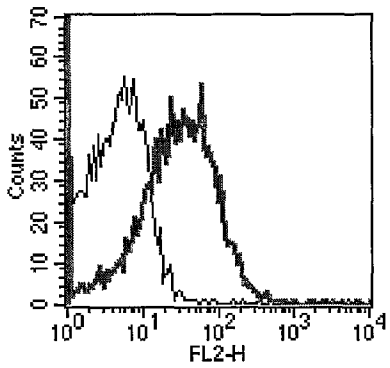

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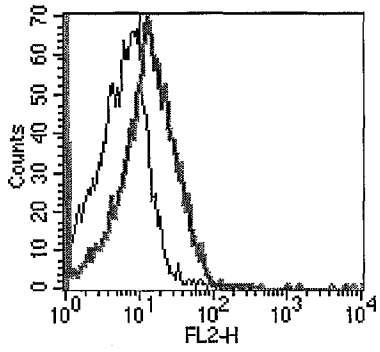

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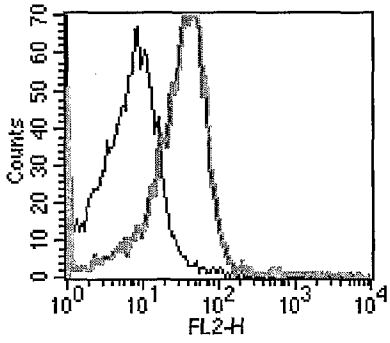

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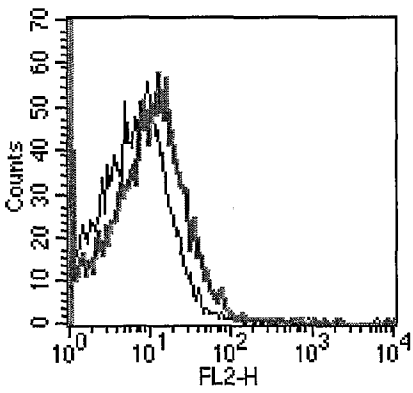

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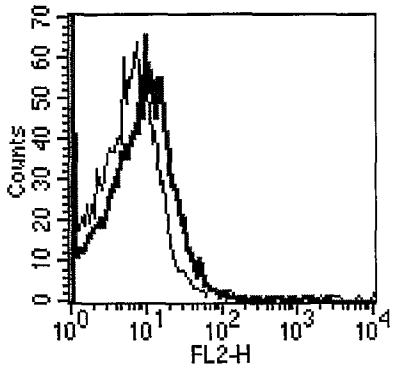

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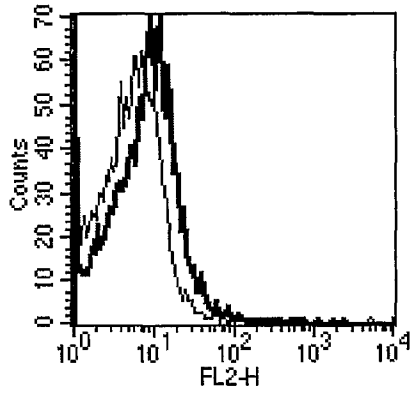

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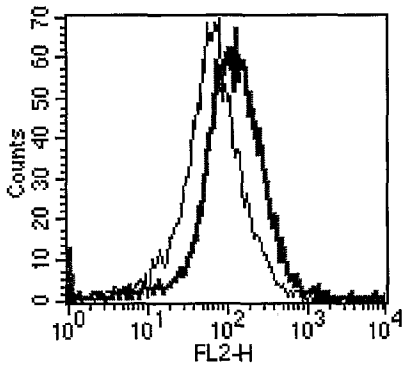

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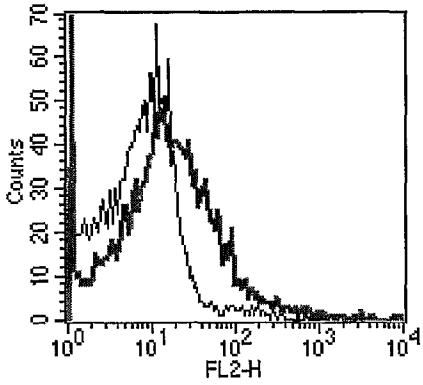

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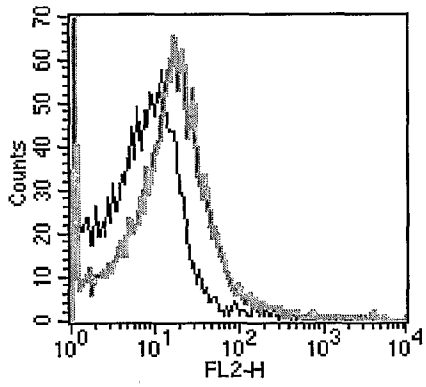

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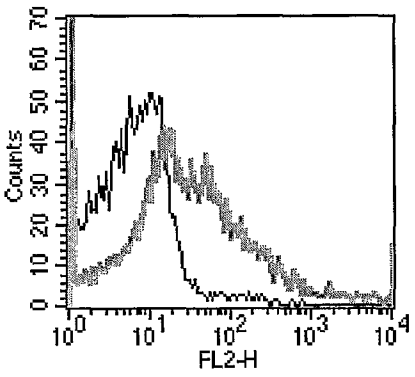

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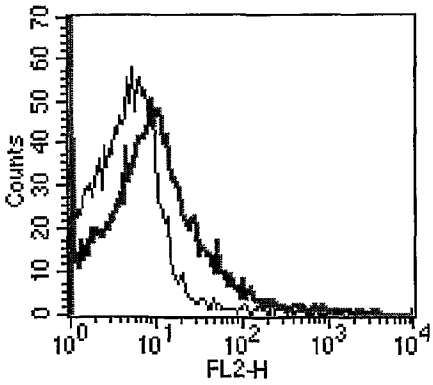

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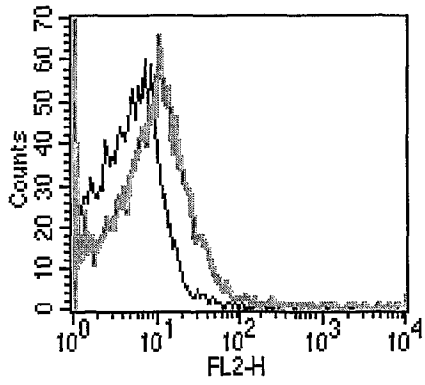


FIGURE 298

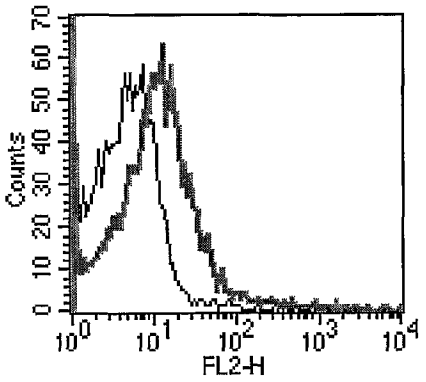
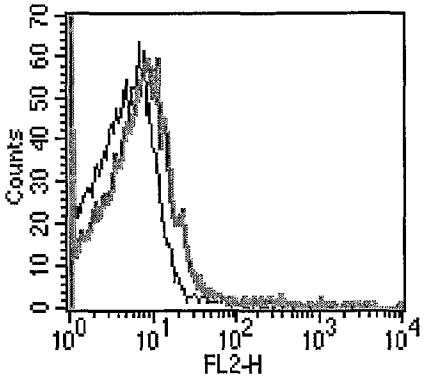


FIGURE 299



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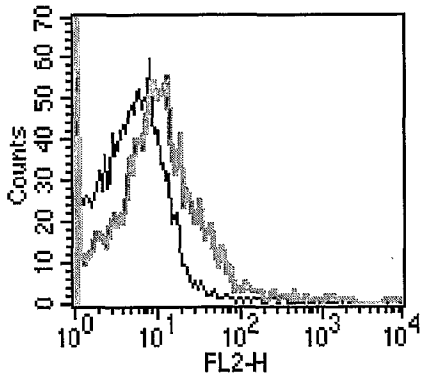

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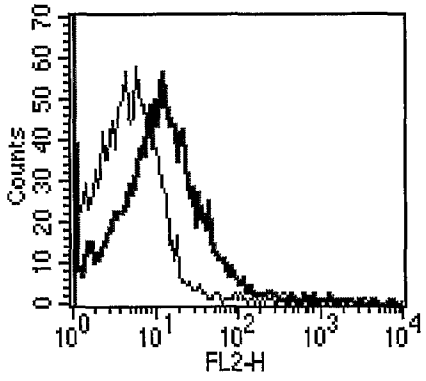

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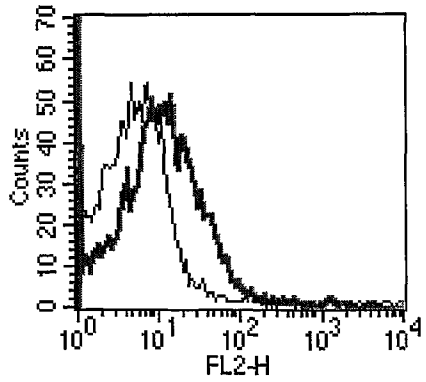

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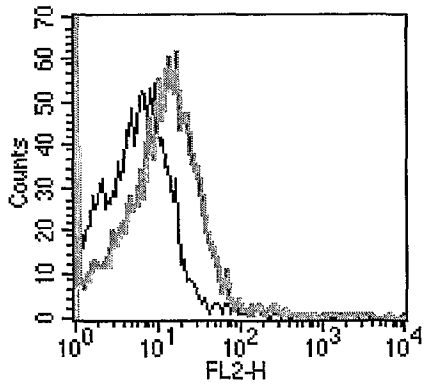

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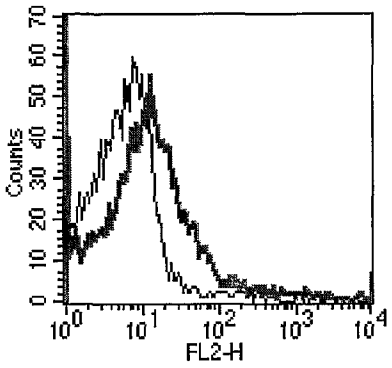

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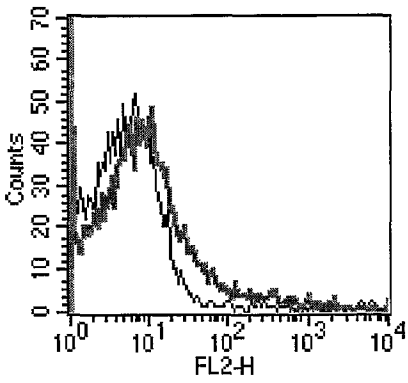

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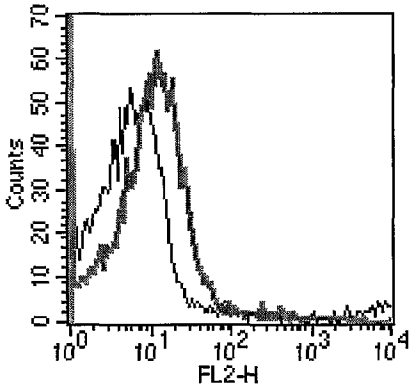

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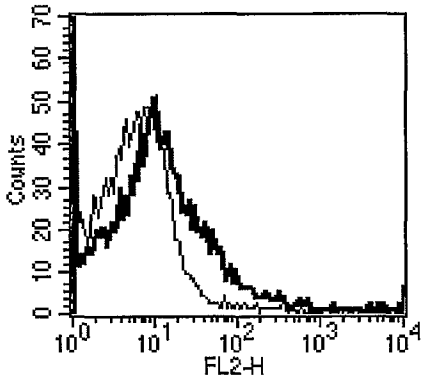

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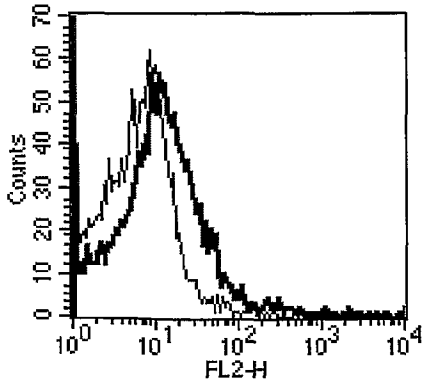

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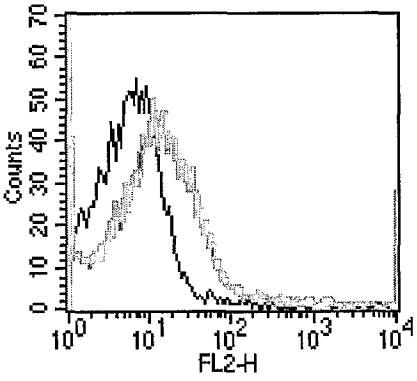

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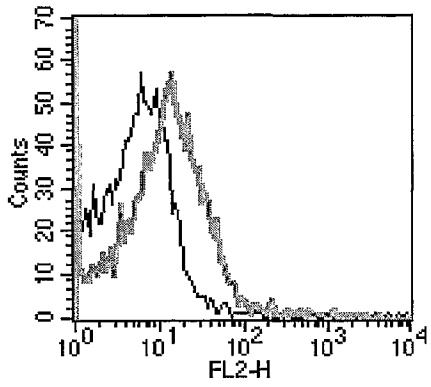

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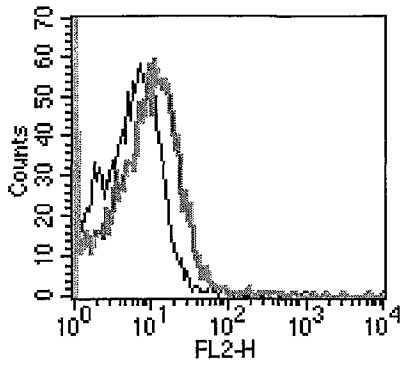

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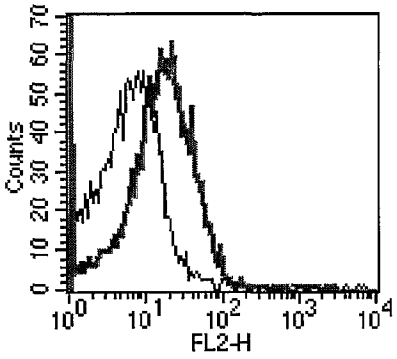

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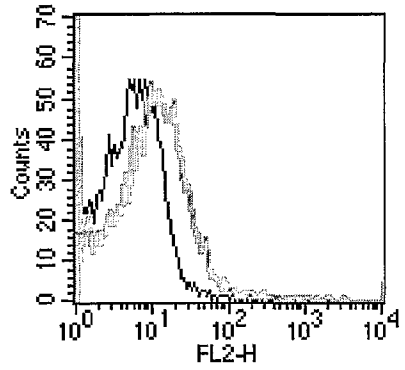

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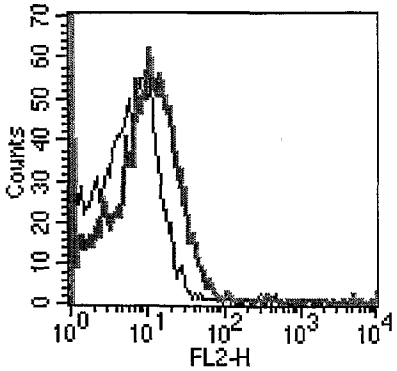

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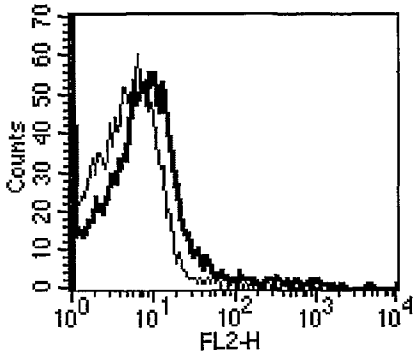

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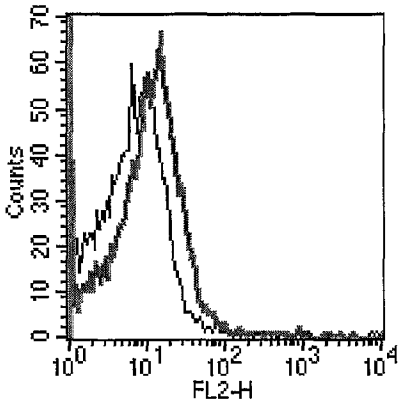

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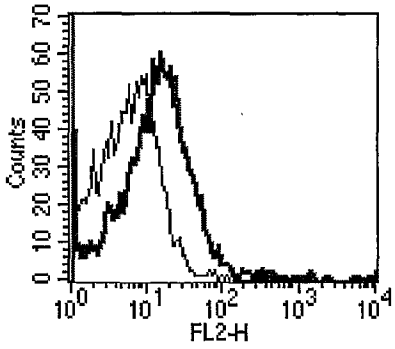

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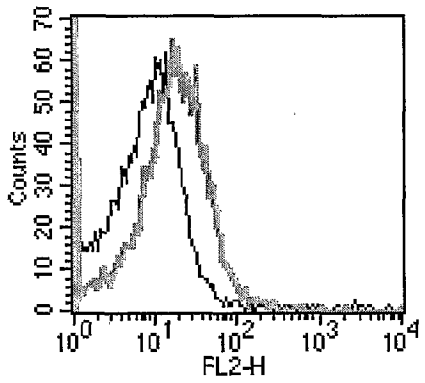

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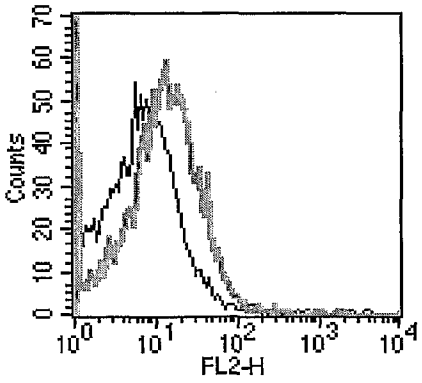

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SEQ ID 11

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AATTTTTTTATTGGAGCGATTATTTTTGGGTTATTAGCTTCTGTTATTATTACTTATATCAAGGAAAACTCTGTCATTAAAGGAGATACGGCTATT
GGTATCACCTTTAGCTCTTTTTTGGCACTGGGAGTCATCTTGATAGGGGTAGCCAATAGTTCGACGGACTTATTTCATATTTTGTTTGGGAATATT
TTAGCTGTGCAAGATAGCGATAAGTGGATTACTATTGGTGTTTCGATTTTTGTTTTAGTGGTTATTAGTCTCTTTTTCAAAGAACTATTATTAACA
TCATTTGATCCTATCTTAGCCAAATCAATGGGTGTGAAGGTCAATGCGTATCATTATTTGTTGATGGTCCTATTAACTTTAGTGGCTGTTACGGCG
ATGCAAAGCGTGGGTACTATCTTGATTGTTGCCTTATTGATTACGCCAGCAGCGACAGCTTATTTATATGCTAATAGCTTAAAAGTAATGTTAGTG
ATGTCATCTTTACTAGGCGCTTTAGCATCGGTTTTAGGGCTTTATTTGGGCTATACCTTTAATGTTGCCGCAGGGTCAAGTATCGTACTGACTTCT
GCGATGATGTTTTTTGATCAGTTTCTTTGTTTCACCCAAGCAAGGCTACCTTAAAAGATGGATGCAAAAAAAAGAAAAAACACCT

SEQ ID 14

MSMKFFEGLMSYHFLQNALITAVVIGIVSGAVGCFIILRSMSLMGDAISHAVLPGVALSFILGVNFFIGAIIFGLLASVIITYIKENSVIKGDTAI
GITFSSFLALGVILIGVANSSTDLFHILFGNILAVQDSDKWITIGVSIFVLVVISLFFKELLLTSFDPILAKSMGVKVNAYHYLLMVLLTLVAVTA
MQSVGTILIVALLITPAATAYLYANSLKVMLVMSSLLGALASVLGLYLGYTFNVAAGSSIVLTSAMMFLISFFVSPKQGYLKRWMQKKEKTP

SEQ ID 15

GTGACCCTAATGGAGACGGGACCGGTGGAAAATCTATATGGAATAGCAAAGATAAAAAGAAAGATTCTGGAAATGGTTTTGTTAATGAAATATCCC
CTTACCTCTACAATATCAGGGGAAGTT

SEQ ID 16

MTLMETGPVENLYGIAKIKRKILEMVLLMKYPLTSTISGEV

SEQ ID 17

ATGAAAAAAATTATTTATCTTGGTTTAGCCTGTGTCAGTATATTAACTTTAAGTGGTTGCGAGTCAATTGAGCGTTCTCTAAAAGGAGACCGTTAT
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CCTCAATTGGACAAGGCTGTTGCCAAAAACGAGGCACAAGTGCTTATAAAAACCTCTAAAGGTGATATAAATATCAAGTTATTTCCAAAATATGCT
CCTTTAGCTGTTGAAAATTTTCTAACACATGCAAAAGAAGGATACTATAATGGGTTAAGTTTCCACAGAGTTATCAAAGATTTTATGATACAATCT
GGTGACCCTAATGGAGACGGGACCGGTGGAAAATCTATATGGAATAGCAAAGATAAAAAGAAAGATTCTGGAAATGGTTTTGTTAATGAAATATCC
CCTTACCTCTACAATATCAGGGGAAGTTTAGCAATGGCAAATGCTGGAGCTGATACTAATGGCAGCCAATTCTTTATCAATCAAAGCCAGCAAGAT
CATTCCAAACAACTGTCAGATAAAAAAGTTCCTAAGGTGATTATTAAAGCCTATTCAGAGGGAGGAAATCCAAGTTTAGATGGTGGTTATACCGTC
TTTGGACAAGTAATCTCTGGCATGGAAACTGTGGATAAAATTGCTTCGGTAGAAGTTACAAAATCAGATCAACCAAAAGAAAAAATTACTATTACA
AGTATCAAAGTTATTAAAGACTACAAATTTAAA

SEQ ID 18

MKKIIYLGLACVSILTLSGCESIERSLKGDRYVDQKLAENSSKEATEQLNKKTKQALKADKKAFPQLDKAVAKNEAQVLIKTSKGDINIKLFPKYA
PLAVENFLTHAKEGYYNGLSFHRVIKDFMIQSGDPNGDGTGGKSIWNSKDKKKDSGNGFVNEISPYLYNIRGSLAMANAGADTNGSQFFINQSQQD
HSKQLSDKKVPKVIIKAYSEGGNPSLDGGYTVFGQVISGMETVDKIASVEVTKSDQPKEKITITSIKVIKDYKFK

SEQ ID 19

ATGAAAAAATTATTATCTCTCAGTTTAGTAGCCATTAGTTTACTTAATTTGAGTGCTTGTGAATCTGTTGACCGCGCTATAAAAGGCGATAAATAC
ATTGATGAAAAAACTGCCAAAGAAGAAAGCGAAGCAGCTTCTAAAGCCTATGAAGAAAGCATTCAAAAAGCTCTCAAAGCTGATGCTAGCCAATTT
CCACAACTAACCAAAGAAGTCGGCAAAGAAGAAGCTAAGGTCGTAATGAGGACAAGTCAAGGGGACATTACCCTTAAGTTATTCCCAAAATATGCT
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GGTGACCCCAAAGGAGATGGCACAGGTGGTGAATCGATTTGGAAAGGCAAGGATCCTAAAAAAGATGCTGGCAATGGCTTTGTCAACGAAATCTCT
CCATTTTTATATCATATTCGCGGTGCTCTTGCCATGGCAAATGCTGGTGCTAATACTAACGGTAGCCAATTTTATATCAACCAAAACAAGAAAAAT
CAAAGCAAGGGATTATCAAGTACCAACTACCCAAAACCTATCATCTCTGCCTATGAGCATGGCGGCAATCCAAGCTTAGATGGCGGTTATACTGTA
TTTGGTCAAGTCATTGATGGTATGGATGTTGTCGATAAAATTGCCGCTACTTCTATCAACCAAAATGATAAACCAGAACAAGACATTACGATTACC
TCAATTGACATTGTCAAAGATTATCGCTTTAAAAAC

SEQ ID 20

MKKLLSLSLVAISLLNLSACESVDRAIKGDKYIDEKTAKEESEAASKAYEESIQKALKADASQFPQLTKEVGKEEAKVVMRTSQGDITLKLFPKYA
PLAVENFLTHAKKGYYDNLTFHRVINDFMIQSGDPKGDGTGGESIWKGKDPKKDAGNGFVNEISPFLYHIRGALAMANAGANTNGSQFYINQNKKN
QSKGLSSTNYPKPIISAYEHGGNPSLDGGYTVFGQVIDGMDVVDKIAATSINQNDKPEQDITITSIDIVKDYRFKN

SEQ ID 21

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CCTAAAAATCAATCCAAAGAAAAGGATTTAGTCCGAAAGAATATCAGAGTTTTAGAAGAAACATTTAGAAGTTTTGGTATCGATGTAAAAGTAGAA
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GCAGGTTATAATACAAAGGTTGAAGAGTTTAATGCTTCCTCTGAGCAAAAACAAATACCTTTGCCTTTAATCGTTGTCATTGTAGATGAATTGGCT
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TTTATTTCAGATGATGATGTTGAAAGGATCGTTGGTTTTATCAAAGACCAAGCCGAGGCTGACTATGATGATGCCTTTGATCCTGGAGAAGTATCT
GAAACAGATAACGGCTCTGGTGGTGGCGGCGGAGTACCTGAAAGTGATCCTCTTTTTGAAGAAGCCAAGGGACTCGTTTTAGAGACGCAAAAAGCA

AGTGCCTCAATGATTCAACGCCGATTGTCTGTTGGTTTCAATAGAGCAACAAGACTAATGGAAGAATTAGAAGCAGCGGGGGTTATTGGTCCAGCA
GAAGGAACCAAGCCACGAAAAGTTTTAATGACTCCAACTCCGAGTGAA

SEQ ID 22

MVFMANKKKTKGKKTRRPTKAEIERQRAIQRMITALVLTIILFFGIIRLGIFGITVYNVIRFMVGSLAYLFIAATLIYLYFFKWLRKKDSLVAGFL
IASLGLLIEWHAYLFSMPILKDKEILRSTARLIVSDLMQFKITVFAGGGMLGALIYKPIAFLFSNIGAYMIGVLFIILGLFLMSSLEVYDIVEFIR
AFKNKVAEKHEQNKKERFAKREMKKAIAEQERIERQKAEEEAYLASVNVDPETGEILEDQAEDNLDDALPPEVSETSTPVFEPEILAYETSPQNDP
LPVEPTIYLEDYDSPIPNMRENDEEMVYDLDDDVDDSDIENVDFTPKTTLVYKLPTIDLFAPDKPKNQSKEKDLVRKNIRVLEETFRSFGIDVKVE
RAEIGPSVTKYEIKPAVGVRVNRISNLSDDLALALAAKDVRIETPIPGKSLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSF
NLARMPHLLVAGSTGSGKSVAVNGIISSILMKARPDQVKFMMIDPKMVELSVYNDIPHLLIPVVTNPRKASKALQKVVDEMENRYELFSKIGVRNI
AGYNTKVEEFNASSEQKQIPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVDVISGLIKANVPSRIAFAVSSGTDSRT
ILDENGAEKLLGRGDMLFKPIDENHPVRLQGSFISDDDVERIVGFIKDQAEADYDDAFDPGEVSETDNGSGGGGGVPESDPLFEEAKGLVLETQKA
SASMIQRRLSVGFNRATRLMEELEAAGVIGPAEGTKPRKVLMTPTPSE

SEQ ID 23

ATGGTTAAAAGAAATCAAAGAAAAAAAAGTGCGCCTAAGAAGCGTTTAACAAAAGCAGAAGTGGAAAAGCAACGTGCCATTAAGAGGATGATTTTA
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TTAGCCTATCCGTTTATGTTTGCCTGGTTAATTTACTTATTTTGTTTTAAATGGTTACGGCAAAAAGATGGAATGATTGCGGGAGTTCTTATTGCC
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CGCAAAAATATCAAGGTGCTTGAAGATACCTTCCAAAGTTTTGGGATTGATGTCAAGGTAGAGCGAGCAGAAATCGGGCCTTCCGTCACCAAATAT
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GGATTTAATCGTGCCACGCGCTTGATGGATGAATTGGAAGAAGCAGGTGTTATCGGTCCAGCAGAAGGAACCAAGCCTCGTAAGGTATTGCAGACA
AAC

SEQ ID 24

MVKRNQRKKSAPKKRLTKAEVEKQRAIKRMILSVLMALLLIFAMLRLGVFGVTTYNMIRFLVGSLAYPFMFAWLIYLFCFKWLRQKDGMIAGVVIA
FLGLLVEWHAFLFAMPRMLDQDIFLGTARLITRDLLALRVTEFVGGGMLGALLYKPIAFLFSNIGSYFIGFLFILLGLFLMTPWDIYDVSHFVKEA
VDKLAVAYQENKEKRFIKREEHRLQAEKEALEKQAQEEEKRLAELTVDPETGEIVEDSQSQVSYDLAEDMTKEPEILAYDSHLKDDETSLFDQEDL
AYAHEEIGAYDSLSALASSEDEMDMDEPVEVDFTPKTHLLYKLPTIDLFAPDKPKNQSKEKNLVRKNIKVLEDTFQSFGIDVKVERAEIGPSVTKY
EIKPAVGVRVNRISNLADDLALALAAKDVRIEAPIPGKSLIGIEVPNSEIATVSFRELWEQSDANPENLLEVPLGKAVNGNARSFNLARMPHLLVA
GSTGSGKSVAVNGIISSILMKARPDQVKFMMIDPKMVELSVYNDIPHLLIPVVTNPRKASKALQKVVDEMENRYELFSKIGVRNIAGYNTKVEEFN
ASSEQKQIPLPLIVVIVDELADLMMVASKEVEDAIIRLGQKARAAGIHMILATQRPSVDVISGLIKANVPSRMAFAVSSGTDSRTILDENGAEKLL
GRGDMLFKPIDENHPVRLQGSFISDDDVERIVNFIKDQTEADYDDAFDPGEVSDNDPGFSGNGGAAEGDPLFEEAKALVLETQKASASMIQRRLSV
GFNRATRLMDELEEAGVIGPAEGTKPRKVLQTN

SEQ ID 25

ATGCATATTGAGACTGTTATTGATTTCAAAGAATTAGGAAAAAGATATCGTTTTAAAAATCCTACAAAAGAATTAATAGCTGATACTTTAGAACAA
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GAAAATGTTAGATTAGCAGATAATTGGACTGCTAATGTTTCTGAGCAAGAATATCAAGAGGCAATTGCTAATATTAAAGGACAAATTAGACAAGGA
AATACTTATCAAGTAAATTATACACTAGAGCTTAGCCAACAATTATGCTCGGATCCCTTTAGTGTTTATGAACGCCTAATGGTAGAACAAGGAGCA
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CTAGTGAATTTATCAAAAAAGTTTTTAACGGCAGAGGTGGTCGTACAAGACTACCCTATTAAATTATCCCCGTTTACTTATTTTAAAACTTCTTAT
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AATGGAAGGTTTTTAACCCCAGATTTATCAGAAGGAGGGTTGAATGGGATTTATCGTCGTCATCTCCTTAAAAACCAAAAAGTAATTGAAGCACCA
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SEQ ID 26

MHIETVIDFKELGKRYRFKNPTKELIADTLEQVLEVIKEVDYYQSQNYYVVGYLSYEASAAFDSHFKVSQQKLAGEHLAYFTVHKDCENEAFPLSY
ENVRLADNWTANVSEQEYQEAIANIKGQIRQGNTYQVNYTLELSQQLCSDPFSVYERLMVEQGAGYNAYIAYDDKRILSVSPELFFKKKDEVLTTR
PMKGTSARKPTYQEDVAERDWLANDPKNRSENMMIVDLLRNDMGRICDVGTVKVKKLCQVEQYATVWQMTSTIEGVLSPEVTLMSIFQALYPCGSI
TGAPKISTMAIINELEKRPRGIYCGTIGLCMPDGQAIFNVPIRTVQMKGQQAYYGVGGGITWESQTDSEYEETRQKSAVLTRVNPKFQLITTGRVT
ENKLLFSQQHVERLVESASYFAYSFDKSKFERELKKYLHQLDEKDYRLKIMLDKTGKVTFEVKQLVNLSKKFLTAEVVVQDYPIKLSPFTYFKTSY
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SEQ ID 27

TTGGGTATGCATAGAAAAACTATTATTGATTTCAAAGAGCTCGGGCAACGCTATCTTTTTGATGAGCCATTAGTAGAATTGGTAGCCAAGTCCTTA
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GACAATGCCCTACAAACCCATAATGACAGACTAGGCAACGAGTACCTTGCCTATTTTACAGTGCACAAAACCTGTCAAAAAAAAGACCTACCTCTT
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CAGGCTGCTGGCTACAATGCCTACATCGCCCATGATGAGTTTGCCGTTATTTCAGCTAGTCCTGAATTGTTCTTTAAACAAGAGGGCAACAGGTTA
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SEQ ID 28

LGMHRKTIIDFKELGQRYLFDEPLVELVAKSLDQVGPVIEKVQHYQQLGYYVVGYLSYEAAAFFDNALQTHNDRLGNEYLAYFTVHKTCQKKDLPL
DYDSITIPNQWVSATQKEAYQKAIETIHREMQQGNTYQVNYTLQLTQELNAADSLAIYNKLVVEQAAGYNAYIAHDEFAVISASPELFFKQEGNRL
TTRPMKGTTKRGVNSWLDQQEHDWLQADGKNRSENMMMIVDLLRNDMGKICQTGSVRVDRLCEVERYSTVWQMTSTIVGDLKADCDLIDILKALFPC
GSITGAPKVSTMAIITSLEPKPRGIYCGSIGICLPDGRRFFNVPIRTIQLSHNQATYGVGGGIIWQSKWEDEYEEVHQKTAFLYRHKQIFDLKTTA
KVEHKKIAFLEQHLNRLKEAATYFAYPYNEKALQKQLSTYLENKNNAAYRLMIRLSKDGKISLSDQPLEPLSADFLTAQLSLQKKDVTASPFTYFK
TSYRPHIEQKSYEQLFYNQAGQLLETSIGNLFVQLGQTLYTPPVAVGILPGLFRQELLATGQAQEKEVTLADLKEASAIFGGNAVRGLYPLNLELT
HLDALLAKSQA

SEQ ID 29

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CAGGTTCAAACCATGCTTGAGAGGGCTTTTCCTGCGGCTTCATACAGCGAAACCATTCTCCACAGCGACCAAGGCTGGCAGTACCAGCACAAGTCC
TACCATCAATTTCTGGAGGACAAAGGCATTCGTCCTTCTATGTCACGGAAGGGGAACAGTCCTGACAACGGTATGATGGAATCTTTCTTTGGGATT
CTAAAATCTGAGATGTTCTATGGCTTGGAGAAGTCTTACAAATCACTTGATGACCTTGAGCAAGCTATCACAGATTACATTTTTTACTACAACAAC
AAGCGAATCAAAGCAAAACTAAAAGGACTTAGTCCTGTGCAATACAGAACTAAATCCTTCACT

SEQ ID 30

MVTGGFRLDLLLEITKIARATYYYQLKKLNKPNKDKAIKSDIQSIYDEHRGNYGYRRIYLELRNRGFVINHKRVQGLMKSMGLTARIRRKRKYASY
KGEVGKKADNLIQRQFEGSKPYEKCYTDVTEFALPEGKLYLSPVLDGYNSEIIDFTLSRSPDLKQVQTMLERAFPAASYSETILHSDQGWQYQHKS
YHQFLEDKGIRPSMSRKGNSPDNGMMESFFGILKSEMFYGLEKSYKSLDDLEQAITDYIFYYNNKRIKAKLKGLSPVQYRTKSFT

SEQ ID 31

ATGCTACTTGAAATCCTTGATTTATCACGCTCCACCTATTACTATCAAGTGAAGCGACTAGCTCAAGGAGATAAGGATATAGAACTAAAGCATGTG
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GTTCAACGTCTCATGAAAGTCATGGGCTTAGCAGCCCGCATTCGTCGGAAGCGCAAGTATTCTTCTTACAAAGGAGAGGTTGGTAAGAAGGCTGAT
AATCTGATTAAACGTCACTTCGAAGGCTCTAAACCTTACGAAAAATGTTACACTGATGTGACGGAGTTGGCCTTACCTGAAGGAAAACTCTACTTA
TCACCTGTTCTTGATGGCTATAACAGTGAGATTATTGATTTCACTCTATCTCGGTCTCCTAACTTGAAACAGGTTCAAACCATGCTTGAGAAGACT
TTTCCAGCAGATTCATACAGCGGAACTATTCTTCATAGTGACCAGGGGTGGCAATACCAACACCAGTCCTACCATGATTTTTTAGAGTCTAAAGGT
ATTCTGGCATCCATGTCCCGCAAAGGGAATAGTCCGGATAACGGCATGATGGAATCCTTCTTTGGCATTCTCAAATCTGAAATGTTTTATGGACTC
GAGACAACTTATCAATCACTTGACAAGCTTGAAGAAGCTATTACAGATTACATTTTTTACTACAACAACAAACGAATTAAAGCAAAACTAAAAGGA
TTTAGTCCTGTCCAATACAGAACTAAATCCTTTCAA

SEQ ID 32

MLLEILDLSRSTYYYQVKRLAQGDKDIELKHVIREIYDEHKGNYGYRRIHMELRNRGFVVNHKKVQRLMKVMGLAARIRRKRKYSSYKGEVGKKAD
NLIKRHFEGSKPYEKCYTDVTELALPEGKLYLSPVLDGYNSEIIDFTLSRSPNLKQVQTMLEKTFPADSYSGTILHSDQGWQYQHQSYHDFLESKG
ILASMSRKGNSPDNGMMESFFGILKSEMFYGLETTYQSLDKLEEAITDYIFYYNNKRIKAKLKGFSPVQYRTKSFQ

SEQ ID 33

ATGAAATTAAGTTATGAAGATAAACTAGAAATATACGAGTTAAGAAAGATCGGGATGTCCTGGTCTCAGATTAGTCAACGATATGATGTTCGTATC
TCGAATCTTAAATACATGATAAAACTCATGGATCGGTATGGTGTAGAAATCGTCGAAAAAGGTAGAAATGAGTATTATCCACCTGAATTAAAGCAG
GAAATGATAGATAAAGTCTTGATTCATGGTTGTTCTCAACTCTCTATCTCGGTCTCCTAACTTGAAACAGGTTCAAACCATGCTTGAGAAGACTT
TCCCAATTTAAGAAAAATGGTTATACTATTGTTGAGAAAACAAGAGGGAGACCGAGTAAAATGGGACGTAAGCGTAAGAAAACTTGGGAAGAAATG
ACAGAGCTCGAGCGACTTCAGGAAGAAAATGAGCGCTTGAGAACGGAGAATGCCTTTCTAAAAAAGTTGAGGGATTTGCGCTTGAGGGACGAAGCC
TTACAGAGCGAACGGCAGAAACAATTAGAGAAATGGTCACAGGAGGATTCCGAC

SEQ ID 34

MKLSYEDKLEIYELRKIGMSWSQISQRYDVRISNLKYMIKLMDRYGVEIVEKGRNEYYPPELKQEMIDKVLIHGCSQLSVSLDYALSNCSILTNWL
SQFKKNGYTIVEKTRGRPSKMGRKRKKTWEEMTELERLQEENERLRTENAFLKKLRDLRLRDEALQSERQKQLEKWSQEDSD

SEQ ID 35

ATGAAATTTAATCAAGAAACGAAAGTTAAGATTTATGAGTTACGGCAAATGGGAGAGTCCATTAAATCCATATCAAAAAAGTTTGATATGGCAGAA
TCCGATCTCAAATATATGATTCGCTTGATTGATAGGTATGGGGTAACCATTGTTCAAAAATGTAAGAATCATTATTATTCTCCAGAACTGAAGCAA
GAGATAATAAATAAAGTCCTGATTGACGGCCAATCTCAGAAACAAACATCCTTAGATTATGCTTTACCAACTTCTAGTATGCTCTCAAGGTGGATA
GCGCAATACAAGAAAAACGGTTATACTATTCTTGAAAAACCAAGAGGGAGACCGAGTAAGATGGGGCGTAAACGTAAGAAAAATTTGGAAGAGATG
ACAGAGGTTGAACGTCTTCAGAAGGAATTAGAATACCCTAGAGCGGAGAATGCTGTGCTAAAAAAGCTGAGAGAATACCGCTTGAGGGACGAAGCA
AAACTCAAAGAGCAACAGAAATCATTCAAGCAT

SEQ ID 36

MKFNQETKVKIYELRQMGESIKSISKKFDMAESDLKYMIRLIDRYGVTIVQKCKNHYYSPELKQEIINKVLIDGQSQKQTSLDYALPTSSMLSRWI
AQYKKNGYTILEKPRGRPSKMGRKRKKNLEEMTEVERLQKELEYPRAENAVLKKLREYRLRDEAKLKEQQKSFKH

SEQ ID 37

TTGAAAAATCAACAAAAATTAATGTATCTAGAGAGTATCGAGCTATACTCAAACATCACTAAAGCCGCTGCACACCTTTTTATTTCTCAACCTTAC
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TATCTATTCTACCTAAAAGAAATTGATATGATTGAGCGTCAAATGGCCAAAGAACTATATCTCATCCGTTCTGATAAAAAAGGAGAAATCACACTT
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AATCAAAATATTTCTGAACAATTGGTAGCGAGTGGTGATATTGACCTAGCTGTTGGGATGGCTCCTATCCTTTATAAAGATGGAATTGCATCAACC
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ATTTCAGTTCTAGACAATGAACCTCTTATCCTAACACCATTAGAGTACGGAATTGGCAAAACAATTGCACAATTCTATGAGCTTCATCACATGTCA
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CGCTATTTGGATAAAGAGTGCAATGTCTACCATTTTCATAAGAATAAGTTATTTTCAGAGTACATTATGATTTATAAAAAAGATGTTGAATTATCT
GGAATTGCTCTCCTACTTTATAAAGCTTTTTTAACCAAG

SEQ ID 38

MKNQQKLMYLESIELYSNITKAAAHLFISQPYLSKVIKQLENELEIKLIQSQGHQTFLTYAGQRYLFYLKEIDMIERQMAKELYLIRSDKKGEITL
GINSGLASSILANVLPKFNLEHPEISVKLLENNQNISEQLVASGDIDLAVGMAPILYKDGIASTTIYRDELFLMIPTTSQLYNAEKRGQIIPFEYP
ISVLDNEPLILTPLEYGIGKTIAQFYELHHMSLNQMITTSTVPTAASLSLSGMGATFVPQTLIHRYLDKECNVYHFHKNKLFSEYIMIYKKDVELS
GIALLLYKAFLTK

SEQ ID 39

TTGATAAGACAAGGAGAATCCTATTTGGATATTAAACAAATTCGTTATTTTATCGCAATCGTTGAAAATCATTTTAACTTGAGCCAGGCGGCGGAA
CTGTTGTATGTGTCGCAGCCGACACTTAGCATGATGATCAATGATTTTGAAAAAAGAGAAAATGTTAAGCTCTTCAAACGAAAAAGAGGTCGTATT
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GGGATTCAATTCAATGTTAAGGAGATTGGTGCTTACCAACTAAAAAATGAACTACTCGTGGGAAATGTTGACGTCGCAGTCTTGTTATCCCCAACA
GGCATCGCTGATAATTTGGTTGAGACTTATGAAATCCAGAGATCAGAATTATCTGTATGCCTGTCTCCACGCCATCGTTTAGCTTCCAAAAAAGTT
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GTCAGACCTAATATTATTTTGACGTCCTCTTCCTGGGATTTTATGCTTAATTCTACCAAGATTAATCACAACGTCTTAACTATTTGTCCCAAACCT
ATTACAGAATTATACCAATTAAAGGACATTAAGTGTATTCCAATGGAACGTCCCATTTCTTGGCGTGTTGTCTTAACACGCCTCCGGAAAAAAAGT
TATTCTGAAATAGAAGCCTACATCATGGACGACTTGCTACAGTCTTTTTTTAAG

SEQ ID 40

LIRQGESYLDIKQIRYFIAIVENHFNLSQAAELLYVSQPTLSMMINDFEKRENVKLFKRKRGRIIGLTYLGDNYYKDAQKVLSLYDDMFLKLHDHS
KGLKGSINIGIPPLILSVVFSEVMPKLILENPGIQFNVKEIGAYQLKNELLVGNVDVAVLLSPTGIADNLVETYEIQRSELSVCLSPRHRLASKKV
IQWEDLTDEQLALFDPSFMVHHLVLEACERHQVRPNIILTSSSWDFMLNSTKINHNVLTICPKPITELVQLKDIKCIPMERPISWRVVLTRLRKKS
YSEIEAYIMDDLLQSFFK

SEQ ID 41

ATGGCCAATGCATCTTTGCGACATCAATTATTTGAAAAACTTGACCAAAAATGTGATCAAATGGTTGCTATTCGTCGCTATTTACATGAAAATCCC
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GAGACAGGGCTTTCTTTTGCTTCAAAAACAGCGGGCGTCATGCATGCTTGTGGACATGATGCCCATACAGCTTATTTATTGATTTTGGCTGAGAGC
TTGATTGAATTAAAATCAGAATTTTCAGGTCATATCCGTATCTTACATCAACCGGCTGAAGAGGTGCCACCAGGCGGAGCAAAAGCAATGATTGAA
GCAGGATGTTTAGATGGCATTGATGCTGTCCTTGGTATCCATGTTATGTCAACGATGGAAGAGGGAACGGTACAATATCACGCAGGTCCCATTCAA
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GATGGAATAGCACAAACTTATGGTGTTAGTTATCAGTTAGACTATCAGAATGATTATCCTGTTTTAGTTAATAACAGTGAAGTGACACAGAAAGTT
GCAAATAGTTTAAAATCTGTTGCTATAAAAGAAATTTTAGATGTCATTGATTGCGACCCTCAAACGCCGTCTGAAGATTTTGCCTATTATGCTCAA
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TTGATGGTATCTGCTAAATCAATGGCAACAGCAGCGCTTGCTATGCTTGTAGAAGGAGAA

SEQ ID 42

MANASLRHQLFEKLDQKCDQMVAIRRYLHENPELSFKETKTAAYISDFYKGKDCHVQTQFGGMNGVVVDIYGDKATDKPIKHIALRADFDALPIQE
ETGLSFASKTAGVMHACGHDAHTAYLLILAESLIELKSEFSGHIRILHQPAEEVPPGGAKAMIEAGCLDGIDAVLGIHVMSTMEEGTVQYHAGPIQ
TGRATFKVILQGKGGHGSMPHRANDTIVAASSFVMAAQTIVSRRVNPFDTAVVTIGSFDGKGSANVIKDSVTLEGDVRVMSEETRGVVEEEFKRIL
DGIAQTYGVSYQLDYQNDYPVLVNNSEVTQKVANSLKSVAIKEILDVIDCDPQTPSEDFAYYAQTIPACFFYVGAHEEGQPYYPHHHPKFQIAESS
LMVSAKSMATAALAMLVEGE

SEQ ID 43

ATGTTAACGACAAAGGAAAATTTCAAAGGAAATAACAAATTATTGGTGGGAATTGTACTCGCTGTACTATCATTTTGGTTATTTGCACAGTCTATT
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ATTGTTGTAACTGGTGGTTTAGCAGATAAACTTGGTCGAGTTAAATTTACTTTTATTGGTCTTTGCTTAAATATTATTGGTTCTCTACTAATTGTT
TTAGCTAATGGAGCAGTGCTATTTATTATGGGACGTATTTTTCAAGGATTGGCAGCAGCTTTTATTATGCCATCAACAATGGCCTTGGTTAAAACG
TACTATGATGGTAAAGATAGACAACGTGCAGTTAGTTTCTGGTCAATCGGATCGTGGGGTGGCTCAGGTCTATGTTCTTATTTTGGTGGAGCGGTG
GCAAGTACTCTAGGTTGGCGTTATGTCTTTATCTTTTCAATCATCGCATCAGTAGTTAGTTTTCTATTAATTTTAGGAACCCCAGAAAGTAAAAAT
GTTGGACAAAAAACTCACTTTGATTACCTTGGTTTAATTATTTTTATTATTTCAATGTTATCGTTAAATATTGGGATATCTATGGCTCAGGAACAT
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ATTGACTTTCATCTGTTTGAAAATCGATTTTACTTAGGTGCGACAATATCAAATTTCTTACTGAATGCAGTTGCAGGAACTCTGATTGTTATTAAT
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CAAGGACCTTTGTATCTTGTGTTAGTCTTTGTTGGTTATGCTTTATTTGGAACAGGCTTGGGGATCTATGCGACACCATCAACAGATACAGCTATT
TCTAGTATTCCTAATGAAAAAGTAGGTTCTGCATCTGGAATTTACAAAATGGCAAGTTCACTAGGTGGTGCAATTGGTGTAGCAACTTCAATTGCG
ATTTATCATGCTTTTTCTGGTAATGCAGATTTTCACAAAGCAGCTTTGTGTGGATTAATTTTAAACCTAGTTTTTTGTAGTCTATCGATCTTATCA
ATTCTTTTTGTTATCCCTAAGAAAATTGAGGATAAA

SEQ ID 44

MLTTKENFKGNNKLLVGIVLAVLSFWLFAQSILNMGPDVQSSLGISSGAMDIGVSSTALFSGLFIVVTGGLADKLGRVKFTFIGLCLNIIGSLLIV
LANGAVLFIMGRIFQGLAAAFIMPSTMALVKTYYDGKDRQRAVSFWSIGSWGGSGLCSYFGGAVASTLGWRYVFIFSIIASVVSFLLILGTPESKN
VGQKTHFDYLGLIIFIISMLSLNIGISMAQEHGLMNVIPLSLFTVMLIGFVLFYYVETRKSNSFIDFHLFENRFYLGATISNFLLNAVAGTLIVIN
TYMQQGRQLTPKVAGEMSLGYLVCVLIAIRVGEKILQRFGARKPMLLGAMSTFVGIFLMTLVNIQGPLYLVLVFVGYALFGTGLGIYATPSTDTAI
SSIPNEKVGSASGIYKMASSLGGAIGVATSIAIYHAFSGNADFHKAALCGLILNLVFCSLSILSILFVIPKKIEDK

SEQ ID 45

ATGTCACATCATCAACAAACCGTTTCAAAACAAACAATTATGGCGATTATCGCCATAGCACTCATTGGTTTTTCAGGAATTTTGTCTGAAACCAGT
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CGCATTCTCAAAATTCCCTCTCTAACCTTTGGCCTGATTCCCTTTTTTGTCTTCCAGCTGATTAATTTAGGCATAAATTTTCTAACGCCAAACTTT
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GCCGAGAAAAATGCCGATGCCACGGCCATTTTTCAGATGATGCAGCAATTTGCTGGCGCTCTAGGAACTGCTATGGCATCACTGATAGCAAATAGT
CAAGCAGAATTCACAAGCGGTGTCCAGTCTGTCTACCTTCTCTTTACTATTTTTGCTCTACTTGATTTTATCTTTTTCTTTGCTATGTTTTACCAT
TTAGGGAAAAAAGGATTAGCC

SEQ ID 46

MSHHQQTVSKQTIMAIIAIALIGFSGILSETSMNVTFPTLMSVYQLPLNSLQWMTTIYLLAVAIMMTTSATLKKNVRERPLFFMATGLFTFGTILA
VLTQSFAIMLLARIFQGIGTGLVMPQMFNIILERVPMHKVGLFMGFAGLIISLAPAFGPTYGGFMISHFSWQWIFICILPVPLIAGILAYYYLEDS
PVSEKVPFDWLAFIALSISLTSALLAITSLENGSVNLYYLGLFILSFILFLYKNLTAKQPFLDIRILKIPSLTFGLIPFFVFQLINLGINFLTPNF
IVMEKIANSSQAGMVLLPGTLLGALLAPAFGKLYDQKGARLSLYLGNALFSLSLIIMTLQTRHFMLLPFTLLYILFTFGRNMGFNNSLATAIRELP
AEKNADATAIFQMMQQFAGALGTAMASLIANSQAEFTSGVQSVYLLFTIFALLDFIFFFAMFYHLGKKGLA

SEQ ID 47

ATGAGTTTATCCATCATGACAAAACACAAACACCTAACTCTCTTAGACCGTAATGACATCCAATCTGGTTTGGATAGAGGAGAAACCTTTAAAGCC
ATCGGGCTTAATCTACTGAAACACCCTACTACTATCGCAAAAGAAGTCAAACGAAATAAGCAACTAAGAGAATCAACCAAAGACTGCCTAGACTGT
CCGCTACTAAGAAAAGCTCCCTATGTTTGTAATGGGTGTCCAAAGAGGAGGATCAACTGTGGTTACAAGAAGACCTTCTATCTTGCTAAGCAAGCT
CAAAGAAACTATGAAAAACTTTTAGTTGAATCTAGAGAAGGAATCCCTTTGAACAAAGAGACCTTCTGGAAAATAGATAGAGTGCTTTCTAATGGG
GTCAAGAAGGGCCAACGTATCTATCATATCCTCAAAACCAACGATCTAGAAGTGAGTTCTTCAACCGTTTATCGACACATCAAGAAAGGCTACCTA
TCCATCACACCAATCGACCTACCCAGAGCTGTGAAGTTCAAAAAAAGGCGAAAGAGCACACTCCCTCCTATTCCAAAAGCGATTAAAGAAGGGCGA
CGGTACGAGGATTTTATAGAACACATAACNNNNNTTAAT

SEQ ID 48

MSLSIMTKHKHLTLLDRNDIQSGLDRGETFKAIGLNLLKHPTTIAKEVKRNKQLRESTKDCLDCPLLRKAPYVCNGCPKRRINCGYKKTFYLAKQA
QRNYEKLLVESREGIPLNKETFWKIDRVLSNGVKKGQRIYHILKTNDLEVSSSTVYRHIKKGYLSITPIDLPRAVKFKKRRKSTLPPIPKAIKEGR
RYEDFIEHITXXN

SEQ ID 49

ATGGCTAAAAAAGTTGAAAAACTTGTAAAACTTCAAATTCCTGCTGGTAAAGCAACTCCAGCTCCACCAGTTGGACCAGCACTTGGTCAAGCAGGA
ATCAACATCATGGGATTCACTAAAGAGTTTAACGCTCGTACAGCTGATCAAGCTGGTATGATTATTCCAGTTGTTATCTCAGTATATGAAGACAAA
TCATTTGATTTCATCACTAAAACACCACCAGCTGCTGTTCTTTTGAAAAAAGCTGCAGGTGTTGAAAAAGGATCAGGTGAACCTAACAAAACTAAA
GTTGCAACAATTACTCGTGCGCAAGTACAAGAAATTGCTGAAACTAAAATGCCAGATTTAAACGCTGCAAACCTTGAGTCTGCAATGCGTATGATC
GAAGGTACTGCTCGTTCTATGGGATTCACTGTTACTGAC

SEQ ID 50

MAKKVEKLVKLQIPAGKATPAPPVGPALGQAGINIMGFTKEFNARTADQAGMIIPVVISVYEDKSFDFITKTPPAAVLLKKAAGVEKGSGEPNKTK
VATITRAQVQEIAETKMPDLNAANLESAMRMIEGTARSMGFTVTD

SEQ ID 51

ATGCAATATTGCATATCTGTGGGAGGTAAAAATCTCAATTACCGCCAAAACCACAACAGGAGGATTTTTAAAATGGCTAAAAAAGTCGAAAAACTT
GTAAAACTTCAAATCCCTGCTGGTAAAGCTACACCAGCTCCACCAGTTGGACCAGCTCTTGGTCAAGCAGGTATCAACATCATGGGCTTCACTAAA
GAATTTAACGCTCGTACAGCTGATCAAGCTGGTATGATCATCCCAGTTGTTATCTCAGTTTATGAAGACAAATCATTTGATTTCATCACTAAAACA
CCACCAGCTGCTGTTCTTTTGAAAAAAGCTGCAGGTGTTGAAAAAGGATCAGGTACACCTAACACTACTAAGGTTGCGACAGTTACTCGTGCACAA
GTACAAGAAATTGCTGAAACTAAGATGCCAGATTTGAACGCTGCAAACATTGAAGCTGCAATGCGTATGATCGAAGGTACTGCTCGTTCTATGGGA
TTCACTGTTACTGAC

SEQ ID 52

MQYCISVGGKNLNYRQNHNRRIFKMAKKVEKLVKLQIPAGKATPAPPVGPALGQAGINIMGFTKEFNARTADQAGMIIPVVISVYEDKSFDFITKT
PPAAVLLKKAAGVEKGSGTPNTTKVATVTRAQVQEIAETKMPDLNAANIEAAMRMIEGTARSMGFTVTD

SEQ ID 53

ATGGCTAAAAAAAGTAAAAACTTACGTGCTGCTCTTGAGAAAATTGATAGCACTAAAGCATACAGCGTAGAAGAAGCTGTAGCTCTTGCAAAAGAA
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TTACCAGCAGGTACTGGTAAAACTTCACGTGTTCTTGTTTTTGCTCGTGGTGCTAAAGCTGAAGAAGCTAAAGCAGCAGGTGCAGACTTTGTCGGT
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CGTGTCCTTGGACCTCGTAACTTGATGCCAAACCCTAAAACTGGTACAGTAACTATGGACGTTGCTAAAGCAGTTGAAGAGTCTAAAGGTGGTAAA
ATTACTTACCGTGCTGATAAAGCAGGTAACGTCCAAGCCCTTATTGGTAAAGTTTCATTTGATGATGCTAAATTAGTTGATAACTTCAAAGCATTT
AATGATGTTATTGTTAAAGCTAAACCAGCTACTGCAAAAGGAACTTACATCACAAACCTTTCAATTACAACAACACAAGGTGTTGGTATCAAAGTT
GATCCTAACTCACTT

SEQ ID 54

MAKKSKNLRAALEKIDSTKAYSVEEAVALAKETNFAKFDATVEVSYNLNIDVKKADQQIRGAMVLPAGTGKTSRVLVFARGAKAEEAKAAGADFVG
EDDLVAKIQGGWLDFDVVIATPDMMALVGRLGRVLGPRNLMPNPKTGTVTMDVAKAVEESKGGKITYRADKAGNVQALIGKVSFDDAKLVDNFKAF
NDVIVKAKPATAKGTYITNLSITTTQGVGIKVDPNSL

SEQ ID 55

ATGGCTAAAAAAAGCAAACAAATGCGTGCTGCACTTGAAAAAGTAGATAGCACAAAAGCGTACAGTGTAGAAGAAGCTGTAGCATTAGTAAAAGAA
ACGAACTTCGCAAAATTTGATGCGTCTGTTGAAGTTGCTTACAACTTGAACATTGACGTTCGTAAAGCAGACCAACAAATCCGTGGCGCAATGGTA
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GAAGACGACCTTGTTGCAAAAATCAATGGTGGATGGCTTGACTTTGACGTTGTTATCGCAACGCCAGACATGATGGCTATCGTAGGTCGTCTTGGA
CGTGTCCTTGGACCTCGTAACTTGATGCCAAACCCTAAAACTGGTACAGTAACGATGGATGTTGCTAAAGCCGTTGAAGAGTCTAAAGGTGGTAAA
ATCACTTACCGTGCTGACAAAGCAGGTAATGTTCAAGCTCTTATTGGTAAAGTTTCATTTGATGCTGACAAATTGGTTGAAAACTTCAAAGCCTTC
CACGATGTAATGGCTAAAGCTAAACCTGCAACAGCTAAAGGAACTTACATGGCAAACGTCTCAATCACATCAACACAAGGTGTTGGTATCAAGGTT
GATCCTAACTCACTT

SEQ ID 56

MAKKSKQMRAALEKVDSTKAYSVEEAVALVKETNFAKFDASVEVAYNLNIDVRKADQQIRGAMVLPNGTGKTQRVLVFARGAKAEEAKAAGADFVG
EDDLVAKINGGWLDFDVVIATPDMMAIVGRLGRVLGPRNLMPNPKTGTVTMDVAKAVEESKGGKITYRADKAGNVQALIGKVSFDADKLVENFKAF
HDVMAKAKPATAKGTYMANVSITSTQGVGIKVDPNSL

SEQ ID 57

TTGGTAAAAATGAGACGTAACATATTATTGAGCATTACTTGTTTATTGATGGTGACTCTGACTGCATGCCATTCACAGGATAGCAAAAGTCATAAA
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AGGAAAGGTGATTTTAAAACCATGCGTTTTGCGCCAGAAGAAAATTCATTCCCATTACGCTATATAGAAAAAAACAATGTATCTAAG

SEQ ID 58

MVKMRRNILLSITCLLMVTLTACHSQDSKSHKLNSDKLTLAWGEDFGDVNPHRYNPDQFVIQDMVYEGLVRYGDNGKIEPALAKSWSISQDGKTYT
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KPIGTGQWVVKSKKQNEYITFKRNENYWGKKPKLKEVTVKVIPDAQTRALAFESGDVDLIYGNGIIGLDTFAQYTKDKKYVTAISQPMSTRLLLLN
AKESIFQDKKVRQAMNHAIDKVSIAKNTFRGTEKPADTIFSKSTSHSDAKLNPYSYNVDKANQLLDQAGWKMGKDKVREKDGKTLTLRLPYIATKA
TDKDLVTYFQGEWRKIGINVSLIAMEEDDYWANAKKGNFDMMLTYSWGAPWDPHAWMSALTAKADHGHPENIALENLATKTEMDRLIKSALVDPKE
ENVDRDYKKVLELLHDEAVYIPLTYQSVISVYRKGDFKTMRFAPEENSFPLRYIEKNNVSK

SEQ ID 59

TTGATTGTGTCAAAATACCTAAAATACTTCTCTATTATCACGTTATTTTTGACTGGGCTTATTTTAGTTGCATGTCAACAACAAAAGCCTCAAACA
AAAGAACGTCAGCGCAAACAACGTCCAAAAGACGAACTTGTCGTTTCTATGGGGGCAAAGCTCCCTCATGAATTCGATCCAAAGGACCGTTATGGA
GTCCACAATGAAGGGAATATCACTCATAGCACTCTATTGAAACGTTCTCCTGAACTAGATATAAAAGGAGAGCTTGCTAAAACATACCATCTCTCT
GAAGATGGGCTGACTTGGTCGTTTGACTTGCATGATGATTTTAAATTCTCAAATGGTGAGCCTGTTACTGCTGATGATGTTAAGTTTACTTATGAT
ATGTTGAAAGCAGATGGAAAGGCTTGGGATCTAACCTTCATTAAGAACGTTGAAGTAGTTGGGAAAAATCAGGTCAATATCCATTTGACTGAGGCG
CATTCGACATTTACAGCACAGTTGACTGAAATCCCAATCGTCCCTAAAAAACATTACAATGATAAGTATAAGAGCAATCCTATCGGTTCAGGACCT
TACATGGTAAAAGAATATAAGGCTGGAGAACAAGCTATTTTTGTTCGTAACCCTTATTGGCATGGGAAAAAACCATACTTTAAAAAATGGACTTGG
GTCTTACTTGATGAAAACACAGCACTAGCAGCTTTAGAATCTGGTGATGTTGATATGATCTACGCAACGCCAGAACTTGCTGATAAAAAAGTCAAA
GGCACCCGCCTCCTTGATATTCCATCAAATGATGTGCGCGGCTTATCATTACCTTATGTGAAAAAGGGCGTCATCACTGATTCTCCTGATGGTTAT
CCTGTAGGAAATGATGTCACTAGTGATCCAGCAATCCGAAAAGCCTTGACTATTGGTTTAAATAGGCAAAAAGTTCTCGATACGGTTTTAAATGGT
TATGGTAAACCAGCTTATTCAATTATTGATAAAACACCATTTTGGAATCCAAAAACAGCCATTAAAGATAATAAAGTAGCTAAAGCTAAGCAATTA
TTGACAAAAGCGGGATGGAAAGAACAAGCAGACGGTAGCCGTAAAAAAGGTGACCTTGATGCAGCGTTTGATCTGTACTACCCTACTAATGATCAA
TTGCGAGCGAACTTAGCCGTTGAAGTAGCAGAGCAAGCCAAGGCCCTAGGGATTACTATTAAACTCAAAGCTAGTAACTGGGATGAAATGGCAACG
AAGTCACATGACTCAGCCTTACTTTATGCCGGAGGACGTCATCACGCGCAGCAATTTTATGAATCGCATCATCCAAGCCTAGCAGGGAAAGGTTGG
ACCAATATTACGTTTTATAACAATCCTACCGTGACTAAGTACCTTGACAAAGCAATGACATCTTCTGACCTTGATAAAGCTAACGAATATTGGAAG
TTAGCGCAGTGGGATGGCAAAACAGGTGCTTCTACTCTTGGAGATTTGCCAAATGTATGGTTGGTGAGCCTTAACCATACTTATATTGGTGATAAA
CGTATCAATGTAGGTAAACAAGGCGTCCACAGTCATGGTCATGATTGGTCATTATTGACTAACATTGCCGAGTGGACTTGGGATGAATCAACTAAG

SEQ ID 60

LIVSKYLKYFSIITLFLTGLILVACQQQKPQTKERQRKQRPKDELVVSMGAKLPHEFDPKDRYGVHNEGNITHSTLLKRSPELDIKGELAKTYHLS
EDGLTWSFDLHDDFKFSNGEPVTADDVKFTYDMLKADGKAWDLTFIKNVEVVGKNQVNIHLTEAHSTFTAQLTEIPIVPKKHYNDKYKSNPIGSGP
YMVKEYKAGEQAIFVRNPYWHGKKPYFKKWTWVLLDENTALAALESGDVDMIYATPELADKKVKGTRLLDIPSNDVRGLSLPYVKKGVITDSPDGY
PVGNDVTSDPAIRKALTIGLNRQKVLDTVLNGYGKPAYSIIDKTPFWNPKTAIKDNKVAKAKQLLTKAGWKEQADGSRKKGDLDAAFDLYYPTNDQ
LRANLAVEVAEQAKALGITIKLKASNWDEMATKSHDSALLYAGGRHHAQQFYESHHPSLAGKGWTNITFYNNPTVTKYLDKAMTSSDLDKANEYWK
LAQWDGKTGASTLGDLPNVWLVSLNHTYIGDKRINVGKQGVHSHGHDWSLLTNIAEWTWDESTK

SEQ ID 61

ATGTATCTAAGTAGTTCGATCATCAAAAAAATATTGTCAGCTTTTTTGGCATTGTTTTTCATATCACTTCTAACATTTATTCTTATCAAACTATCA
ACAGTTAATTCAGCAGAAAATTACCTTCGTTTATCAAAAATAAGTGTTAGTCCAGAAGCGCTAAAAGAAGCAGAGCACTATTTAGGTTTAGATAAG
CCATTATGGAAGCAGTACTGGCTGTGGTTCCAAAAAGCATTAACAGGAGATTTTGGATATTCTTATGTGCTCAGGTTGCCAGTATTAGATTTGGTT
TTACAACGGTTTTTGGCTACTTTATTTTTAGGCACGAGTGCCTTCTTGCTAATTGTTACCATTTCTACCCCGTTAGGTGTGTGGGCTGGCTTACAT
GAATCTGCTCGGAGTGATCACTTGATTCGATTTTTGAGTTTTTCTAGTGTGTCTATGCCAAATTTTTGGGTTGCTTACTTGTTGATGCTGCTATTT
TCGGCAAAATTAAATCTTCTGCCTGTTTCAGGAGGTAACGATTTACAAAGTTTAATTTTGCCAAGTATTACCTTAAGTTTTTCTACCGTAGGTCAA
TACATAGCCCTTATTCGAAAAGCTATTAGTCAAGAAAATAGAAGTTTAAATGTGGAAAATGCCCGATTAAGAGGAGTAAAAGAACGTTATATTGTC
ACACATCACCTCCTTAGAAATGCCTTACCTGCGATAATGACAGCACTTAGCTTGACTTGGGTTTACTTATTAACAGGATCAATTATTGTTGAAGAA
ATTTTTTCATGGAATGGAATAGGACGTTTATTTGTGACCAGTCTAAGAACTTCAGATCTTCCAGTAATACAAGCTTGTATGCTAATTTTTGGAACC
TTATTTTTAGCTAATAATTTTATGACACAGTGTTTTATGAATTGGGTTGATCCTCGGTTACGAAAGTCAAGGGAGAAA

SEQ ID 62

MYLSSSIIKKILSAFLALFFISLLTFILIKLSTVNSAENYLRLSKISVSPEALKEAEHYLGLDKPLWKQYWLWFQKALTGDFGYSYVLRLPVLDLV
LQRFLATLFLGTSAFLLIVTISTPLGVWAGLHESARSDHLIRFLSFSSVSMPNFWVAYLLMLLFSAKLNLLPVSGGNDLQSLILPSITLSFSTVGQ
YIALIRKAISQENRSLNVENARLRGVKERYIVTHHLLRNALPAIMTALSLTWVYLLTGSIIVEEIFSWNGIGRLFVTSLRTSDLPVIQACMLIFGT
LFLANNFMTQCFMNWVDPRLRKSREK

SEQ ID 63

GTGAAACGTACTACCATTATTATCATCTGGAAAATCATCAGATGTGTCACGCTTATTTTTGGGGTATCTGTTTTGACCTTCGTTTTGTTAAAACAA
TCTCCAGTAGATCCAGTCATGGCAAGTGTCAATTATGACACATCACTAACCCCTGCTCAGTACAAAGCGATTGCTCACCACTATGGCTTGGATAAG
CCAGCTCTAGTCCAATATTTTATTTGGTTGAAAAATGTGATACAGGGAGATTTAGGGACCTCGCTCGTTTATCGGCAACCTGTTAGTGATATTATT
AGATCACGGGCAGGTGCTTCTTTCATACTTATGGGACTCTCTTGGATCTTATCGGGTCTTATTGGATTTATCTTAGGAACGTTATCCGCTTTCCAT
CAAGGGAAATTACTTGACCGAGTTGTCAGGTGGTTTTCATACCTTCAGATATCAGTACCAACGTTTTGGATTGGACTCATTTTTTTATTAATCTTT
TCTGTCCAGCTGGGGTGGTTCCCGATTGGTATTTCTTCCCCGATAGGCACTTTGAGTCAAGATATTACGTTAGCTGATCGAGTTAAGCACCTTATG

TTACCTGTTTTCACGCTAAGTATTCTAGGCATTGCCAATGTCACCCTTCATACGAGAACTAAAATGATGTCGGTGCTTTCTAGTGAATATGTCTTA
TTTGCCAGAGCGCGTGGGGAAACACAGTGGCAAATTTTTAAACATCATTGCCTTAGAAATGCTATCGTACCAGCTATTACACTGCATTTTTCCTAT
TTTGGAGAATTGTTTGGAGGATCTGTTCTTGCTGAGCAAGTTTTCTCATATCCTGGCTTAGGGTCTACCCTCACTGAAGCAGGACTTAAAAGTGAT
ACACCGCTCCTTCTAGCTATTGTGATGATAGGGACATTATTTGTTTTTGCGGGCAATCTTATTGCGGATATTTTAAATAGCATCATCAATCCACAG
TTAAGGAGAAAAGTA

SEQ ID 64

VKRTTIIIIWKIIRCVTLIFGVSVLTFVLLKQSPVDPVMASVNYDTSLTPAQYKAIAHHYGLDKPALVQYFIWLKNVIQGDLGTSLVYRQPVSDII
RSRAGASFILMGLSWILSGLIGFILGTLSAFHQGKLLDRVVRWFSYLQISVPTFWIGLIFLLIFSVQLGWFPIGISSPIGTLSQDITLADRVKHLM
LPVFTLSILGIANVTLHTRTKMMSVLSSEYVLFARARGETQWQIFKHHCLRNAIVPAITLHFSYFGELFGGSVLAEQVFSYPGLGSTLTEAGLKSD
TPLLLAIVMIGTLFVFAGNLIADILNSIINPQLRRKV

SEQ ID 65

TTGTTAGTGATTAGTGCCATTTTTGCCCCTATTCTATCTAGCTTTGATCCACAATACGTAGATTTATCACAAAAATTATTGGCTCCCAATAATGTT
CATTTGTTAGGGACTGACCAATTGGGTAGAGATGTATTATCTCGCTTGCTTTATGGTGCTAGATATTCACTGTTTTTAGCTATTATTATTAGCTTA
TTGGAATTAACGATTGGTATGTTTGTGGGTCTTATTGTTGGTTGGTATCAAGGAAAGTTAGAAAACCTCTTTTTATGGATAGCTAATATTATTTTA
GCTTTTCCGAGCTTTTTGCTCTCTCTTGCAACCGTGGGAATCTTAGGTCATGGTCTAGGGAATTTAATTTTTGCAATTGTCTTTGTGGAATGGGTT
TACTATGCTAAATTAATGACCAATTTAGTTAAGAGTGCAAAAAAAGAGCCTTATGTGATAAATGCGCAAATTATGGGACTTTCAGTCTGGCATATT
TTAAGAAAACATATTTTTCCTTTTGTGTATCAGCCAATCCTCGTTATGGTCCTTATGAATATAGGAAATATTATTTTAATGATTTCTGGCTTTTCT
TTCTTAGGGATTGGTGTGCAACCTAATGTCACAGAATGGGGAATGATGTTGCACGATGCTAGAGGATATTTTAGGACAGCTACTTGGATGATGTTA
TCTCCTGGAATTGCGATTTTTTTAACAGTATTTTCCTTTAATACTTTAGGCGATGCCATAGATAAAAAAGATTGGAAACGACAATGGAACAGT

SEQ ID 66

MLVISAIFAPILSSFDPQYVDLSQKLLAPNNVHLLGTDQLGRDVLSRLLYGARYSLFLAIIISLLELTIGMFVGLIVGWYQGKLENLFLWIANIIL
AFPSFLLSLATVGILGHGLGNLIFAIVFVEWVYYAKLMTNLVKSAKKEPYVINAQIMGLSVWHILRKHIFPFVYQPILVMVLMNIGNIILMISGFS
FLGIGVQPNVTEWGMMLHDARGYFRTATWMMLSPGIAIFLTVFSFNTLGDAIDKKDWKRQWNS

SEQ ID 67

ATGATATTGAAACGTCGAACGATGGTTTTATGGCAACTGGGTATCGCCATTTCTCTCATTCTTAGTATTCTAGCCTTAAACCTTTATTTCTATAGG
ACGCCTTTGGAAACCAATGCAGCTTTACGCAACCTCGCTCCTTCCTTAAACCATCTTTTTGGGACAGATGGTTTAGGTAGGGATATGTTTGTCAGA
ACGATTAAAGGGCTTTATTTCTCTTTACAAGTCGGCTTATTAGGCGCCCTTATGGGAGTCTTTCTTGCGACCGTTTTTGGAGTGCTTGCAGGTCTA
GGAAATAGCCTTATTGATAAAATAATAGCCTGGTTGGTTGATTTGTTTATTGGTATGCCTCATTTGATTTTTATGATTCTCATTTCTTTTGTTGTT
GGGAAAGGGGCTCAAGGGGTTATCATTGCAACAGCTGTTACCCATTGGCCCTCTCTAGCAAGGCTTATCCGCAATGAAGTCTATGATCTAAAGAAT
AAAGCCTTTGTCCAGCTCTCTAAAAGCATGGGAAAAACGCCTTATTATATTGTGAGGCATCATATCCTGCCTTTGATTGCTTCTCAAATTTTCATT
GGGTTTATCCTCTTATTTCCGCACGTCATCTTGCATGAAGCATCCATGACTTTCTTAGGATTTGGCCTTTCTGCCGAACAACCTTCGGTTGGTATC
ATTTTGTCAGAGGCAGCTAAGCATATCTCTCTTGGCAATTGGTGGTTGGTGATTTTTCCAGGCCTTTATCTTATTTTGGTTGTCAATGCCTTTGAT
ACTATCGGAGAATCTTTAAAGAAACTCTTTTACCCTCAAACGGATCATTTT

SEQ ID 68

MILKRRTMVLWQLGIAISLILSILALNLYFYRTPLETNAALRNLAPSLNHLFGTDGLGRDMFVRTIKGLYFSLQVGLLGALMGVFLATVFGVLAGL
GNSLIDKIIAWLVDLFIGMPHLIFMILISFVVGKGAQGVIIATAVTHWPSLARLIRNEVYDLKNKAFVQLSKSMGKTPYYIVRHHILPLIASQIFI
GFILLFPHVILHEASMTFLGFGLSAEQPSVGIILSEAAKHISLGNWWLVIFPGLYLILVVNAFDTIGESLKKLFYPQTDHF

SEQ ID 69

TTGGAAACGACAATGGAACAGTTAGAAATAAGAAAATTGTCATTACAGATAGGAGAGGTCCCTGTACTAAGAGATTTTAGTTGTAAAATAGATATG
GGAGAATCGCTAACTATTATTGGTGAGAGTGGTTCAGGGAAAACCCTCTTGGCAAAATTATTGGTTGGTCACATTCCACAAGGTATGACAGTTAGA
GGAAACATATTTTTTAAGGGAGTTGATTTAGGTAAACTAACTGTAAAGCAGTGGCAGAAATTAAGGGGACGAGATATTGCCTATTTAGTGCAAAAT
CCCATGTCTATGTTTAATCCTTTTCAAAAAATTGAAGCGCATATTTTGGAAACAATCCTTAGTCATGAGAAATGTTCAAAGAGAGTAGCCTTATCT
AAAGCGTTAGAATGGATGAAACGTTTAAATTTAGATGATGCGATATCCCTGTTAAAAAAATACCCTTTTGAGCTTAGTGGAGGAATGCTACAAAGA
ATTATGTTAGCCACTATATTATCTCTTGATCCTCAGGTAATCATATTAGATGAGCCGACCTCAGCGGTTGATTGTCATAATTGTTCTACTATATCA
GCTATTTTGCAGGAATTGCAAAATAATGGAAAAACCTTGATTACTGTAACGCATGATTATCAGTTAGCTAGAGACCTGGGGGGACAATTATTAGTT
ATAAGTGAGGGAGAAGTTGTTGAACAGGGACAAACCCAAGCTATTTTAAGCAATCCTCAACATAACTATACGAAAGCACTGACAGTGCAAATGGAG
TATGAAGGAGATATTCTTAATGTTGGTTTG

SEQ ID 70

METTMEQLEIRKLSLQIGEVPVLRDFSCKIDMGESLTIIGESGSGKTLLAKLLVGHIPQGMTVRGNIFFKGVDLGKLTVKQWQKLRGRDIAYLVQN
PMSMFNPFQKIEAHILETILSHEKCSKRVALSKALEWMKRLNLDDAISLLKKYPFELSGGMLQRIMLATILSLDPQVIILDEPTSAVDCHNCSTIS
AILQELQNNGKTLITVTHDYQLARDLGGQLLVISEGEVVEQGQTQAILSNPQHNYTKALTVQMEYEGDILNVGL

SEQ ID 71

ATGACAAAAGAAAATAATGTAATCTTAACTGCCAAAGATGTGGTGGTAGAATTTGATGTGCGTGATCGTGTTTTAACAGCTATCCGTAACGTCTCA
CTGGAACTTGTTGAAGGAGAAGTCCTTGCTTTTGTAGGGGAATCAGGCTCAGGTAAATCTGTTTTAACAAAGACCTTTACAGGGATGTTGGAGTCT
AATGGACGCATTGCTAATGGTTCAATTGTCTATCGTGGGCAAGAATTGACAGATTTAAAAACAAATAAAGAGTGGGCAAAGATTCGCGGCTCAAAA
ATCGCAACGATTTTCCAAGACCCAATGACCAGTCTTAGTCCCATTAAAACTATCGGTAGCCAAATCACAGAAGTGATTATTAAGCACCAAAAAGTA
AGTCATGCCAAAGCTAAAGAAATGGCCCTTGATTACATGAATAAAGTGGGTATCCCAAATGCCAAAAAACGCTTTGAAGATTACCCATTTGAGTAT
TCAGGAGGAATGCGTCAACGTATTGTTATCGCTATTGCTTTAGCTTGTCGCCCAGATATTCTTATCTGTGATGAGCCAACAACAGCCCTTGATGTG
ACTATTCAAGCTCAAATCGTTGAGTTATTGAAGTCGCTTCAACGAGAATATCATTTCACCATTATCTTTATTACGCACGATTTAGGTGTTGTGGCA
AGCATTGCAGATAAAGTGGCTGTCATGTATGCAGGAGAAATTGTTGAATTTGGAACAGTCGAAGAGATTTTCTATGATCCAAGACACCCCTATACA
TGGAGTTTGCTGTCTAGCTTACCGCAGTTGGCAGATGAATCTGGTGAACTTTACGCTATTCCAGGAACGCCTCCATCACTTTATTCACCAATTATC
GGAGATGCCTTTGCACTTCGCTCAGAATATGCTATGGTTTTAGACTTTGAAAAAGCACCTCCGGCGATTAACGTATCTGAGACTCATTGGGCCAAA
ACATGGCTTTTACACCCAGAGGCTCCAAAAGTTCAAAAACCAGAAGTCATTCAAGATTTGCATCAAAAAATCTTAAGAAAAATGTCACAACAGGAG
GAAGGAAATGTC

SEQ ID 72

MTKENNVILTAKDVVVEFDVRDRVLTAIRNVSLELVEGEVLAFVGESGSGKSVLTKTFTGMLESNGRIANGSIVYRGQELTDLKTNKEWAKIRGSK
IATIFQDPMTSLSPIKTIGSQITEVIIKHQKVSHAKAKEMALDYMNKVGIPNAKKRFEDYPFEYSGGMRQRIVIAIALACRPDILICDEPTTALDV
TIQAQIVELLKSLQREYHFTIIFITHDLGVVASIADKVAVMYAGEIVEFGTVEEIFYDPRHPYTWSLLSSLPQLADESGELYAIPGTPPSLYSPII
GDAFALRSEYAMVLDFEKAPPAINVSETHWAKTWLLHPEAPKVQKPEVIQDLHQKILRKMSQQEEGNV

SEQ ID 73

ATGAAGGAGATATTCTTAATGTTGGTTTGTAATCATGTCGGAAAAACATTTGGACGACAAGAGGTTTTAAAGGACTGTCATTTTCATCTTAAAAGA
GGAGAAATAATTGGTATAATGGGTAAAAGTGGCAGTGGTAAAAGTAGCCTTGCCCGACTCATTATAGGACTAGATAGTCCTACTTGTGGTTCGATA
TATTTTCAAGGAAAAATTTACACACCTAAAGATGGTAAGGCGCAGATTATCCTTGTTTTTCAAGATGCGCTTAGTTCGGTCAATCCATATTTTAGT
ATTGAGGAAATTTTGAATGAAGCTTTTTATGGAAAAAAAACAACTTTTGAATTATGTCAAATATTAGAAGCGGTGGGTTTAGATGGAACTTATCTA
AAATATAAAGCTAGACAACTTAGTGGTGGTCAGCTACAGAGAGTTTGTATCGCTAGAGCTTTACTCTTAAAGCCTAAAATTATTATTTTTGATGAA

TCCTTAAGTGGATTAGACCCAGTAACTCAAATTAAAATGCTACGTTTATTACAAAAAATAAAACGCCGTTATGAATTAAGTTTTATAATGATTTCT
CATGACCCTAAAATTTGTCAAGCTATCTGTAACCGGGTCTTTCTGATAAAAAATGGTTATTTAGTAGAAGATAATGAATTCTTGAAGAGAGCGTGT
TCTACTAACTGTTTGACCAATCTC

SEQ ID 74

MKEIFLMLVCNHVGKTFGRQEVLKDCHFHLKRGEIIGIMGKSGSGKSSLARLIIGLDSPTCGSIYFQGKIYTPKDGKAQIILVFQDALSSVNPYFS
IEEILNEAFYGKKTTFELCQILEAVGLDGTYLKYKARQLSGGQLQRVCIARALLLKPKIIIFDESLSGLDPVTQIKMLRLLQKIKRRYELSFIMIS
HDPKICQAICNRVFLIKNGYLVEDNEFLKRACSTNCLTNL

SEQ ID 75

ATGAATGAAGCAATAATTCAATTAGATCATATTGATATTACCTTCCGTCAAAAAAAACGGGTTATCGAAGCTGTTAAAGATGTCACGGTTCATATC
AATCAAGGAGATATTTATGGCATTGTTGGGTATTCAGGTGCCGGGAAATCAACTCTTGTGCGTGTGATTAACCTGCTACAGGCACCAACAAACGGG
AAAATCACTGTTGATGGGGATGTGACTTTTGACCAGGGGAAAATTCAATTGTCAGCTGATGCCCTTCGCCAAAAACGACGTGATATTGGTATGATC
TTCCAACATTTCAATTTGATGGCCCAAAAAACAGCCAAAGAAAATGTAGCATTTGCGCTCCGTCATTCGTCGTTAAGTAAGACTGAGAAAGAACAC
AAAGTTATCGAACTGCTAGAACTTGTAGGTTTATCAGAGCGAGCAGATAACTACCCTGCCCAGTTATCGGGTGGGCAAAAACAAAGGGTGGCTATT
GCGCGTGCTCTAGCTAACGATCCAAAAATTTTGATTTCAGATGAGGCCACATCAGCACTAGATCCAAAAACCACTAAACAAATTTTGGCGCTCTTG
CAAGAATTAAACCGCAAACTTGGCCTTACCATTGTTATGATTACTCATGAAATGCAAATTGTTAAGGATATTTGTAATCGTGTTGCTGTTATGCAA
AATGGTGTTTTGATTGAAGAAGGTTCTGTCCTTGATATCTTTTCAAATCCAAAAGAAGCCTTGACACAGGAATTTATCACAACAGCTACAGGGATT
GATGAGGCTTTAGAAAAAATTAACCAACAAGACATTGTTAAACATTTGCCTGCAAATGCCCTTCTAGCTCAGTTGAAATATGCAGGAACTTCTACG
GATGAGCCTCTACTTAATAGCATTTACCGTCAGTTTGAAGTGACAGCTAATATTTTGTATGGCAATATTGAGATTTTAGATCATATTCCAGTTGGT
GACATGATTGTTGTCTTGGAAGGGCAAGCTGAAAATATTCTTGCGGCTGAGAAAGCCTTGCATGAAGCTGGTGTTGATGTTAGTATTTTAAAGAGA
GGAGCC

SEQ ID 76

MNEAIIQLDHIDITFRQKKRVIEAVKDVTVHINQGDIYGIVGYSGAGKSTLVRVINLLQAPTNGKITVDGDVTFDQGKIQLSADALRQKRRDIGMI
FQHFNLMAQKTAKENVAFALRHSSLSKTEKEHKVIELLELVGLSERADNYPAQLSGGQKQRVAIARALANDPKILISDEATSALDPKTTKQILALL
QELNRKLGLTIVMITHEMQIVKDICNRVAVMQNGVLIEEGSVLDIFSNPKEALTQEFITTATGIDEALEKINQQDIVKHLPANALLAQLKYAGTST
DEPLLNSIYRQFEVTANILYGNIEILDHIPVGDMIVVLEGQAENILAAEKALHEAGVDVSILKRGA

SEQ ID 77

GTGGAACCTAAATATCAACGTATATTAATTAAGTTATCTGGTGAAGCATTGGCGGGAGATAAGGGTGTCGGTATTGACATTCCTACCGTTCAATCT
ATTGCAAAAGAAATTGCCGAAGTACACAATTCAGGTGTTCAAATAGCGCTTGTCATTGGTGGAGGTAATCTTTGGCGTGGAGAACCTGCAGCAGAA
GCAGGGATGGATCGTGTTCAAGCTGATTATACAGGGATGTTAGGGACAGTAATGAATGCTCTTGTAATGGCTGATAGCCTTCAACAATATGGGGTA
GATACTAGAGTTCAAACAGCTATTCCAATGCAAACTGTTGCTGAGCCTTACGTACGTGGTCGTGCTTTACGTCATCTAGAGAAGAATCGTATTGTT
GTCTTTGGAGCGGGTATTGGTTCGCCTTATTTCTCAACTGATACAACAGCAGCGCTTCGTGCTGCTGAGATTGAGGCAGAAGCAATTTTAATGGCT
AAAAATGGAGTAGATGGTGTTTATAATGCTGATCCAAAGAAAGATGCCAATGCTGTCAAATTTGATGAATTAACTCACGTTGAAGTAATAAAACGA
GGGTTAAAAATCATGGATGCAACCGCATCAACTATTTCAATGGATAATGATATTGACCTTGTTGTTTTCAATATGAATGAGACTGGTAATATTAAG
CGTGTTGTTCTTGGAGAACAAATCGGAACAACTGTTTCAAACAAAGCATCTGAA

SEQ ID 78

MEPKYQRILIKLSGEALAGDKGVGIDIPTVQSIAKEIAEVHNSGVQIALVIGGGNLWRGEPAAEAGMDRVQADYTGMLGTVMNALVMADSLQQYGV
DTRVQTAIPMQTVAEPYVRGRALRHLEKNRIVVFGAGIGSPYFSTDTTAALRAAEIEAEAILMAKNGVDGVYNADPKKDANAVKFDELTHVEVIKR
GLKIMDATASTISMDNDIDLVVFNMNETGNIKRVVLGEQIGTTVSNKASE

SEQ ID 79

GTGGAACCTAAATATCAACGTATATTAATTAAGTTATCTGGTGAAGCATTAGCAGGTGAAAAAGGAGTTGGCATTGACATTCCAACTGTTCAGGCT
ATTGCAAAAGAAATTGCCGAAGTTCATGTGTCGGGAGTACAGATCGCTCTTGTTATTGGTGGAGGCAATCTCTGGCGTGGAGAGCCTGCAGCAGAC
GCTGGAATGGACCGTGTTCAGGCTGATTACACTGGCATGCTTGGAACGGTGATGAATGCCCTAGTCATGGCTGATAGTCTTCAACATTATGGTGTT
GATACCCGTGTGCAAACAGCTATTCCTATGCAAAATGTAGCAGAACCTTATATTCGCGGACGTGCCTTGCGCCATCTAGAAAAAAATCGGATTGTT
GTTTTTGGAGCTGGTATTGGCTCGCCTTATTTTTCAACAGACACCACCGCGGCACTGCGTGCTGCTGAGATTGAAGCAGATGCTATTTTAATGGCA
AAAAATGGTGTGGATGGGGTCTATAATGCTGATCCTAAAAAAGATGCTAATGCGGTTAAATTTGATGAATTAACACATGGTGAAGTGATCAAACGT
GGTCTCAAAATCATGGATGCAACGGCATCGACCTTATCGATGGATAACGATATTGATTTGGTGGTTTTCAATATGAATGAAGCTGGCAATATTCAA
CGTGTTGTCTTTGGAGAACATATTGGAACTACTGTATCAAATAAAGTTTGTGAC

SEQ ID 80

VEPKYQRILIKLSGEALAGEKGVGIDIPTVQAIAKEIAEVHVSGVQIALVIGGGNLWRGEPAADAGMDRVQADYTGMLGTVMNALVMADSLQHYGV
DTRVQTAIPMQNVAEPYIRGRALRHLEKNRIVVFGAGIGSPYFSTDTTAALRAAEIEADAILMAKNGVDGVYNADPKKDANAVKFDELTHGEVIKR
GLKIMDATASTLSMDNDIDLVVFNMNEAGNIQRVVFGEHIGTTVSNKVCD

SEQ ID 81

TTGATTGATGATTTATCAAATGGTGAAATTAAAAGAACACGAGCTTCAGGTACAGTAATAGAAGCTAATTGGTTAAGGGGGGTTGGCGCTCCA

SEQ ID 82

MIDDLSNGEIKRTRASGTVIEANWLRGVGAP

SEQ ID 83

ATGACTAAGGAAATCGTTACAAAAGCTCAAGAGCGTTTTGAGCAATCACACCAAAGTTTATCAAGAGAATTTGCAGGGATTCGTGCAGGACGTGCT
AATGCTAGCTTGCTTGATCGTATTCAAGTTGAGTATTATGGAGCGCCAACCCCCCTTAACCAATTAGCTTCTATTACTGTACCTGAAGCTCGTGTT
CTTTTAATTTCACCATTTGATAAATCATCAATCAAAGATATTGAGCGTGCTATTAACGAATCAGATTTAGGTATTAATCCTGCAAATGATGGTTCA
GTTATTCGTCTTGTTATTCCAGCTTTGACAGAAGAAACACGTCGTGATTTAGCTAAAGAAGTGAAAAAAGTCGGAGAAAATGCTAAGATTGCTATC
CGTAATATTCGCCGTGATGCTATGGATGAAGCTAAGAAGCAAGAAAAGAATAAAGAAATTACAGAAGATGACTTGAAATCTCTTGAAAAAGATATT
CAAAAGGCTACTGATGATGCTGTAAAACATATTGATGAGATGACTGCTAATAAAGAAAAAGAATTGTTGGAAGTT

SEQ ID 84

MTKEIVTKAQERFEQSHQSLSREFAGIRAGRANASLLDRIQVEYYGAPTPLNQLASITVPEARVLLISPFDKSSIKDIERAINESDLGINPANDGS
VIRLVIPALTEETRRDLAKEVKKVGENAKIAIRNIRRDAMDEAKKQEKNKEITEDDLKSLEKDIQKATDDAVKHIDEMTANKEKELLEV

SEQ ID 85

ATGGCAAATGCAATTATTGAAACTGCAAAAGAACGTTTTGCACAATCCCATCAGTCTTTATCACGTGAATATGCCAGCATTCGTGCGGGTCGTGCC
AACGCTAGTCTTTTAGACCGTATCCAAGTTGATTATTACGGGGCACCGACACCATTAAATCAATTGGCTTCAATCACTGTACCAGAAGCGCGTGTC
TTATTGATCTCGCCTTTTGATAAATCTTCTATCAAAGATATCGAGCGCGCTCTTAACGCATCAGATTTAGGCATTACACCTGCTAACGATGGCTCT
GTCATTCGTTTGGTTATTCCAGCTTTGACCGAAGAAACACGTAAAGAATTAGCCAAAGAAGTGAAAAAAGTTGGTGAAAATGCTAAAATTGCAATC
CGTAATATCCGCCGCGATGCTATGGATGATGCTAAAAAGCAAGAAAAAGCAAAAGAAATCACTGAAGATGAGTTAAAAACACTTGAGAAAGATATC
CAAAAAGCAACCGATGATGCTATCAAAGAAATTGACCGCATGACGGCTGAAAAAGAAAAAGAATTGCTCTCAGTG

SEQ ID 86

MANAIIETAKERFAQSHQSLSREYASIRAGRANASLLDRIQVDYYGAPTPLNQLASITVPEARVLLISPFDKSSIKDIERALNASDLGITPANDGS
VIRLVIPALTEETRKELAKEVKKVGENAKIAIRNIRRDAMDDAKKQEKAKEITEDELKTLEKDIQKATDDAIKEIDRMTAEKEKELLSV

SEQ ID 87

TTGGCAAGTAATAAAATGATTATGGAGGTAACTGATAGAATCAAAACCAGATGGATTTGGTTTGTCGGTTACCTTTTTAAAAGGAGAAAAATGAAT
ACATTATTAGCGACAGTCATAACAGGCTTAGTAACTGATGAAAACAAAGATTTTTACTTTATCCAAAAAGATGGCTTTACCTTTGCATTATCAAAG
TCAGAAGGAGAGCATCACATTGGTGAAATGGTTAAAGGATTCGCCTATACAGATATGCAACAAAAAGCACGTCTTACAACTAAAGAAACATTTGCG
ACTCGAGATCATTATGGTTGGGGGACAGTTACTGAGGTACGTAAAGACTTGGGAGTATTTCTTGATACTGGTCTTCCAGATAAGCAAGTGGTTGTT
TCTTTGGATGTTCTTCCTGAATTGAAAGAACTTTGGCCTAAAAAAGGTGATCGCCTCTACGTTTGCTTAGATGTTGATAAAAAAGATCGTCTCTGG
GCTCTCCCTGCAGATCCTGAAGTGTTTCAACGAATGGCAACCCCTGCATATAACAATATGCAAAATCAAAATTGGCCAGCAATCGTTTATCGCTTA
AAATTGTCAGGAACTTTTGTTTATCTACCAGAAAATAATATGCTCGGCTTTATTCACCCTAGTGAACGTTACAGTGAACCTCGTTTAGGGCAAGTG
CTGGATGCACGAGTTATTGGCTTCAGAGAAGTTGATAGAACCTTAAATTTATCATTAAAGCCTCGTTCTTTTGAAATGTTAGAAAATGACGCACAA
ATGATTTTAACGTATTTAGAAAGTAACGGAGGATTCATGACTTTAAATGATAAATCTTCTCCAGAGGAAATTAAAGCTACTTTTGGAATTTCCAAA
GGTCAGTTTAAAAAAGCACTTGGAGGACTCATGAAAGCTAAAAAGATCAAACAAGATCAGCTAGGTACAGAATTATTA

SEQ ID 88

MASNKMIMEVTDRIKTRWIWFVGYLFKRRKMNTLLATVITGLVTDENKDFYFIQKDGFTFALSKSEGEHHIGEMVKGFAYTDMQQKARLTTKETFA
TRDHYGWGTVTEVRKDLGVFLDTGLPDKQVVVSLDVLPELKELWPKKGDRLYVCLDVDKKDRLWALPADPEVFQRMATPAYNNMQNQNWPAIVYRL
KLSGTFVYLPENNMLGFIHPSERYSEPRLGQVLDARVIGFREVDRTLNLSLKPRSFEMLENDAQMILTYLESNGGFMTLNDKSSPEEIKATFGISK
GQFKKALGGLMKAKKIKQDQLGTELL

SEQ ID 89

ATGAATGATTTACTAGCAACAGTCATTACTGGGCTTATTAAAGAAGAAAACGCTAATGACTATTTTATCCACAAAGAAGGGTTTACCTTTACCTTG
TCTAAAGCAGAAGGAGAACGCCAGATTGGTGATATGGTCACAGGCTTTGCCTATACAGACATAGAGCAAAAGGCACGTCTCACAACCAAAGAGATC
CGTTCAACACGGACAAGTTATGGCTGGGGGGAAGTGACAGAGGTTCGTCGTGACCTAGGCGTTTTTGTCGATACAGGAATTCCAAATAAAGAAATT
GTGGTTTCTTTGGACGTGTTGCCTGAGATGAAAGAACTATGGCCTAAAAAAGGGGATAAACTTTACATTCGTTTGGATGTGGATAAAAAAGACCGT
ATTTGGGGACTTCCAGCAGAGCCTGAGGTCTTTCAAAAGATGGCTAGCCCTGCTTACAATAACATGCAAAATCAACATTGGCCAGCAATTGTTTAC
CGCCTAAAATTAACAGGAACGTTTGTTTACCTGCCTGAAAACAACATGTTGGGCTTTATTCACTCAAGTGAACGCTACGCAGAACCGCGCTTAGGT
CAGGTTTTAGATGCCCGTGTGATTGGGTTTAGAGAGGTCGATCGTACCTTGAATTTATCGTTGAAACCACGTTCTTTTGAGATGTTGGAGAATGAC
GCTCAGATGATTGTTACTTATCTGGAAGCCAATGGTGGTTTCATGACTTTAAATGACAAATCAAGTCCAGAAGAGATTAAAGCAAGCTTTGGTATT
TCAAAAGGCCAGTTTAAAAAAGCCTTGGGTGGATTGATGAAAGCTAAACGTATCAAACAAGACGCCACAGGAACTGAATTAATAGGA

SEQ ID 90

MNDLLATVITGLIKEENANDYFIHKEGFTFTLSKAEGERQIGDMVTGFAYTDIEQKARLTTKEIRSTRTSYGWGEVTEVRRDLGVFVDTGIPNKEI
VVSLDVLPEMKELWPKKGDKLYIRLDVDKKDRIWGLPAEPEVFQKMASPAYNNMQNQHWPAIVYRLKLTGTFVYLPENNMLGFIHSSERYAEPRLG
QVLDARVIGFREVDRTLNLSLKPRSFEMLENDAQMIVTYLEANGGFMTLNDKSSPEEIKASFGISKGQFKKALGGLMKAKRIKQDATGTELIG

SEQ ID 91

TTGGCTTTTTTTGTTATAATGTATCTATTAAAAAGAATGGAGAACGATATGGAACGTGCGATTTTTGCTGGAGGTTGTTTTTGGTGTATGGTACAA
CCATTTGAAGAATTAGATGGTATTGAATCTGTTTTATCTGGATACACTGGAGGACATGTTGAGAATCCAACTTATAAAGAAGTTTGTAGTAAAACT
ACTGGACATACAGAAGCTGTTGAAATTATTTTTAATCCTGAAAAAATCTCTTATGCAGATTTAGTTGAGTTATATTGGGCACAAACAGATCCAACA
GACGCTTTTGGTCAGTTTGAAGATCGTGGGGATAATTATCGTCCTGTCATCTTTTATGAGAATGAAGAGCAACGTCAGATTGCTCAAAAATCAAAA
GATAAGCTACAAGCTTCGGGTAGATTTGATAGACCAATTGTAACCAGCATTGAGCCTGCTGATACTTTTTACCCAGCAGAAGACTATCATCAAGCA
TTCTATCGGACTAACCCTGCTCGTTACGCCTTGAGTAGTGCCAGAAGACATGCATTTCTAGAGGAGAACTGGCAT

SEQ ID 92

MAFFVIMYLLKRMENDMERAIFAGGCFWCMVQPFEELDGIESVLSGYTGGHVENPTYKEVCSKTTGHTEAVEIIFNPEKISYADLVELYWAQTDPT
DAFGQFEDRGDNYRPVIFYENEEQRQIAQKSKDKLQASGRFDRPIVTSIEPADTFYPAEDYHQAFYRTNPARYALSSARRHAFLEENWH

SEQ ID 93

ATGGAAAGAGCCATTTTTGCAGGAGGTTGTTTCTGGTGTATGGTGCAACCTTTTGAGGAGCAAGCAGGTATTTTGTCAGTCAGAAGTGGCTACACA
GGTGGGCATCTCCCAAATCCTAGCTATGAACAAGTTTGTGCCAAAACAACAGGACATACAGAAGCTGTTGAAATTATTTTTGACCCTAAGCAAATC
GCTTATAAAGATTTGGTAGAGCTCTATTGGACGCAGACGGATCCAACAGACGCCTTTGGGCAATTTGAAGATCGTGGGGACAACTACCGTCCTGTC
ATTTACTACACAACGGAAAGACAAAAAGAAATTGCAGAGCAATCAAAAGCAAACTTGCAAGCTTCAGGACGTTTTGACCAACCCATTGTCACCACT
ATTGAACCAGCAGAGCCATTTTATCTCGCAGAGGATTATCACCAAGGATTTTATAAAAAGAATCCCAAGCGGTATGCACAAAGCAGTGCTATTCGT
CATCAGTTTTTAGAGGAGAATTGGTCA

SEQ ID 94

MERAIFAGGCFWCMVQPFEEQAGILSVRSGYTGGHLPNPSYEQVCAKTTGHTEAVEIIFDPKQIAYKDLVELYWTQTDPTDAFGQFEDRGDNYRPV
IYYTTERQKEIAEQSKANLQASGRFDQPIVTTIEPAEPFYLAEDYHQGFYKKNPKRYAQSSAIRHQFLEENWS

SEQ ID 95

TTGAGAAAATCATTTTACAGTTGGTTGATGACACAAAGAAATCCAAAATCAAATGAACCAGTAGCAATCCTAGCAGATTACGCTTTTGATGAAACC
ACTTTTCCAAAACATAGTTCGGATTTTGAAACAGTTAGTCGCTATTTAGAAGATGAGGCCAGTTTTTCCTTTAATTTAACAGATTTTGATGATATT
TGGGAAGATTATCTCAATCAT

SEQ ID 96

MRKSFYSWLMTQRNPKSNEPVAILADYAFDETTFPKHSSDFETVSRYLEDEASFSFNLTDFDDIWEDYLNH

SEQ ID 97

TTGGTCATGAGAAAATCATTTTACAGCTGGCTGATGACACAACGTAACCCTAAATCAAATGAACCTGTGGCGATTTTAGCAGATTTGGTGTTTGAT
GACACCACTTTTCCAAAGCATACCAATGATTTTGAACTCATTAGTCGGTATCTAGAAGATCAAGCTAGTTTTTCCTTTAATTTAGGTCAATTTGAT
GAAATCTGGGAAGATTATCTAGCACAT

SEQ ID 98

LVMRKSFYSWLMTQRNPKSNEPVAILADLVFDDTTFPKHTNDFELISRYLEDQASFSFNLGQFDEIWEDYLAH

SEQ ID 99

TTGTTTATGAGATATACAAATGGAAATTTTGAAGCCTTTGCAAGACCTCGAAAACCTGAAGGTGTGGATAAAAAATCCGCTTATATTGTTGGTTCT
GGTTTAGCAGGATTAGCTGCCGCTGTCTTTTTAATACGTGACGGTCAAATGGATGGTCAACGTATTCATATTTTTGAAGAACTACCTCTTTCTGGA
GGATCACTTGACGGTGTCAAACGACCTGATATCGGTTTTGTAACGCGTGGTGGTCGTGAAATGGAAAATCACTTCGAATGTATGTGGGATATGTAC
CGTTCCATCCCCTCTCTCGAAGTTCCAGATGCTTCTTATCTAGATGAATTTTATTGGCTTGACAAGGATGATCCCAATTCATCTAACTGTCGCCTC
ATTCATAAACAGGGGAATCGCTTAGAATCTGATGGTGATTTTACACTCGGAACACATTCCAAAGAGTTAGTTAAGCTAGTCATGGAGACTGAAGAG
TCTTTAGGTGCTAAGACGATTGAAGAAGTTTTTTCAAAAGAATTTTTTGAAAGTAATTTTTGGACTTATTGGGGTACTATGTTTGCCTTTGAGAAA
TGGCATTCAGCGATTGAAATGCGTCGATATGCTATGCGCTTTATCCATCATATTGGTGGTCTGCCTGATTTCACTTCATTAAAATTTAATAAATAT
AATCAATATGATTCTATGGTGAAACCAATCATCAGTTATTTAGAGTCTCATAATGTAGATGTTCAATTTGATAGCAAGGTAACTAATATCTCCGTA
GACTTTAAGAACGGTCAGAAGCTTGCAAAAGCTATTCATCTCACAGTTGGTGGTGAAGCAAAAACAATTGATCTTACTCCAAATGATTTTGTTTTT
GTAACGAATGGTTCTATCACTGAAAGTACGAACTATGGTAGTCATGATACTGTAGCTAAACCTAATACCGATTTGGGAGGTTCTTGGAATCTTTGG
GAAAACTTAGCTGCTCAATCTGATGAATTTGGACATCCTAAAGTCTTCTACAAAGATATTCCAAAAGAGTCATGGTTTGTTTCTGCTACTGCAACA
ATAAAAGATCCAGCTATTGAACCTTATATAGAGCGTTTAACACATCGTGACCTCCATGATGGTAAAGTAAATACCGGAGGCATTGTTACAGTTACA

GATTCTAATTGGATGATGAGTTTTGCTATCCATCGCCAACCGCATTTCAAAGAGCAAAAGGAAAATGAAACAATTGTTTGGATTTATGGACTCTAT
TCAAATGTGGAAGGTAATTATATTAAAAAACCAATTGAAGAATGTACTGGTCGAGAAATCACAGAAGAGTGGTTATATCACTTAGGTGTTCCTGAA
ATGAAGATTCATGATTTATCTGATAAACAATATGTAAGTACAGTTCCTGTTTATATGCCTTACATTACTAGTTATTTCATGCCTCGAGTTAAAGGT
GACCGACCAGATGTTATCCCACAAGGATCTGTTAACCTAGCCTTCATTGGTAATTTTGCAGAATCTCCATCCAGAGATACAGTATTTACAACGGAA
TATTCTATTAGAACTGCTATGGAAGCTGTTTATACTTTCTTAAATATTGAACGTGGTGTTCCAGAAGTCTTTAATTCAGCATTTGATATTCGTGTC
TTGTTGCAATCTTTATACTATCTCAATGATAAGAAATCTGTTGAAGATATGGATTTACCAATACCTGCCTTAATGCGTAAAGTAGGCATGAAAAAA
ATTAGAGGAACTTATTTAGAAGAATTACTTCGAGAAGCTCATCTTTTA

SEQ ID 100

MFMRYTNGNFEAFARPRKPEGVDKKSAYIVGSGLAGLAAAVFLIRDGQMDGQRIHIFEELPLSGGSLDGVKRPDIGFVTRGGREMENHFECMWDMY
RSIPSLEVPDASYLDEFYWLDKDDPNSSNCRLIHKQGNRLESDGDFTLGTHSKELVKLVMETEESLGAKTIEEVFSKEFFESNFWTYWGTMFAFEK
WHSAIEMRRYAMRFIHHIGGLPDFTSLKFNKYNQYDSMVKPIISYLESHNVDVQFDSKVTNISVDFKNGQKLAKAIHLTVGGEAKTIDLTPNDFVF
VTNGSITESTNYGSHDTVAKPNTDLGGSWNLWENLAAQSDEFGHPKVFYKDIPKESWFVSATATIKDPAIEPYIERLTHRDLHDGKVNTGGIVTVT
DSNWMMSFAIHRQPHFKEQKENETIVWIYGLYSNVEGNYIKKPIEECTGREITEEWLYHLGVPEMKIHDLSDKQYVSTVPVYMPYITSYFMPRVKG
DRPDVIPQGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVYTFLNIERGVPEVFNSAFDIRVLLQSLYYLNDKKSVEDMDLPIPALMRKVGMKK
IRGTYLEELLREAHLL

SEQ ID 101

GTGATGATATCACTTTGCTTGACTATTCAAGGAGGTCTTGAAATGTATTATACTAGTGGTAATTACGAAGCTTTTGCAACACCTCGAAAACCCGAA
GGGGTAGATCAGAAATCAGCTTATATTGTTGGTACTGGTTTAGCTGGTTTAGCAGCAGCTGTTTTCCTTATTCGCGATGGGCATATGGCTGGGGAA
CGCATTCATCTGTTTGAGGAATTGCCTTTAGCAGGTGGTTCTTTAGATGGTATTGAAAAGCCTCATCTTGGTTTTGTGACCCGTGGTGGTCGTGAG
ATGGAAAATCATTTTGAGTGTATGTGGGACATGTATCGGTCTATTCCCTCACTGGAAATTCCCGGTGCGTCTTATTTAGATGAATTTTATTGGTTG
GATAAGGATGATCCTAACTCATCCAACTGTCGTTTGATTCACAAGAGAGGAAATCGTGTGGATGATGACGGCCAGTATACGCTCGGTAAACAGTCA
AAAGAATTAATCCATTTAATCATGAAGACAGAAGAATCTCTAGGAGACCAAACCATTGAAGAGTTCTTCTCAGAAGATTTCTTTAAGAGTAATTTT
TGGGTGTATTGGGCAACCATGTTTGCTTTTGAAAAATGGCATTCTGCTGTAGAAATGCGACGCTATGCGATGAGGTTTATCCACCATATTGATGGT
TTGCCAGATTTCACCTCCCTCAAGTTCAACAAATATAACCAATATGACTCTATGGTCAAACCGATTATTGCTTACCTAGAATCACACGACGTTGAC
ATCCAATTTGACACAAAAGTCACTGATATTCAGGTGGAGCAAACAGCTGGTAAAAAGGTAGCAAAAACCATCCATATGACGGTGTCTGGGGAGGCT
AAGGCGATTGAGCTAACACCTGATGATTTGGTTTTTGTGACCAATGGTTCTATTACTGAAAGCAGCACATACGGTAGTCATCACGAAGTGGCTAAG
CCAACCAAAGCGTTAGGTGGTTCTTGGAATTTATGGGAAAATCTAGCTGCTCAATCAGATGATTTTGGTCATCCTAAAGTGTTTTACCAGGACTTG
CCTGCTGAAAGCTGGTTTGTGTCTGCTACAGCAACCATAAAACACCCAGCTATCGAGCCTTATATAGAACGTTTGACCCACCGTGACTTGCACGAT
GGCAAAGTGAACACTGGCGGCATCATCACTATTACAGATTCTAACTGGATGATGAGCTTTGCCATTCACCGTCAACCTCATTTTAAAGAACAAAAA
GAAAATGAGACCACTGTCTGGATTTACGGTCTTTATTCCAATAGTGAGGGCAATTACGTCCACAAGAAAATTGAGGAGTGTACAGGTCAAGAAATC
ACAGAAGAATGGTTGTACCACCTTGGGGTACCTGTTGATAAAATCAAGGACTTAGCGAGTCAGGACTATATCAATACAGTTCCTGTTTACATGCCT
TATATTACGAGTTACTTTATGCCACGCGTCAAAGGAGACCGTCCGAAAGTTATCCCAGATGGTTCAGTCAACTTGGCCTTTATTGGTAACTTTGCG
GAATCTCCATCTCGAGATACGGTCTTTACGACTGAGTATTCTATTCGTACTGCCATGGAAGCAGTGTATAGCTTCTTGAATGTGGAACGAGGCATC
CCAGAAGTCTTTAATTCAGCCTATGATATTCGTGAATTGCTCAAAGCCTTTTATTACCTTAATGATAAAAAGGCAATCAAGGATATGGATTTGCCA
ATTCCTGCACTGATTGAGAAAATCGGACATAAAAAAATCAAGGATACCTTTATCGAAGAATTGCTCAAAGATGCTAATCTTATG

SEQ ID 102

VMISLCLTIQGGLEMYYTSGNYEAFATPRKPEGVDQKSAYIVGTGLAGLAAAVFLIRDGHMAGERIHLFEELPLAGGSLDGIEKPHLGFVTRGGRE
MENHFECMWDMYRSIPSLEIPGASYLDEFYWLDKDDPNSSNCRLIHKRGNRVDDDGQYTLGKQSKELIHLIMKTEESLGDQTIEEFFSEDFFKSNF
WVYWATMFAFEKWHSAVEMRRYAMRFIHHIDGLPDFTSLKFNKYNQYDSMVKPIIAYLESHDVDIQFDTKVTDIQVEQTAGKKVAKTIHMTVSGEA
KAIELTPDDLVFVTNGSITESSTYGSHHEVAKPTKALGGSWNLWENLAAQSDDFGHPKVFYQDLPAESWFVSATATIKHPAIEPYIERLTHRDLHD
GKVNTGGIITITDSNWMMSFAIHRQPHFKEQKENETTVWIYGLYSNSEGNYVHKKIEECTGQEITEEWLYHLGVPVDKIKDLASQDYINTVPVYMP
YITSYFMPRVKGDRPKVIPDGSVNLAFIGNFAESPSRDTVFTTEYSIRTAMEAVYSFLNVERGIPEVFNSAYDIRELLKAFYYLNDKKAIKDMDLP
IPALIEKIGHKKIKDTFIEELLKDANLM

SEQ ID 103

ATGAAATTTTGTTATAATGTAGTCACTTACTGTACGAAAAGGAAGAATAATTTGCAAGAATACTCTATCGAAATTACTTTACAACATCCAGATGAT
ATGATGTCACTCTTTGGCAGCAATGAGCGCCATTTAAAATTAATCGAAGAAAATTTAGATGTTATCATTCATGCTAGAACTGAACGTGTTCAGGTA
TTAGGTGACTCTGAAGAAGCAGTAGAAACCGCTCGGTTAACCATTGAAGCATTATTAGTGCTTGTTAACCGCGGGATGACTGTGAATACTTCAGAT
GTTGTAACAGCCTTATCCATGGCACAAAATGGTTCAATTGATAAATTCGTTGCCCTTTATGAGGAAGAAATTATTAAGGATAGCTATGGTAAGCCT
ATCCGTGTTAAGACTTTAGGGCAAAAAATATACGTTGATAGCGTTAAAAATCATGATGTTGTTTTTGGTATTGGGCCTGCTGGAACGGGAAAAACT
TTTTTAGCAGTCACTCTAGCAGTAACGGCACTAAAGCGTGGTCAAGTTAAACGAATAATCTTAACGAGACCAGCGGTTGAAGCTGGTGAAAGCCTT
GGTTTCTTGCCTGGAGATCTCAAAGAGAAAGTTGATCCTTATTTGAGACCAGTTTATGATGCCCTATATCAAATTTTAGGTAAAGAGCAAACAAGT
CGCTTAATGGAGCGTGAAATCATCGAAATTGCTCCATTGGCTTACATGCGTGGTCGTACTTTAGATGATGCATTTGTCATATTAGATGAAGCGCAA
AACACCACTATAATGCAAATGAAAATGTTCCTAACACGTCTTGGCTTCAATTCTAAAATGATTGTAAATGGCGATGTTAGCCAAATTGACTTACCA
AAGAATGTTAAATCTGGTTTGATTGATGCTGTTGAGAAATTACGAAATATCAAAAAGATTGACTTTATTCATTTATCAGCAAAGGATGTTGTAAGA
CACCCTGTCGTTGCTGAAATAATAAATGCTTATTCAGATTCAGAAAGTAGTCACAAGCTACAATCTGATAAGGAC

SEQ ID 104

MKFCYNVVTYCTKRKNNLQEYSIEITLQHPDDMMSLFGSNERHLKLIEENLDVIIHARTERVQVLGDSEEAVETARLTIEALLVLVNRGMTVNTSD
VVTALSMAQNGSIDKFVALYEEEIIKDSYGKPIRVKTLGQKIYVDSVKNHDVVFGIGPAGTGKTFLAVTLAVTALKRGQVKRIILTRPAVEAGESL
GFLPGDLKEKVDPYLRPVYDALYQILGKEQTSRLMEREIIEIAPLAYMRGRTLDDAFVILDEAQNTTIMQMKMFLTRLGFNSKMIVNGDVSQIDLP
KNVKSGLIDAVEKLRNIKKIDFIHLSAKDVVRHPVVAEIINAYSDSESSHKLQSDKD

SEQ ID 105

TTGCAAGAGTATTCTATTGACATTACCTTAACCCATCCTGATGATGTTTTAGCTCTTTTTGGTAGCAACGAGCGTCATTTGAAGCTAATAGAAGCT
CATTTAGGAGTTATTGTTCACGCAAGAACCGAGCGAGTCCAAGTGATTGGTGATGATGAAGAAGCTGTGGAATTGGCTCGATTGACCATCAAAGCC
CTACTGGTTCTAGTGGGTCGTGGCATGGTGGTCAACACATCAGATGTGGTGACAGCTTTATCTATGGCAGAATCTCATCAGATTGACCAATTTATG
GCGCTTTATGAAGAAGAAATCATTAAAGATAACTATGGTAAGGCAATACGAGTCAAAACATTAGGTCAAAAAACCTATGTTGATAGTGTCAAACGT
CATGATGTGGTTTTTGGTGTAGGACCTGCAGGGACAGGTAAAACCTTCTTAGCTGTTACGCTTGCAGTCACTGCTCTGAAAAGAGGACAGGTAAAG
CGTATTATTTTGACGCGTCCTGCGGTAGAAGCTGGCGAAAGCCTAGGTTTTTTACCAGGCGATTTGAAAGAAAAGGTGGATCCTTACCTCAGACCT
GTTTACGATGCCCTTTATCACATTTTAGGCAAGGAACAAACCACACGCCTGATGGAACGAGATGTGATTGAGATTGCTCCGTTAGCTTATATGCGA
GGTCGTACTCTGGATGACGCTTTTGTTATCTTAGATGAGGCTCAAAACACGACCATCATGCAAATGAAGATGTTTTTGACCCGTCTTGGTTTTAAT
TCTAAAATGATTGTCAATGGAGATACGAGTCAGATTGACCTCCCTCGAAATGTCAAGTCTGGTTTGATTGATGCTACTCAGAAATTACAAGGCATT
AAACAGATTGATTTTGTCTATTTCTCTGCTAAGGATGTTGTCCGACATCCTGTTGTGGCTGATATTATCAAGGCTTATGAAACGTCCTCAGAGGAG
ATGAAGGACTTACTAAAACCTAAGGCTAGTGACGTTGAAGCTGATTACCAGCCAGGCTTGACAAAATACCCTGTGATCGGTCAAGAGCAC

SEQ ID 106

LQEYSIDITLTHPDDVLALFGSNERHLKLIEAHLGVIVHARTERVQVIGDDEEAVELARLTIKALLVLVGRGMVVNTSDVVTALSMAESHQIDQFM
ALYEEEIIKDNYGKAIRVKTLGQKTYVDSVKRHDVVFGVGPAGTGKTFLAVTLAVTALKRGQVKRIILTRPAVEAGESLGFLPGDLKEKVDPYLRP

VYDALYHILGKEQTTRLMERDVIEIAPLAYMRGRTLDDAFVILDEAQNTTIMQMKMFLTRLGFNSKMIVNGDTSQIDLPRNVKSGLIDATQKLQGI
KQIDFVYFSAKDVVRHPVVADIIKAYETSSEEMKDLLKPKASDVEADYQPGLTKYPVIGQEH

SEQ ID 107

ATGGACCATTTCACAAAACTCTGGCAAGATTTCTCTAAACTTCCAAATGTTGTTGCTATAGCACTCGGAGGCTCACGCTCTGGTGACAGTTTTGAC
CAATCTTCCGATTATGATTTGTATGTTTATTGTGCAGCAACTCCTGATATCACTAGTCGTAAACGTATCCTTAACAAGCACTGTCATTACATTGAA
CTTAACAATCATTACTGGGAGCTTGAAGATAATGGTACTTTAAACGACGGAACTGATATTGATATTCTCTATCGTAACATAGATAACTTTTTATCA
GACTTAGAAGATGTCGTTGAACACCACAATTCTCGAATTGGATACACTACTTGTTTTTGGCATAACCTCATCAATTGCCAAATACTCTATGATCCT
GAAAATCAATTACAATCACTCAAAGAGAGATTCGAAGTTTCTTATCCCAGTCAGTTACAAAAACAAATTATCATTCAAAATCGTAACTTATTAACT
GGCAAGCTTCCCTCTTACGATAAACAAATTATAAAAGCCCTTAAACGCCAAGACTTTGTTAGTACTCACCATAGAACTACTGCTTTCTTAGATTCC
TACTTTGATATTATTTTTGCACTTAATAAGTTGACACATCCTGGCGAAAAAAGAATGATTTCCTATGCTAAGAAGAATGCTACATTGCTTCCTAAA
CATTTCGAAGAAAATATCATTAAACTATGTCATCACAACTCCAACGAACACACTGTTAAAGAAACATTAAACGATATAATAATGCATCTCGACGTC
ATGCTTAAAGAAAATTTTCAACACTTTATAGGT

SEQ ID 108

MDHFTKLWQDFSKLPNVVAIALGGSRSGDSFDQSSDYDLYVYCAATPDITSRKRILNKHCHYIELNNHYWELEDNGTLNDGTDIDILYRNIDNFLS
DLEDVVEHHNSRIGYTTCFWHNLINCQILYDPENQLQSLKERFEVSYPSQLQKQIIIQNRNLLTGKLPSYDKQIIKALKRQDFVSTHHRTTAFLDS
YFDIIFALNKLTHPGEKRMISYAKKNATLLPKHFEENIIKLCHHNSNEHTVKETLNDIIMHLDVMLKENFQHFIG

SEQ ID 109

ATGAAACAAGATTATATTTCCTACATTAGGTCAAAAGTTGGACATGAGACTATCTTTTTAACATATTCTGGTGGTATTTTGACAGATGGTAAGGGA
CGTGTCTTACTCCAATTAAGAGCTGATAAGAATTCTTGGGGAATTATTGGTGGATGTATGGAGTTAGGTGAGTCATCAGTAGATACATTGAAAAGA
GAATTTTTCGAAGAAACTGGATTGAGAGTGGAACCAATCAGACTGTTAAATGTTTATACTAACTTTCAAGACTCTTATCCCAATGGCGATAAAGCA
CAAACCGTCGGTTTTATTTATGAAGTAAGCTGTCCAAAACCAGTTAATATAGAAGGTTTTCATAATGAGGAAACATTGCAATTGGACTATTTTTCT
AAAGAAGACGTCAAAAATATTACGATCGTAAATGAACAACACCAATTAATTTTAGATGAATATTTTTCACAAACATTCCAAATGGGGCGT

SEQ ID 110

MKQDYISYIRSKVGHETIFLTYSGGILTDGKGRVLLQLRADKNSWGIIGGCMELGESSVDTLKREFFEETGLRVEPIRLLNVYTNFQDSYPNGDKA
QTVGFIYEVSCPKPVNIEGFHNEETLQLDYFSKEDVKNITIVNEQHQLILDEYFSQTFQMGR

SEQ ID 111

TTGGCTATAATGAGAAAGAATACTAACATAGTAAAGCGAGATCATATGCCACAAGACTACATTTCTTATATCCGCTCCAAAGTTGGGCATGATAAG
ATTATTCTTAACTTTGCTGGTGGGATTTTGACCAATGATGACGGCAAGGTGCTGATGCAGCTGCGTGGTGATAAGAAAACCTGGACTATTCCTGGT
GGCACTATGGAACTGGGTGAGAGCTCTTTAGAGACTTGCAAACGTGAGTTCTTAGAGGAAACCGGAATTGAGGTTGAAGCTGTTCGCTTACTGAAT
GTTTACACTCATTTTGAGGAAGTTTATCCCAACGGTGATGCTGTTCAGACTATTGTCTTTATCTATGAACTAACGGCTGTTTCTGATATGGCTATT
GATAACTTTCATAATGAGGAAACGCTCAAGTTACAATTTTTCTCTCATGAGGAGATAGCAGAGTTAGAGAGTGTCTCAGCCAAACATCGCCTGATG
TTAGAGGAATATTTTAGTGATAGCTTTGCTATGGGGCAT

SEQ ID 112

LAIMRKNTNIVKRDHMPQDYISYIRSKVGHDKIILNFAGGILTNDDGKVLMQLRGDKKTWTIPGGTMELGESSLETCKREFLEETGIEVEAVRLLN
VYTHFEEVYPNGDAVQTIVFIYELTAVSDMAIDNFHNEETLKLQFFSHEEIAELESVSAKHRLMLEEYFSDSFAMGH

SEQ ID 113

GTGACTGTTTTTTTTAGAAAGCATAAGAAGTACACAAAAAGAAAATTATGGAATATTTGATGGTGGGGATATGCTTTACTTACGGTATTGGAATGAT
ATACTTAAAGAAATCCAGTTT

SEQ ID 114

MTVFLESIRSTEKENYGIFDGGDMLYLRYWNDILKEIQF

SEQ ID 115

ATGAAGATAACATTACACGGCGTTGCTGAAACGTTATTAATCACCTTATATATTAGGGCTAAAGATGCGATGGCTAAACATCCGATACTTAATGAT
CAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAATTCGATAATTCAGAAGCTTCTTTTTATGCAACATTAGCTAGAATTCGC
GTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCTTTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTC
GATAATGGACAAATTAGGTGGTATAACCTTGATTTGCCAGAGGTTATGGAGATAAGAAAATTATTTTTTGAAGAGCATGAAAGAGTTACTAATATA
GCAAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCCCCTTTTCTAATCGTGTCAGAAGGTGTTTTAATGTTTCTAAAA
GAAGATGACGTAGAGACTTTTCTTCATATCCTGACAAATTCATTTAGCCAATTTATGGCACAATTTGATTTGTGTCATAAGGAAATGATTAATAAA
GGAAAGCAACATGATACAGTAAAGTATATGGATACAGAATTTCAGTTTGGTATCACAGATGGTCATGAGATTGTGGATTTAGACCCTAAATTAAAG
CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAAATTTAATAATTGT
TTAGGTGTGTACGAATATAAAGCATCTGAGAAAAAG

SEQ ID 116

MKITLHGVAETLLITLYIRAKDAMAKHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLDTRFERV
DNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPQNAPFLIVSEGVLMFLKEDDVETFLHILTNSFSQFMAQFDLCHKEMINK
GKQHDTVKYMDTEFQFGITDGHEIVDLDPKLKQINLINFTDEMSKFELGTLRSLLPTIRKFNNCLGVYEYKASEKK

SEQ ID 117

ATGTACGTTGAAATGATTGATGAAACTGGACAAGTTTCAGAAGATATCAAAAAGCAAACTCTTGATTTGTTAGAGTTTGCAGCACAAAAAACAGGT
AAAGAGAATAAAGAAATGGCTGTAACGTTTGTCACTAATGAACGTAGCCATGAATTGAATTTAGAGTATCGAGATACCGATCGTCCGACTGATGTT
ATCAGTTTAGAATATAAGCCTGAGGTTGATATTTCTTTTGATGAAGAAGATCTGGCTGAAAATCCTGAACTTGCTGAGATGCTAGAAGATTTTGAT
TCTTATATTGGTGAACTTTTTATTTCTATTGATAAAGCTAAAGAACAAGCAGAAGAGTACGGTCACTCTTATGAACGTGAAATGGGTTTTTTAGCT
GTACATGGTTTTTTGCATATTAACGGTTATGATCATTATACACCCGAAGAAGAAAAAGAGATGTTCAGCTTACAGGAAGAAATTTTAACTGCTTAT
GGACTTAAACGACAA

SEQ ID 118

MYVEMIDETGQVSEDIKKQTLDLLEFAAQKTGKENKEMAVTFVTNERSHELNLEYRDTDRPTDVISLEYKPEVDISFDEEDLAENPELAEMLEDFD
SYIGELFISIDKAKEQAEEYGHSYEREMGFLAVHGFLHINGYDHYTPEEEKEMFSLQEEILTAYGLKRQ

SEQ ID 119

GTGCCCAACATACCAAATGAGGTGGGCAGCCCTTCCCTAACAATTAACCTTATGTATATCGAGATGATTGACGAAACGGGACAAGTTTCGCAAGAG
ATTATGGAGCAAACACTTGATTTGCTCAATTTTGCTGCTCAAAAGACGGGCAAAGAAGAAAAAGAAATGTCTGTGACCTTTGTGACCAATGAAAGA
AGTCATGAACTCAACTTAGAATACCGAGATACTGATCGTCCAACAGATGTGATTTCTCTAGAATATAAGCCAGAAACGCCTATTTTATTTAGTCAA
GAGGATTTGGCTGCTGATCCTAGTTTGGCAGAGATGATGGCAGAGTTTGATGCTTATATTGGCGAATTGTTTATTTCTATTGACAAGGCGCGTGAG
CAGTCCCAAGAATATGGGCACTCTTTTGAGCGTGAAATGGGATTTTTGGCTGTTCATGGATTCTTACATATTAATGGGTATGATCACTACACCCTT
GAAGAAGAAAAAGAGATGTTTACCTTACAGGAAGAGATTTTGACTGCTTATGGCCTTACACGACAA

SEQ ID 120

VPNIPNEVGSPSLTINLMYIEMIDETGQVSQEIMEQTLDLLNFAAQKTGKEEKEMSVTFVTNERSHELNLEYRDTDRPTDVISLEYKPETPILFSQ
EDLAADPSLAEMMAEFDAYIGELFISIDKAREQSQEYGHSFEREMGFLAVHGFLHINGYDHYTLEEEKEMFTLQEEILTAYGLTRQ

SEQ ID 121

ATGTCAGAAAATCCTGATGCCTATATTATTCGTAGTCAAAATTTGCATAATCAGGATTTCCCAAGTAACCTCAAAGCTATTGCTAGGGCGGGTGCA
GGAACAAATAATATTCCTATTGAAGAGGCAAGTGCACAGGGAATAGTCGTGTTTAATACCCCAGGTGCAAATGCTAATGCTGTAAAAGAAGCGGTC
ATTGCTGCCTTATTACTTTCAGCTCGTGATTATTTAGGAGCTAACCGATGGGTTAATACTCTAACTGGAACAGATATTCCCAAACAAATTGAAGCA
GGAAAGAAAGCTTTTGCTGGTAATGAAATTGCAGGAAAAAAATTGGGAGTTATCGGCCTTGGTGCCATTGGAGCTAGAATTGCGAATGATGCTAGA
CGCTTAGGAATGACAGTTCTTGGTTATGATCCCTATGTTTCAATTGAAACAGCTTGGAATATTTCAAGCCATGTTCAAAGGGTTAAAGAGATTAAG
GATATTTTTGAAACTTGTGACTATATCACAATTCATGTTCCCTTAACAAATGAAACTAAGCATACTTTTGATGCGAAAGCTTTTTCAATCATGAAA
AAAGGAACTACGATTATCAACTTTGCTCGTGCAGAATTAGTCAATAACCAAGAGCTATTTGAAGCGATAGAAACTGGTGTTGTCAAGCGCTATATT
ACTGATTTTGGAGACAAAGAATTATTAAACCAAAAG

SEQ ID 122

MSENPDAYIIRSQNLHNQDFPSNLKAIARAGAGTNNIPIEEASAQGIVVFNTPGANANAVKEAVIAALLLSARDYLGANRWVNTLTGTDIPKQIEA
GKKAFAGNEIAGKKLGVIGLGAIGARIANDARRLGMTVLGYDPYVSIETAWNISSHVQRVKEIKDIFETCDYITIHVPLTNETKHTFDAKAFSIMK
KGTTIINFARAELVNNQELFEAIETGVVKRYITDFGDKELLNQK

SEQ ID 123

TTGATGAAATTAAAATTATATAATGTTAGAGGCGAAGAAGCAGTCTTAGCAAAAAAATGGGCTGATGACAATGGGATTGAGATTTCCTTGACGGAG
TCTCCCTTAACTCCTGAAACGGTTAAAGAAGCTGAAGGCTTTGACGGGATTGCCAATGCCCAAATTGGTCCTTTAGATGATGCGATTTATCCTCTC
TTAAAGGAAATGGGGATTAAACAAATCGCTCAGCACAGTGCTAGTGTCGATATGTATAACCTTGATTTGGCCACCGAAAATGACATTATTATCACA
AATGTTCCTAGCTATTCTCCAGAATCCATTGCAGAATTTACGGTTACTATTGTCCTTAATTTAATTCGTCATGTGGAGTTGATTCGTGAAAATGTT
AAAAAACAAAATTTCACTTGGGGACTCCCTATCCGCGGCCGTGTTTTAGGTGATATGACAGTTGCGATTATCGGAACTGGACGTATTGGTCTAGCT
ACTGCTAAAATCTTTAAAGGTTTTGGCTGCAAGGTCGTTGGATATGATATTTACCAAAGCGATGCTGCCAAAGCTGTCTTGGACTATAAGGAATCT
GTAGAAGAAGCGATTAAAGATGCTGATCTTGTTTCCTTACACATGCCACCAACTGCAGAGAACACACACCTTTTCAATTCTGATTTATTTAAATCA
TTCAAAAAAGGGGCTATTTTGATGAATATGGCGCGTGGTGCCGTCATTGAGACGCAAGATTTACTGGATGCTTTGGATGCAGGCTTACTGAGCGGA
GCTGGTATTGACACTTACGAATTTGAAGGACCTTATATACCTAAGAATTTTGAAGGTCAAGAAATTACAGATTCACTATTTAAAGCTTTGATTAAC
CATCCTAAGGTTATTTATACACCTCATGCAGCTTATTATACTGATGAAGCCGTTAAAAACCTAGTTGAAGGTGCCCTTAATGCTACAGTAGAGATT
ATCAAAACTGGGACAACGACAACTCGTGTTAAC

SEQ ID 124

LMKLKLYNVRGEEAVLAKKWADDNGIEISLTESPLTPETVKEAEGFDGIANAQIGPLDDAIYPLLKEMGIKQIAQHSASVDMYNLDLATENDIIIT
NVPSYSPESIAEFTVTIVLNLIRHVELIRENVKKQNFTWGLPIRGRVLGDMTVAIIGTGRIGLATAKIFKGFGCKVVGYDIYQSDAAKAVLDYKES
VEEAIKDADLVSLHMPPTAENTHLFNSDLFKSFKKGAILMNMARGAVIETQDLLDALDAGLLSGAGIDTYEFEGPYIPKNFEGQEITDSLFKALIN
HPKVIYTPHAAYYTDEAVKNLVEGALNATVEIIKTGTTTTRVN

SEQ ID 125

ATGCTTTTCATGAGAGATAATTTAGATTCTTTGATTCAGCCTGTTATTGATGAGATGGCTAAACATTATCAATGGTCTGATCAAGACAAAACTTTC
TATGAAGAAGAATTACATGAGACTCTAAAAGACAATGACTTGGCAGCTTTGAANNNNNTTAAT

SEQ ID 126

MLFMRDNLDSLIQPVIDEMAKHYQWSDQDKTFYEEELHETLKDNDLAALXXXN

SEQ ID 127

ATGGAATTTTCAAGAGAAACAAGACGCTTAGCTCTCCAAAAAATGCAAGAAAGAGATTTAGACCTACTGATTATTGGGGGAGGTATTACGGGTGCT
GGTGTGGCACTTCAGGCGGCAGCTAGTGGCCTAGATACGGGTCTGATTGAGATGCAAGATTTTGCTCAAGGAACCTCTAGCCGTTCAACCAAATTG
GTTCACGGGGGGCTTCGTTACTTGAAACAATTTGATGTGGAGGTGGTTTCAGATACGGTGTCAGAGCGGGCTGTGGTGCAACAAATTGCACCCCAC
ATTCCAAAACCAGACCCTATGTTATTACCTGTTTATGACGAACCTGGCAGTACCTTTAGCATGTTCCGTTTGAAGGTCGCTATGGATTTGTATGAT
CTTTTAGCAGGCGTGTCCAATACGCCAGCGGCCAACAAGGTGTTAACCAAAGAAGAAGTCTTAAAACGAGAACCAGACTTAAAACAAGAAGGCTTG
CTTGGTGGTGGGGTTTACCTTGATTTCCGCAATAATGACGCAAGGCTTGTTATTGAAAATATCAAACGAGCTAATCGTGATGGGGCTCTTATTGCT
AGTCATGTGAAAGCAGAAGATTTCTTGCTAGATGACAATGGTAAGATTATTGGTGTGAAGGCGCGTGATCTGCTGTCAGATCAAGAAATCATTATC
AAGGCTAAATTAGTCATCAACACCACAGGTCCATGGAGTGATGAGATTCGTCAATTCTCTCATAAGGGACAACCGATTCATCAAATGCGCCCTACA
AAAGGGGTGCATCTGGTAGTGGACCGTCAAAAATTACCAGTGTCTCAACCTGTCTATGTTGACACAGGGTTAAATGATGGTCGTATGGTCTTTGTC
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AATAGTGCTTCTGACTACAATGGTGGCAACAGCGGTAAAGTCAGTGATGATAGTTTTGATCACTTGGTTGATACTGTCAAAGCCTATATTAACCAC
GAAGATAGCCGAGAAGCTGTTGAAAAAGCTATTAAGCAGGTTGAAACCAGCACATCTGAAAAAGAATTGGATCCGTCTGCAGTGTCACGAGGTTCA
AGTTTTGAGCGTGATGAGAATGGACTCTTTACCTTGGCAGGTGGTAAGATTACCGACTATCGCAAAATGGCTGAAGGAGCATTGACAGGGATTATT
CAAATCCTCAAAGAAGAGTTTGGCAAATCCTTCAAGCTTATCAATTCAAAAACCTATCCTGTTTCAGGAGGTGAAATCAATCCAGCCAATGTAGAT
TCGGAAATAGAAGCCTATGCTCAATTAGGAACTCTTAGTGGTCTTTCGATGGATGATGCTAGGTATTTGGCAAACCTTTATGGTTCTAATGCGCCA
AAAGTCTTTGCCTTAACTCGTCAATTAACAGCAGCTGAAGGGTTAAGTTTAGCTGAAACCTTGTCCTTACATTATGCGATGGATTATGAAATGGCT
CTTAAACCGACAGATTATTTCTTGAGAAGAACAAATCACCTCTTATTTATGCGAGATAGCCTAGATGCTTTGATTGACCCAGTGATTAATGAAATG
GCTAAACATTTTGAATGGTCTGATCAGGAAAGAGTGGCACAAGAAGACGATCTTCGTCGCGTGATTGCAGACAATGATTTGAGTGCCTTAAAAGGC
CATCAGGAGGGT

SEQ ID 128

MEFSRETRRLALQKMQERDLDLLIIGGGITGAGVALQAAASGLDTGLIEMQDFAQGTSSRSTKLVHGGLRYLKQFDVEVVSDTVSERAVVQQIAPH
IPKPDPMLLPVYDEPGSTFSMFRLKVAMDLYDLLAGVSNTPAANKVLTKEEVLKREPDLKQEGLLGGGVYLDFRNNDARLVIENIKRANRDGALIA
SHVKAEDFLLDDNGKIIGVKARDLLSDQEIIIKAKLVINTTGPWSDEIRQFSHKGQPIHQMRPTKGVHLVVDRQKLPVSQPVYVDTGLNDGRMVFV
LPREEKTYFGTTDTDYTGDLEHPQVTQEDVDYLLGVVNNRFPNANVTIDDIESSWAGLRPLLSGNSASDYNGGNSGKVSDDSFDHLVDTVKAYINH
EDSREAVEKAIKQVETSTSEKELDPSAVSRGSSFERDENGLFTLAGGKITDYRKMAEGALTGIIQILKEEFGKSFKLINSKTYPVSGGEINPANVD
SEIEAYAQLGTLSGLSMDDARYLANLYGSNAPKVFALTRQLTAAEGLSLAETLSLHYAMDYEMALKPTDYFLRRTNHLLFMRDSLDALIDPVINEM
AKHFEWSDQERVAQEDDLRRVIADNDLSALKGHQEG

SEQ ID 129

ATGGTTCGTACAACTCGTCCAACAACTGATAAGGTTAAAGGCGCTATTTTTAATATGATTGGTCCTTTTTTTTGAAGGTGGTCGTGTTTTAGACCTT
TTTTCTGGCAGTGGTAGCTTAGCTATTGAGGCGATCTCAAGGGGAATGGACCAAGCTGTCCTAGTTGAAAAAGATAGGCGTGCGCAGGTCGTTATT
CAAGAAAATATTGCAATGACTAAGAGTCCGGAGCAATTTCAATTATTAAAAATGGAAGCCAACCGTGCTTTAGAACAATTAACGGGACAATTTGAT
TTGGTCTTGTTGGACCCGCCATATGCTAAGGAAGAAATTGTAAAGCAAATCCAAATCATGGATAGCAAGGGTTTATTAGGCGATGATATCATGATT
GCTTGTGAAACGGACAAATCAGTTGATTTACCTGAAGAAATTGCTTCTTTTGGGATATGGAAACAGAAAATTTATGGCATTTCTAAAGTAACGGTC
TACGTTCGT

SEQ ID 130

MVRTTRPTTDKVKGAIFNMIGPFFEGGRVLDLFSGSGSLAIEAISRGMDQAVLVEKDRRAQVVIQENIAMTKSPEQFQLLKMEANRALEQLTGQFD
LVLLDPPYAKEEIVKQIQIMDSKGLLGDDIMIACETDKSVDLPEEIASFGIWKQKIYGISKVTVYVR

SEQ ID 131

ATGAGAGTTGTATCAGGTGAATTTGGTGGGCGTCCTTTAAAGACGCTCGATGGAAAGATAACACGCCCTACTTCAGACAAAGTTAGAGGTGCGATT
TTTAATATGATAGGACCTTACTTTAATGGTGGTCGTGTTTTAGATTTGTTTGCAGGTTCAGGTGGATTAGCCATTGAGGCTGTTTCTCGTGGGATG
TCTGCTGCAGTTTTGGTTGAGAAGAATCGTAAAGCGCAAGCTATTATTCAAGACAATATTATAATGACTAAAGCTGAGAATCGGTTTACCTTGTTA
AAAATGGAAGCTGAGCGAGCTATTGATTGCTTGACTGGTCGATTTGACTTAGTCTTTTTAGACCCTCCTTATGCCAAAGAAACAATTGTGGCAACT
ATTGAAGCTTTAGCAGCTAAAAACTTATTGAGTGAACAGGTTATGGTTGTCTGTGAGACAGATAAAACAGTCTTGTTGCCAAAAGAGATTGCAACG
TTAGGTATTTGGAAAGAAAAAATTTATGGAATTAGTAAGGTAACAGTTTATGTTAAC

SEQ ID 132

MRVVSGEFGGRPLKTLDGKITRPTSDKVRGAIFNMIGPYFNGGRVLDLFAGSGGLAIEAVSRGMSAAVLVEKNRKAQAIIQDNIIMTKAENRFTLL
KMEAERAIDCLTGRFDLVFLDPPYAKETIVATIEALAAKNLLSEQVMVVCETDKTVLLPKEIATLGIWKEKIYGISKVTVYVN

SEQ ID 133

ATGACAAAGAAAGCTTTATTTACAGGTTCATTTGATCCTGTTACTAATGGACATTTAGATATTATTGAGCGCGCCAGCTATCTATTTGATCATGTT
TACATTGGGTTATTTTATAACCTTGAGAAGCAAGGTTACTTTTCGATTGAGTGCCGTAAAAAAATGTTAGAAGAAGCTATCCGTCAGTTTAAGAAT
GTTTCAGTTTTAGTGGCGCAAGATAGACTGGCTGTTGACTTAGCAAGGGAAGTGGGAGCAAAATATTTTGTTCGAGGTCTGCGTAATAGCCAGGAT
TTTGATTATGAAGCCAATTTGGAGTTTTTTAATAAACAGTTGGCAGATGATATTGAGACAGTTTATTTATCAACGTCGCCATCTTTGAGTCCGATA
TCATCTAGTCGCATCCGTGAATTGATACATTTTAAGGCTTCTGTGAAGCCTTTTGTTCCAAAGAGTGTTGTTAGAGAAGTGGAGAAAATGAGTGAA
GAA

SEQ ID 134

MTKKALFTGSFDPVTNGHLDIIERASYLFDHVYIGLFYNLEKQGYFSIECRKKMLEEAIRQFKNVSVLVAQDRLAVDLAREVGAKYFVRGLRNSQD
FDYEANLEFFNKQLADDIETVYLSTSPSLSPISSSRIRELIHFKASVKPFVPKSVVREVEKMSEE

SEQ ID 135

ATGTTAACTAAAATAGGACTTTATACAGGGTCATTTGATCCTGTTACAAACGGTCATCTCGATATTGTTAAACGGGCAAGTGGCCTATTTGATCAA
ATATATGTTGGGATTTTTGATAATCCTACCAAAAAAAGCTATTTTAAACTAGAAGTTCGTAAAGCAATGCTTACTCAAGCTCTGGCTGATTTTACA
AATGTAATTGTAGTAACTTCGCACGAACGTTTAGCTATTGATGTAGCTAAAGAATTACGAGTAACTCACTTGATTAGAGGCTTGCGAAATGCAACT
GACTTTGAGTATGAAGAAAATTTGGAATATTTTAATCACCTTTTAGCTCCAAATATTGAAACCGTCTATTTGATATCAAGAAATAAATGGCAGGCC
CTTAGCTCTAGTCGTGTGAGAGAGCTAATTCATTTTCAGTCTTCCTTAGAAGGTTTGGTTCCTCAGTCGGTTATTGCTCAAGTGGAGAAAATGAAT
GAAAAGACT

SEQ ID 136

MLTKIGLYTGSFDPVTNGHLDIVKRASGLFDQIYVGIFDNPTKKSYFKLEVRKAMLTQALADFTNVIVVTSHERLAIDVAKELRVTHLIRGLRNAT
DFEYEENLEYFNHLLAPNIETVYLISRNKWQALSSSRVRELIHFQSSLEGLVPQSVIAQVEKMNEKT

SEQ ID 137

TTGGATCTCTATTCTTCACTCATTTTCTCCACTTCTCTAACAACACTCTTTGGAACAAAAGGCTTCACAGAAGCCTTAAAATGTATCAATTCACGG
ATGCGACTAGATGATATCGGACTCAAAGATGGCGACGTTGATAAA

SEQ ID 138

MDLYSSLIFSTSLTTLFGTKGFTEALKCINSRMRLDDIGLKDGDVDK

SEQ ID 139

GTGAAGAATAGAGATCCAAAAAGAAAACATAAAAGTTTACTAGGTCTGCTTAAATGGTGGATTATAGGTTTTGCTTTTTTATTGTTAGTATTAGCA
AGCCTTGTAGTGAGACTACCTTATTATTTGGAAATGCCAGGTGGAGCTTATGATATCCGTTCGGTATTGAAAGTGAATAAAAAGGCTGATAAAGCT
AAGGGTTCGTACAATTTTGTAGCGGTATCTGTCAGTCAAGCAACGCCAGCTCAGGTTCTTTATGCTTGGTTAACTCCTTTTACAGAATTATCTAGT
AAAGAGGAGACAACAGGTGGCTTTAGTAATGACGATTATCTCAGAATTAATCAATTCTACATGGAGACTTCTCAAAATGAGTCCATCTATCAAGCT
TTAAAGTTAGCTAATAAGCAAGTATCTCTTACTTATAAAGGAGTTTATGTGCTTAACTTAGCTAAAAATTCGACATTTAAAGATAGATTACATTTA
GCTGATACAGTCACAGGAGTTAATGGCAAAAGTTTCAAAAATTCTTCTCAACTTATCAAATATGTTGCAGCTCTTCATCTAGGTGATAAAGTAAAG
GTACAATACACAAGTCAAGGTAAAAAGAAAGAATCAGTTGGTAAAGTTATTAAACTATCAAACGGTAAAAATGGTATTGGTATCGGTTTGACAGAC
CATACAGAAGTATTATCTGATGTTCCTGTGGACTTTAATACTGAAGGTGTTGGAGGACCAAGTGCAGGTTTAATGTTTACTTTAGCGATTTACGAC
CAATTGGTTAAAGAAGATTTACGTAAAGGACGTAAGATTGCAGGTACTGGTACTATTGAGCAAAATGGGCATGTTGGCGATATTGGTGGAGCAGGT
TTGAAAGTTGTTTCAGCGGCTAAAAAAGGAATGGATATTTTCTTTGTTCCTAATAATCCGATCGATAAAAATGCTAAAAAAGGCAAAACAAAGGTT
CAGACGAATTATCAAGAGGCAAAAGCAGCAGCTAAGCGATTAGGTACGAAGATGAAAATTGTACCAGTTCAAAATGTTCAGCAAGCTATTGATTAT
TTGAAAAAAACAAAA

SEQ ID 140

MKNRDPKRKHKSLLGLLKWWIIGFAFLLLVLASLVVRLPYYLEMPGGAYDIRSVLKVNKKADKAKGSYNFVAVSVSQATPAQVLYAWLTPFTELSS
KEETTGGFSNDDYLRINQFYMETSQNESIYQALKLANKQVSLTYKGVYVLNLAKNSTFKDRLHLADTVTGVNGKSFKNSSQLIKYVAALHLGDKVK
VQYTSQGKKKESVGKVIKLSNGKNGIGIGLTDHTEVLSDVPVDFNTEGVGGPSAGLMFTLAIYDQLVKEDLRKGRKIAGTGTIEQNGHVGDIGGAG
LKVVSAAKKGMDIFFVPNNPIDKNAKKGKTKVQTNYQEAKAAAKRLGTKMKIVPVQNVQQAIDYLKKTK

SEQ ID 141

ATGAAAAGACTTAAAAAAAATCAAATGGTGGTTAGTGGGTCTGCTAGCTTTAATCTCTTTGTTGCTAGCGTTATTTTTTCCGCTACCTTATTATATT
GAAATGCCTGGAGGCGCTTACGATATTCGGACTGTCTTACAAGTCAATGGCAAAGAAGACAAACGAAAAGGAGCTTACCAGTTTGTTGCAGTGGGC
ATTAGTCGTGCCAGCCTCGCTCAGCTATTATATGCTTGGCTGACACCGTTTACTGAAATTAGTACAGCAGAAGATACAACAGGCGGATACAGCGAT
GCTGATTTCCTTCGAATTAATCAATTTTACATGGAAACATCACAAAATGCAGCTATTTATCAAGCTTTATCCTTAGCTGGAAAACCAGTTACATTA
GATTATAAAGGCGTATATGTTTTAGACGTAAACAACGAATCTACTTTTAAAGGAACGCTACACTTAGCAGATACTGTAACAGGTGTAAATGGTAAA
CAGTTTACTAGTTCAGCAGAACTTATTGACTATGTTTCTCACCTAAAACTAGGGGATGAAGTTACGGTTCAGTTTACGAGTGATAATAAGCCTAAA
AAAGGAGTTGGCCGTATTATCAAACTGAAAAATGGGAAAAATGGGATTGGCATTGCCTTGACTGATCATACAAGTGTCAATTCAGAAGACACAGTG
ATCTTTAGTACTAAAGGAGTAGGAGGACCTAGTGCTGGTCTAATGTTTACTCTTGATATATATGATCAAATAACTAAAGAAGATTTACGCAAGGGC
CGTACAATTGCAGGTACAGGAACTATTGGCAAGGATGGCGAAGTAGGAGATATTGGTGGTGCAGGTCTTAAAGTAGTTGCAGCAGCTGAAGCTGGT
GCAGATATATTTTTTGTTCCGAATAATCCTGTTGATAAGGAAATTAAAAAAGTTAATCCAAATGCTATAAGTAATTACGAAGAAGCCAAACGGGCA
GCCAAACGACTAAAGACCAAAATGAAGATTGTTCCTGTTACGACTGTTCAAGAGGCACTGGTTTATCTTCGCAAA

SEQ ID 142

MKRLKKIKWWLVGLLALISLLLALFFPLPYYIEMPGGAYDIRTVLQVNGKEDKRKGAYQFVAVGISRASLAQLLYAWLTPFTEISTAEDTTGGYSD
ADFLRINQFYMETSQNAAIYQALSLAGKPVTLDYKGVYVLDVNNESTFKGTLHLADTVTGVNGKQFTSSAELIDYVSHLKLGDEVTVQFTSDNKPK
KGVGRIIKLKNGKNGIGIALTDHTSVNSEDTVIFSTKGVGGPSAGLMFTLDIYDQITKEDLRKGRTIAGTGTIGKDGEVGDIGGAGLKVVAAAEAG
ADIFFVPNNPVDKEIKKVNPNAISNYEEAKRAAKRLKTKMKIVPVTTVQEALVYLRK

SEQ ID 143

ATGACAGAGCTTATAAGAATACTACATTTAAATGATCTGCACTCTCATTTTGAGAATTTTCCTAAGGTAAAACGATTTTTTCATGACAATCAAGCG
CAGCCAATAGAGACGATTTCACTTGACTTGGGGGATAATATTGATAAAAGCCATCCTTTGACAGAAGCAAGCTCGGGAAAGGCTAATGTCCAATTG
ATGAATGAACTGGGTATTGAGCTTGCTACTATTGGTAATAATGAAGGAGTTGGTTTATCCAAAAAAGACTTGGACCAAGTCTACAAAGATTCAGAT
TTTACGGTTATTGTTGGCAATCTAAAAGATAACATAATCGAACCGAGTTGGGCAAAACCTTACATTATTTATGAGACGCAGCAAGGAACTAAGCTT
GCCTTTTTAGCTTATACTTTTCCTTATTATAAAACCTATGAACCTAATGGGTGGACGATAGAAGATCCAATTGACTGTCTTAAATGCCATTTACAA

ATAAATCAGATAAAAGAGGCAAATTGTCGCATTTTGATGAGTCATTTAGGTATTCGTTTTGATACAAGGATTGCTCAAGAATTTTCAGAAATTGAC
CTTATTATAGGTGCACATACACACCATTTATTTGAGGAAGGGGAGCTAATTAACGGTACATATCTTGCAGCAGCTGGTAAATATGGTCGCTTTGTT
GGGAGTATTGATATAACTTTTGATAATCATACACTAAAAGATATTTTAATCTCAACATGTGATACAAAACAACTAACTGGTTATCCTTCGGACAGT
GACTGGCTAAGAAGATTGAGTCAGAAGGTAAAGAACAGCTTAGAAAAGAAAGTT

SEQ ID 144

MTELIRILHLNDLHSHFENFPKVKRFFHDNQAQPIETISLDLGDNIDKSHPLTEASSGKANVQLMNELGIELATIGNNEGVGLSKKDLDQVYKDSD
FTVIVGNLKDNIIEPSWAKPYIIYETQQGTKLAFLAYTFPYYKTYEPNGWTIEDPIDCLKCHLQINEIKEANCRILMSHLGIRFDTRIAQEFSEID
LIIGAHTHHLFEEGELINGTYLAAAGKYGRFVGSIDITFDNHTLKDILISTCDTKQLTGYPSDSDWLRRLSQKVKNSLEKKV

SEQ ID 145

ATGGATGCGATGCTGTTTTACGCAGGTGCAGATGTTGCTATTATCAATTCTGGCTTAATTGTTCAGCCATTTGAAAAAGACTTTTCGAGGAAAAAT
CTCCACGAATCATTACCTCATCAAATGCGCCTCGCTAAATTGACAGTGAGTAGTCAAGAACTTTTAGAGATTTATGAAACTATTTATCAACAAGGT
CAATTTTTAGCGCAACAAAAGATTCATGGTATGGGCTTTCGTGGCAAGTGCTTTGGAGAAGTTTTACATTCGGGATTTGATTACAAAAATGGAAAA
ATAGTGTATAATGAGAAAGATATTGATGCCAAAGAAGAAGTGATTCTTGTAATCGTTGATCAGTATTATTTTGCATCGTATTTTGAGTGTTTAAAA
ACGAAAAAAGTAGACTTGCTTTTCCTGAATTACTCAGAGATGTGGCAGCAGATTATT

SEQ ID 146

MDAMLFYAGADVAIINSGLIVQPFEKDFSRKNLHESLPHQMRLAKLTVSSQELLEIYETIYQQGQFLAQQKIHGMGFRGKCFGEVLHSGFDYKNGK
IVYNEKDIDAKEEVILVIVDQYYFASYFECLKTKKVDLLFLNYSEMWQQII

SEQ ID 147

ATGCGAAAAGAAGTGACACCAGAGATGCTTAACTATAATAAGTATCCTGGCCCACAGTTCATTCACTTTGAAAATATCGTTAAAAGTGATGATATT
GAATTTCAACTTGTTATTAATGAAAAATCAGCTTTTGATGTGACTGTCTTTGGACAACGTTTTTCTGAGATTTTATTAAAATATGATTTTATCGTT
GGCGATTGGGGTAACGAGCAGTTGAGGCTAAGAGGCTTTTACAAAGATGCTAGTACAATTAGAAAAAATAGCCGGATTTCACGTTTAGAAGATTAT
ATTAAAGAGTATTGTAACTTTGGTTGTGCTTATTTTGTGTTGGAGAATCCAAATCCTAGAGATATTAAATTTGATGATGAAAGACCTCATAAGCGT
CGTAAGTCAAGATCCAAATCACAATCATCAAAGTCACAAACTAGAAATAATCGTTCCCAGTCAAATGCCAATGCTCATTTTACAAGTAAAAAGCGT
AAAGACACAAAACGCCGTCAAGAACGTCATATTAAAGAAGAGCAAGATAAGGAAATGACCTCTGCAAAGCAGCATTTTGTTATTCGTAAGAAAAAA

SEQ ID 148

MRKEVTPEMLNYNKYPGPQFIHFENIVKSDDIEFQLVINEKSAFDVTVFGQRFSEILLKYDFIVGDWGNEQLRLRGFYKDASTIRKNSRISRLEDY
IKEYCNFGCAYFVLENPNPRDIKFDDERPHKRRKSRSKSQSSKSQTRNNRSQSNANAHFTSKKRKDTKRRQERHIKEEQDKEMTSAKQHFVIRKKK

SEQ ID 149

ATGGATTTTTCAGAAAGGTGTCAAATGAAAAAAGAAATTTCGCCAGAAATGTACAACTATAATAAATTTCCAGGTCCCAAATTTATTCATTTTGAA
GAGCAAGTTAAGGCTGAAGGCATTGATTTGTTACTCTTAGAAGATGTTAAGAACGCTTTTGATACGACTAGCTTTGGTCAACGTTATACAGAAGTT
CTCCTAAAGTATGACTATATTGTTGGCGATTGGGGAAATGAACAGCTTCGTCTTAAAGGGTTTTATAAGGATAGTGACGATATCAAGAAAACGAAT
CGCATCTCACGTTTAGAAGATTATATTAAAGAATTTTGCAATTTTGGTTGTGCTTATTTTGTTTTAGAAAATCTTCATCCACAAGATATTAAATTT
GAAGAGGAGCGCCAACCAAGACGAAAGAAATCACCTAAATCAAAATCAAATCGTCGCAAGCCAAACTATTCAAATCAGCAGCCCGCAACACCTAAG
AGCAAATCGAAGCGGGCATCAAAAGAAAAGCAACCTGAAAACCAAGCGTTTACCAGTCAAAAACGTCGAAGTAATACTAAGCATAAAGAAAAGTCA
AAACGTAATCAGACTAGTCAACTTAATACCAAAATTAGTCATTTTATCATCAGAAAGAAAGATAAA

SEQ ID 150

MDFSERCQMKKEISPEMYNYNKFPGPKFIHFEEQVKAEGIDLLLLEDVKNAFDTTSFGQRYTEVLLKYDYIVGDWGNEQLRLKGFYKDSDDIKKTN
RISRLEDYIKEFCNFGCAYFVLENLHPQDIKFEEERQPRRKKSPKSKSNRRKPNYSNQQPATPKSKSKRASKEKQPENQAFTSQKRRSNTKHKEKS
KRNQTSQLNTKISHFIIRKKDK

SEQ ID 151

ATGAAGAAAGAAAATATTATGCCTAAAAAAACTGATACACCCGCCTATAAACCCTCTATTTATAGCTTAACTCGCGATGAACTAATAGCTTGGGCT
ATTGAACATGGAGAAAAGAAATTCCGTGCTTCACAAATCTGGGACTGGCTCTATAAAAAGCGTGTGCAAAGCTTCGATGAAATGACTAACATTTCC
AAAGATTTTATTGCACTTTTGAACGAGAATTTTGTTGTTAATCCTCTAAAACAACGTATTGTTCAAGAATCTGCTGATGGAACTGTTAAATACCTT
TTTGAATTACCTGATGGCATGCTGATTGAGACGGTTTTGATGCGTCAACATTATGGTTTATCAGTATGTGTAACGACTCAAGTTGGTTGTAACATT
GGTTGCACTTTCTGTGCAAGTGGTTTAATAAAGAAACAACGTGATCTTAACAATGGCGAAATCACTGCTCAAATTATGCTTGTTCAAAAATATTTT
GATGAACGTGGACAAGGTGAGCGCGTTAGTCACATTGTGGTCATGGGAATAGGTGAACCCTTTGATAACTATACCAATGTATTAAAATTCTTGCGT
ACAGTTAATGATGATAATGGATTAGCTATTGGTGCACGTCACATTACAGTGTCTACTTCAGGTTTAGCACATAAAATTCGTGAATTTGCAAATGAA
GGTGTACAAGTTAACTTAGCAGTATCTCTTCATGCTCCAAATAACGATTTACGATCAAGTATCATGCGTATTAATCGTTCTTTCCCTCTTGAAAAG
TTGTTTGCGGCTATTGAATATTATATTGAGACGACTAACCGTCGTGTAACATTTGAGTATATTATGTTAAATGGTGTCAACGATACCCCAGAAAAT
GCTCAAGAGTTAGCAGATTTAACGAAAAAGATTCGCAAATTATCTTATGTCAATTTAATTCCTTACAATCCTGTCTCAGAACATGACCAGTATAGT
CGTAGTCCTAAAGAGCGTGTAGAAGCTTTCTATGACGTTTTGAAGAAAAATGGAGTTAACTGTGTTGTTCGTCAAGAACATGGTACGGACATTGAT
GCAGCTTGCGGGCAATTACGTTCAAACACAATGAAACGCGATCGTCAAAAAGCGAAGGTAGGGCAG

SEQ ID 152

MKKENIMPKKTDTPAYKPSIYSLTRDELIAWAIEHGEKKFRASQIWDWLYKKRVQSFDEMTNISKDFIALLNENFVVNPLKQRIVQESADGTVKYL
FELPDGMLIETVLMRQHYGLSVCVTTQVGCNIGCTFCASGLIKKQRDLNNGEITAQIMLVQKYFDERGQGERVSHIVVMGIGEPFDNYTNVLKFLR
TVNDDNGLAIGARHITVSTSGLAHKIREFANEGVQVNLAVSLHAPNNDLRSSIMRINRSFPLEKLFAAIEYYIETTNRRVTFEYIMLNGVNDTPEN
AQELADLTKKIRKLSYVNLIPYNPVSEHDQYSRSPKERVEAFYDVLKKNGVNCVVRQEHGTDIDAACGQLRSNTMKRDRQKAKVGQ

SEQ ID 153

ATGAAACCATCGATTTATAGCTTAACACGCGATGAACTGATCGCGTGGGCAGTTGAACGCGGCCAAAAACAGTTTAGAGCTACTCAAATTTGGGAT
TGGCTCTATAAAAAAAGAGTTCAATCTTTTGAGGAGATGACGAATATTTCTAAAGATTTTGTTTCTATTTTAAATGATAGTTTCTGTGTCAATCCT
TTAAAACAGCGAGTTGTACAAGAGTCAGCTGATGGTACAGTAAAATATTTATTTGAACTGCCCGATGGTATGTTAATTGAAACAGTTTTAATGCGT
CAACATTATGGTCATTCTGTTTGTGTGACGACTCAAGTTGGCTGTAACATTGGCTGTACTTTTTGTGCTAGTGGATTGATCAAAAAGCAACGTGAT
CTAAACAGTGGGGAAATTACAGCTCAAATCATGTTAGTCCAAAAATATTTTGACGATAGAAAGCAAGGTGAGCGGGTTAGCCATGTTGTCGTAATG
GGCATTGGTGAACCTTTTGATAATTACAAAAATGTCATGTGCTTTCTTCGCGTCATCAACGATGATAATGGCTTAGCAATTGGTGCCCGTCATATT
ACAGTCTCTACCTCAGGGTTAGCTCACAAGATTCGGGATTTTGCAAACGAGGGAGTACAGGTTAACTTAGCAGTCTCGTTGCATGCACCAAATAAT
GATTTACGTTCAAGTATTATGCGAGTAAATCGCTCTTTTCCGCTTGAAAAGCTCTTTTCAGCTATAGAATACTATATTGAAAAAACGAATCGTCGT
GTCACTTTTGAATACATTATGCTAAATGAAGTTAACGATAGCATTAAGCAAGCTCAAGAATTAGCAGACTTAACTAAAACTATTCGTAAGTTATCT
TATGTTAACTTGATTCCGTATAATCCTGTTTCAGAACATGATCAGTATAGTAGAAGTCCTAAAGAGCGAGTTCTAGCGTTTTATGATGTGCTAAAG
AAAAATGGAGTTAACTGTGTGGTGCGTCAAGAGCACGGAACAGATATTGATGCAGCCTGTGGCCAGTTACGTTCTAAAACGATGAAAAAAGATCGC
GAAAAGGTTACAGCGACAAAA

SEQ ID 154

MKPSIYSLTRDELIAWAVERGQKQFRATQIWDWLYKKRVQSFEEMTNISKDFVSILNDSFCVNPLKQRVVQESADGTVKYLFELPDGMLIETVLMR
QHYGHSVCVTTQVGCNIGCTFCASGLIKKQRDLNSGEITAQIMLVQKYFDDRKQGERVSHVVVMGIGEPFDNYKNVMCFLRVINDDNGLAIGARHI
TVSTSGLAHKIRDFANEGVQVNLAVSLHAPNNDLRSSIMRVNRSFPLEKLFSAIEYYIEKTNRRVTFEYIMLNEVNDSIKQAQELADLTKTIRKLS
YVNLIPYNPVSEHDQYSRSPKERVLAFYDVLKKNGVNCVVRQEHGTDIDAACGQLRSKTMKKDREKVTATK

SEQ ID 155

ATGCTTAAAAGATTACTTACTGAAGATGGGGAATTGACAAAGATTAGTCGTCGTTTCGTTTGGATGTTAGTGATTATCTATTGTCTTATTATTGTC
AGGATGTGTTTTGGGCCTCAAATTATGATTGAGGGGGTATCAACTCCGAATGTTCAGCGCTTCGGAAGAATTGTAGCTCTTTTAGTACCATTTAAT
TCTTTTCGTAGTTTAGATCAGCTAACTAGCTTTAAAGAGATTTTTTGGGTTATTGGTCAAAATGTAGTGAATATTTTACTGCTGTTTCCTCTCATT
ATAGGGTTACTATCCCTAAAGCCAAGTTTACGGAAATATAAAAGCGTTATATTACTTGCTTTCTTGATGTCTATTTTCATAGAGTGTACTCAAGTT
GTTTTAGATATTTTAATAGATGCTAATCGGGTTTTTGAAATCGACGATCTATGGACAAATACCTTAGGCGGTCCTTTCGCCCTATGGACTTATCGA
AACATAAAAGGTTGGCTTCTAACTATTAGAAAA

SEQ ID 156

MLKRLLTEDGELTKISRRFVWMLVIIYCLIIVRMCFGPQIMIEGVSTPNVQRFGRIVALLVPFNSFRSLDQLTSFKEIFWVIGQNVVNILLLFPLI
IGLLSLKPSLRKYKSVILLAFLMSIFIECTQVVLDILIDANRVFEIDDLWTNTLGGPFALWTYRNIKGWLLTIRK

SEQ ID 157

ATGTCTATTATAAAAAATTTGTGGTGGTTTTTTAAGGAAGAAAAGAAGCGCTATCTTATTGGAATTTTGTCATTAAGTTTGGTTGCGGTGTTAAAT
CTTATCCCTCCTAAAATCATGGGATCAGTTATTGATGCTATTACAACTGGAAAATTAACAAGACCACAATTGCTCTGGAATTTATTAGGTTTGGTT
TTGTCAGCTTTAGCTATGTATGGGCTGCGTTATATTTGGCGTATGTATATTTTAGGGACTTCTTACAAATTGGGTCAAGTTGTCAGATACCGTTTA
TTTGAACATTTTACAAAAATGTCTCCTTCTTTTTATCAGAAATATCGTACAGGTGATTTAATGGCGCACGCGACCAACGACATCAATTCTCTAACA
CGTCTTGCAGGAGGAGGAGTTATGTCAGCAGTGGATGCCTCTATCACAGCATTAGTAACGCTTATCACCATGTTCTTTACTATTTCGTGGCAAATG
ACATTAATTGCGGTTATCCCTTTGCCCTTAATGGCCTTAGCAACTAGTAAATTGGGGCGAAAAACCCATGAAACCTTCAAAGAATCTCAGGCAGCC
TTTTCAGAATTAAATAATAAAGTGCAAGAAAGTGTCTCTGGCGTCAAAGTGACTAAATCATTTGGTTATCAAGAACAAGAAATTGCTTCTTTTCAA
GAGGTTAATCAGATGACTTTCGTGAAGAACATGCGGACCATGACTTATGATGTCATGTTTGATCCTTTAGTTCTTCTTTTTATAGGTGCCTCCTAC
GTATTAACATTGGCTATGGGAGCTTTTATGATTTCAAAAGGTCAAGTTACTGTTGGTGACTTGGTAACATTTGTGACGTATTTAGATATGTTGGTA
TGGCCCTTGATGGCGATTGGTTTCTTGTTCAATATGGTACAGCGTGGTAGTGTTTCTTATAACCGTATTAATAGCCTACTTGAGCAAGAATCGGAT
ATAACTGACCCTTTAAATCCTATCAGACCTGTTGTCAATGGAACATTAAGATATGATATTGATTTCTTTAGATACGACAATGAAGAAACCTTAGCC
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CATGATGTGACTCAGGGAAAAATTACTTTAAATAAACATGATATACGTGATTATCGATTGTCTGAGTTACGTCAACTAATCGGTTATGTTCCTCAA
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CATGTTTACGATGACATTAAACAGATGCCAGCAGGATTTGAGACTCTAATTGGAGAAAAAGGAGTCTCATTATCTGGTGGACAAAAACAAAGGATT
GCGATGAGTCGTGCCATGATTTTAGATCCAGATATTCTTATTTTGGATGATTCTCTATCAGCAGTGGACGCTAAAACGGAACATGCCATTATTGAA
AATCTTAAAACGAATCGTCAAGGGAAATCGACTATTATTTCAGCACATCGATTATCAGCTGTTGTGCACGCAGACCTTATCTTAGTTATGCAAGAC
GGCAGAGTCATCGAGCGAGGTCAGCATCAAGAGTTGCTAAATAAAGGTGGTTGGTATGCTGAAACGTATGCCTCACAGCAATTAGAAATGGAGGAA
GCATTTGATGAAGTC

SEQ ID 158

MSIIKNLWWFFKEEKKRYLIGILSLSLVAVLNLIPPKIMGSVIDAITTGKLTRPQLLWNLLGLVLSALAMYGLRYIWRMYILGTSYKLGQVVRYRL
FEHFTKMSPSFYQKYRTGDLMAHATNDINSLTRLAGGGVMSAVDASITALVTLITMFFTISWQMTLIAVIPLPLMALATSKLGRKTHETFKESQAA
FSELNNKVQESVSGVKVTKSFGYQEQEIASFQEVNQMTFVKNMRTMTYDVMFDPLVLLFIGASYVLTLAMGAFMISKGQVTVGDLVTFVTYLDMLV
WPLMAIGFLFNMVQRGSVSYNRINSLLEQESDITDPLNPIRPVVNGTLRYDIDFFRYDNEETLADIHFTLEKGQTLGLVGQTGSGKTSLIKLLLRE
HDVTQGKITLNKHDIRDYRLSELRQLIGYVPQDQFLFATSILENVRFGNPTLSINAVKKATKLAHVVDDIKQMPAGFETLIGEKGVSLSGGQKQRI
AMSRAMILDPDILILDDSLSAVDAKTEHAIIENLKTNRQGKSTIISAHRLSAVVHADLILVMQDGRVIERGQHQELLNKGGWYAETYASQQLEMEE
AFDEV

SEQ ID 159

GTGATGAAAACAGCACGTTTTTTCTGGTTTTATTTTAAACGCTATCGTTTCTCATTTACTGTCATTGCTGTTGCCGTTATCTTAGCAACTTATTTA
CAAGTAAAAGCTCCTGTCTTCTTAGGAGAGTCCTTGACTGAGTTGGGAAAAATCGGTCAGGCTTATTACGTTGCTAAGATGAGTGGCCAGACACAT
TTTAGCCCTGATTTATCAGCTTTTAATGCCGTGATGTTTAAGCTTTTGATGACTTATTTCTTTACTGTTTTAGCTAATCTAATATATAGTTTCTTA
CTTACACGTGTTGTCTCACATTCGACTAACCGCATGCGCAAGGGCTTATTTGGTAAATTAGAACGTTTAACCGTCGCCTTTTTTGACCGCCATAAA
GATGGGGAGATTCTTTCTCGTTTCACGAGTGATTTGGATAATATTCAAAACTCGCTGAACCAATCCTTGATTCAAGTGGTGACTAATATTGCCCTT
TACATCGGCCTGGTCTGGATGATGTTTAGGCAAGATAGCCGTTTAGCTTTGTTAACCATCGCATCAACCCCAGTTGCTCTCATTTTTTTAGTGATT
AACATCCGTTTGGCAAGAAAATACACCAATATCCAACAGCAAGAAGTCAGTGCTTTAAATGCTTTTATGGATGAAACCATTTCAGGACAAAAGGCT
ATTATTGTACAAGGTGTCCAAGAAGATACGATGACAGCCTTTTTAAAGCATAATGAAAGGGTTCGACAAGCCACCTTCAAACGCCGTCTGTTCTCA
GGACAATTATTTCCAGTCATGAATGGAATGAGCCTTATTAACACGGCTATCGTGATTTTTGTCGGTTCAACAATTGTCCTCAGTGACAAATCTATG
CCAGCAGCGGCAGCGCTTGGTTTAGTGGTTACTTTTGTACAATATTCCCAGCAATATTACCAACCCATGATGCAAATCGCGTCTAGTTGGGGAGAA
TTGCAGCTGGCCTTTACCGGTGCTCACCGTATTCAAGAAATGTTTGATGAAACCGAAGAAGTTCGTCCACAAAATGCACCAGCGTTCACCAGCTTA
AAAGAAGCAGTGGCGATTAACCACGTCGATTTTGGGTATCTTCCTGGGCAAAAAGTTTTATCAGATGTGTCAATCGTTGCACCCAAGGGCAAAATG
ATTGCCGTGGTTGGACCGACAGGTTCTGGAAAGACCACTATTATGAACTTGATTAACCGTTTCTACGATGTGGATGCAGGTTCGATTACCTTTGAT
GGCCGTGATATTCGTGACTACGATTTGGATAGTCTTCGTCAAAAGGTAGGGATTGTGTTGCAAGAGTCAGTTCTTTTTCAGGAACCATTACGGAT
AATATTCGTTTTGGTGATCAGACCATTAGTCAAGACATGGTTGAAACTGCTGCGCGTGCGACCCATATTCATGACTTTATCATGTCCTTACCAAAA
GGGTACAATACCTATGTCTCAGATGATGACAATGTCTTTTCAACAGGTCAAAAGCAGTTGATTTCTATTGCTAGGACGCTACTGACTGACCCTGAA
GTGTTGATTTTGGATGAGGCCACTTCAAATGTTGATACGGTTACCGAAAGTAAAATTCAACGGGCCATGGAAGCTATCGTGGCAGGTCGAACTAGC
TTTGTCATTGCTCACCGCCTCAAAACCATTTTAAATGCCGATCACATTATTGTGTTGAAAGATGGCAAGGTCATTGAGCAAGGAAATCATCATGAG
CTATTGCATCAAAAAGGCTTTTATGCCGAATTGTATCACAATCAATTTGTCTTTGAA

SEQ ID 160

VMKTARFFWFYFKRYRFSFTVIAVAVILATYLQVKAPVFLGESLTELGKIGQAYYVAKMSGQTHFSPDLSAFNAVMFKLLMTYFFTVLANLIYSFL
LTRVVSHSTNRMRKGLFGKLERLTVAFFDRHKDGEILSRFTSDLDNIQNSLNQSLIQVVTNIALYIGLVWMMFRQDSRLALLTIASTPVALIFLVI
NIRLARKYTNIQQQEVSALNAFMDETISGQKAIIVQGVQEDTMTAFLKHNERVRQATFKRRLFSGQLFPVMNGMSLINTAIVIFVGSTIVLSDKSM
PAAAALGLVVTFVQYSQQYYQPMMQIASSWGELQLAFTGAHRIQEMFDETEEVRPQNAPAFTSLKEAVAINHVDFGYLPGQKVLSDVSIVAPKGKM
IAVVGPTGSGKTTIMNLINRFYDVDAGSITFDGRDIRDYDLDSLRQKVGIVLQESVLFSGTITDNIRFGDQTISQDMVETAARATHIHDFIMSLPK
GYNTYVSDDDNVFSTGQKQLISIARTLLTDPEVLILDEATSNVDTVTESKIQRAMEAIVAGRTSFVIAHRLKTILNADHIIVLKDGKVIEQGNHHE
LLHQKGFYAELYHNQFVFE

SEQ ID 161

TTGATGAAGTCTAATCAATGGCAAGTCTTTAAGAGATTAATCTCCTATTTACGCCCTTATAAATGGTTTACAGTATTAGCTCTATCTCTCTTATTG
TTGACGACTGTTGTTAAAAATATTATTCCTTTAATTGCTTCACATTTTATTGATCACTATCTGACAAATGTTAATCAAACAGCAGTTCTTATTTTA
GTGGGATATTATTCAATGTATGTCTTGCAGACCTTAATTCAATATTTTGGGAATCTCTTTTTTTGCGCGTGTTTCTTATAGTATTGTTAGAGATATT
CGTAGAGATGCTTTTGCTAATATGGAAAGGCTTGGCATGTCTTATTTTGATAGGACACCGGCAGGATCTATAGTGTCACGTATTACTAATGATACT
GAAGCAATATCTGATATGTTTTCGGGTATTTTATCGAGTTTTATCTCGGCGATATTTATTTTTACAGTTACTCTGTACACTATGTTGATGCTAGAC
ATTAAACTAACAGGACTTGTCGCTCTTTTATTACCTGTTATCTTTATATTAGTGAATGTCTATCGGAAAAAATCAGTCACTGTCATTGCTAAAACG
AGAAGTTTACTTAGTGATATCAACAGTAAATTATCAGAAAGTATTGAAGGAATTCGCATTGTACAGGCTTTTGGTCAAGAAGAGCGCTTGAAGACT
GAATTTGAGGAAATTAACAAAGAGCATGTTGTGTATGCCAATCGTTCTATGGCTCTTGATAGTCTCTTCTTAAGACCGGCGATGTCTCTTTTAAAA
CTCCTAGCATATGCTGTTCTTATGGCTTATTTTGGATTTACAGGAGTTAAAGGAGGTCTTACGGCAGGATTGATGTATGCTTTTATTCAGTACGTT

AATCGTCTCTTTGACCCTTTAATTGAAGTAACGCAAAATTTTTCAACCTTACAAACATCAATGGTATCAGCAGGGCGTGTGTTTGATTTGATTGAT
GAAACAGGTTTTGAACCAAGCCAAAAAAATACAGAAGCTTTTGTGAGAGAAGGAAATATCGAATTTAAAAATGTATCATTCTCATATGATGGAAAA
AAACAAATCCTTGATAATGTTTCTTTTAGTGTTAAAAAAGGTGAAACGATTGCTTTTGTAGGAGCGACAGGTTCTGGAAAATCATCTATTATTAAT
GTCTTTATGAGGTTTTACGAATTTCAATCTGGACAAGTTTTATTAGATGGGAAGGATATTAGGGATTACTCACAAGAACAATTGCGAAAGAATATT
GGACTCGTCTTACAAGACCCCTTTTTATATCATGGCACTATTAAATCTAATATCAAAATGTACCAAGACATCACCGATCAAGAGGTACAGGACGCA
GCAGAGTTTGTTGATGCTGATCAATTTATTCAGAAGTTGCCAGATAAGTACGATGCAGCTGTTTCAGAACGTGGGTCAAGTTTTTCGACTGGACAA
CGCCAACTATTGGCGTTTGCCAGAACTGTGGCTAGTAAACCTAAAATTTTAATCTTAGATGAAGCGACAGCAAATATTGATTCGGAAACAGAGCAG
ATTGTACAAGATTCGTTAGCAAAAATGCGTCAAGGTCGAACAACAATTGCCATTGCTCACCGCTTATCAACCATTCAAGATGCTAATTGTATCTAT
GTTCTTGATAGAGGAAAGATAATTGAAAGTGGGAATCACGAGTCTTTATTAGACCTAAAAGGGACTTATTATCGTATGTACCAATTACAAGCTGGC
ATGATGGAGGTC

SEQ ID 162

MMKSNQWQVFKRLISYLRPYKWFTVLALSLLLLTTVVKNIIPLIASHFIDHYLTNVNQTAVLILVGYYSMYVLQTLIQYFGNLFFARVSYSIVRDI
RRDAFANMERLGMSYFDRTPAGSIVSRITNDTEAISDMFSGILSSFISAIFIFTVTLYTMLMLDIKLTGLVALLLPVIFILVNVYRKKSVTVIAKT
RSLLSDINSKLSESIEGIRIVQAFGQEERLKTEFEEINKEHVVYANRSMALDSLFLRPAMSLLKLLAYAVLMAYFGFTGVKGGLTAGLMYAFIQYV
NRLFDPLIEVTQNFSTLQTSMVSAGRVFDLIDETGFEPSQKNTEAFVREGNIEFKNVSFSYDGKKQILDNVSFSVKKGETIAFVGATGSGKSSIIN
VFMRFYEFQSGQVLLDGKDIRDYSQEQLRKNIGLVLQDPFLYHGTIKSNIKMYQDITDQEVQDAAEFVDADQFIQKLPDKYDAAVSERGSSFSTGQ
RQLLAFARTVASKPKILILDEATANIDSETEQIVQDSLAKMRQGRTTIAIAHRLSTIQDANCIYVLDRGKIIESGNHESLLDLKGTYYRMYQLQAG
MMEV

SEQ ID 163

GTGTATAATGAGGTCAAAGTGCAAGGAAAGGTCTATAAAATGTTACTATTGGTAGATAATTACGATTCTTTTACCTATAATTTAAAGCAATATTTA
AGTGTCTATAAAGAGGTATTCGTCATAAAAAATGATGTTCCTAACCTTTTTTTATTAGCTGAGAGCGCAGAAGCCATCGTCTTATCACCTGGACCA
GGACACCCAAAGGATGCTGGGAAAATGGTAGAATTAATCAATCAGTTTATAGGAAAGAAACCTATTCTAGGTATCTGTTTGGGGCATCAAGCGCTT
GCCGAGTGCTTGGGTGGGCGATTAAATTTAGCAAATCACGTTATGCATGGTAAACAAAGTTGGGTAACAATAAACGACCATACTAGTTTGTTTAAG
GGAATTGATAGTCCAACCCAAGTTATGCGTTATCATTCATTGGTAGTGACTGATTTACCAGAGAAATATTGCTGTTATTGCACGATCAAATGAGGAT
AATGAAATCATGGCATTCCATTGCCCCAGCTTAAAGGTATATGCGATGCAGTTTCATCCTGAGTCAATCGGGAGTATTGATGGAATGAAAATGATT
GAAAACTTTTTGACGTTAATTAATGAC

SEQ ID 164

MYNEVKVQGKVYKMLLLVDNYDSFTYNLKQYLSVYKEVFVIKNDVPNLFLLAESAEAIVLSPGPGHPKDAGKMVELINQFIGKKPILGICLGHQAL
AECLGGRLNLANHVMHGKQSWVTINDHTSLFKGIDSPTQVMRYHSLVVTDLPENIAVIARSNEDNEIMAFHCPSLKVYAMQFHPESIGSIDGMKMI
ENFLTLIND

SEQ ID 165

ATGATACTCTTAATTGATAATTACGATTCATTTACCTACAACCTCGCCCAATATTTAAGTGAATTTGACGAGACGATTGTCTTGTATAACCAAGAC
CCAAACTTATATGACATGGCCAAAAAAGCTAACGCTCTAGTCCTCTCACCTGGTCCTGGTTGGCCCAAGGAAGCCAACCAAATGCCAAAACTCATT
CAAGACTTTTACCAAACAAAACCTATCTTAGGAGTGTGTCTGGGACACCAAGCTATCGCTGAAACTTTAGGGGGAACCTTACGCTTGGCCAAACGC
GTCATGCATGGGAGACAAAGCACCATTGAAACGCAAGGCCCTGCTAGTCTTTTTCGCTCCCTGCCACAAGAGATCACCGTCATGCGCTACCATTCC
ATCGTTGTGGATCAGTTACCAAAAGGTTTTAGCGTAACCGCTAGAGACTGTGACGATCAAGAAATCATGGCATTTGAACACCACACCCTGCCACTT
TTTGGGCTACAATTTCACCCAGAAAGCATCGGAACTCCTGATGGCATGACCATGATTGCCAACTTCATCGCAGCCATTCCCCGT

SEQ ID 166

MILLIDNYDSFTYNLAQYLSEFDETIVLYNQDPNLYDMAKKANALVLSPGPGWPKEANQMPKLIQDFYQTKPILGVCLGHQAIAETLGGTLRLAKR
VMHGRQSTIETQGPASLFRSLPQEITVMRYHSIVVDQLPKGFSVTARDCDDQEIMAFEHHTLPLFGLQFHPESIGTPDGMTMIANFIAAIPR

SEQ ID 167

ATGAAAACAAGAACAACTACCTATATTGCACTCATGGTTGCACTACTTATTGTTTTAGGTTTTATCCCAGGGATCCCATTAGGTTTCATTCCAGTC
CCAATTGTTTTACAAAATCTTGGTGTTATGCTGGCAGGTGCTCTGCTTGGTAGTAGGAAGGGTTTCCTAGCTGTGGCTATTTTCTTGCTCTTAGTT
GCTATTGGTGCACCATTTTTACCAGGAGGACGGTCAGGTCTCGTAACGCTGTTTGGGCCAACAGCAGGCTATCTGCTGACTTATCCATTTGCAGCT
TTTTTTATCGGCCTAGGGCTTGAGAAAGTGAAAACAACAAAACTCTGGGTTCAATTCCTTATTATTTGGATATTTGGCGTACTATTGATTGATATT
TGTGGTAGCATCGTTCTTTCCTTTCAAACTTCTCTACCCTTAACTAAATCACTATTTTCTAACCTTATTTTTATTCCTGGGGATACCTTAAAAGCA
TCCATTTGCTTGATTATTTATCGTAAATTTGCAAACAGATTAACTCATCTATACAAC

SEQ ID 168

MKTRTTTYIALMVALLIVLGFIPGIPLGFIPVPIVLQNLGVMLAGALLGSRKGFLAVAIFLLLVAIGAPFLPGGRSGLVTLFGPTAGYLLTYPFAA
FFIGLGLEKVKTTKLWVQFLIIWIFGVLLIDICGSIVLSFQTSLPLTKSLFSNLIFIPGDTLKASICLIIYRKFANRLTHLYN

SEQ ID 169

ATGTTTACAACCAAAGAACTTGTTAAGGTGGCTATGATGACCACTTTGATTATTATTTTAGGCTTTATTCCTGCTATCCCGCTAGGCTTTATCCCA
GTCCCTATTGTTTTACAAAACTTAGGTGTCATGTTGGCTGGATTGATGCTGGGTGGTAAAAAGGGAACCTTATCTGTTTTCTTATTTTTAGTGATT
GGCCTTTTCTTACCTGTTTTCTCAGGCTCAAGAACAACCATTCCAGTATTGATGGGGCCATCTGCTGGCTATGTTATTGCCTACCTTCTTGTGCCT
ATTGTCTTTTCATTACTTTACCGCAATTGGTTCTCAAAAAGCACGCCATTAGCATTCCTAGCTCTTTTAATCTCAGGAGTTGTACTGGTTGATGTT
CTGGGTGCTATCTGGTTGTCAGCCTACACTGGCATGTCTCTTGTGACATCGCTTTTATCAAACTTGGTCTTTATTCCAGGAGATACCATCAAAGCA
ATCATTGCGACCATTATCGCTGTTAAATACAAAGATAGTTTTTTGAATACAAAACAG

SEQ ID 170

MFTTKELVKVAMMTTLIIILGFIPAIPLGFIPVPIVLQNLGVMLAGLMLGGKKGTLSVFLFLVIGLFLPVFSGSRTTIPVLMGPSAGYVIAYLLVP
IVFSLLYRNWFSKSTPLAFLALLISGVVLVDVLGAIWLSAYTGMSLVTSLLSNLVFIPGDTIKAIIATIIAVKYKDSFLNTKQ

SEQ ID 171

GTGACTAATGATTCAAAATTCTCAAAATGGACCTCTCGTCCAGCGCTTAATCTTAATTCCTTGAAAGGAAAAACAAAACGCAACATGGCCATAATT
TTTAAGCATTTAATGGGAGTCAAA

SEQ ID 172

MTNDSKFSKWTSRPALNLNSLKGKTKRNMAIIFKHLMGVK

SEQ ID 173

ATGCTATTATTAATTTCGTTAAAGGAGGCTATCATGTCATTTCAAACAAATTATATCCATTTGGCTGACGAAATATTATCTGGAAAGACTAGCATT
TCTTATGAACAAGCGCTGGAAATTCTAAATAGCGATGAGAACTGGTGGGAAATCTACGCTGCTGCCTTATACCTTAAAAATCAAGTTAGCCGAAAT
AATATTCGCCTTAACGTTTTATTAAGTGCTAAGCAAGGACTTTGTGCAGAAAATTGTGGTTACTGTTCTCAATCTAAAGAAAGCACTGCTGACATT
GATAAATTTGGTCTGCTTCCTCAAAATGTCATTCTAAAACAGGCTATTGTCGCTCATCAAAATGGTGCTAGCGTCTTTTGTATTGCGATGAGTGGA
ACTAAGCCTAGCAAGAGAGAAATTGAGCAGTTATGTCAAGTCATCCCTGAAATCAAAAAAAGCCTCCCTCTAGAAATATGCCTTACCGCTGGTTTT
TTGGATAGAGAACAACTTCATCAGCTAAAACAAGCAGGAATTGACCGTATCAATCATAATCTCAACACCCCCGAAGAAAACTACCCCAACATTGCA
ACGACGCATAGCTTCAAAGATCGTTGTGATACTTTAGAAAGAATTCACAATGAAGACATTGATGTTTGTTCTGGATTCATTTGTGGTATGGGAGAG
AGCGATGAGGGGCTCATCACATTAGCTTTCAGACTAAAAGAGCTGGACCCCTATTCTATCCCTGTCAATTTTTTACTTGCTGTTGAAGGAACACCT
CTTGGAAAATATAACTATTTGACTCCCATTAAATGCTTAAAAATTATGGCCATGTTGCGTTTTGTTTTTCCTTTCAAGGAATTAAGATTAAGCGCT

GGACGAGAGGTCCATTTTGAGAATTTTGAATCATTAGTCACCTTACTTGTTGACTCAACTTTTTTGGGAAATTACCTAACAGAGGGCGGTCGCAAT
CAACATACCGATATTGAATTCTTGGAAAAATTACAACTAAATCATACTAAAAAGGAATTAATT

SEQ ID 174

MLLLISLKEAIMSFQTNYIHLADEILSGKTSISYEQALEILNSDENWWEIYAAALYLKNQVSRNNIRLNVLLSAKQGLCAENCGYCSQSKESTADI
DKFGLLPQNVILKQAIVAHQNGASVFCIAMSGTKPSKREIEQLCQVIPEIKKSLPLEICLTAGFLDREQLHQLKQAGIDRINHNLNTPEENYPNIA
TTHSFKDRCDTLERIHNEDIDVCSGFICGMGESDEGLITLAFRLKELDPYSIPVNFLLAVEGTPLGKYNYLTPIKCLKIMAMLRFVFPFKELRLSA
GREVHFENFESLVTLLVDSTFLGNYLTEGGRNQHTDIEFLEKLQLNHTKKELI

SEQ ID 175

ATGATATACTGGTCTTATATTTTGACGGGAGATAAGATGAAAAAACTATTTAAAAAAGCGATAGCTATGTGCCGAGATTTGCCGCTTAATTTTGTA
ATTGTTGAACTTAGTTTGTATCAAAGAGAGGATGGCTCATCTGATAATATTAAATGGATTTCTAAGAGAATTCTTGAGGTAACGGTAACTGATCAG
CAATGGATTTACCATTTGAGGATGCTTAATTTACCAAAACTTAAGCCAATGTCACTAGCATCCAGTGACTGTCCTGCAAGGGAAGAGAAGGCTAGT
CTTATTTCAATAGAAGAATGTCAAAAATTCACTAGCTTAGTGCGAGATAAAAATCCTTTTCACCAAGGGGAAGCAGCTATTGTGCCTGCGGCTCTA
TTATTGGAAAAAATAATGGAAGTTAGAAAAGGAAAAATAAAGGAGATTCATTTGACTTTTTTATCTCCAGTAAGGGTGAATCAAGAATTCTCAGTG
CAAGTAGTGGATAACACAGTGATTATTTTTCAGCATCAAATATTATGG

SEQ ID 176

MIYWSYILTGDKMKKLFKKAIAMCRDLPLNFVIVELSLYQREDGSSDNIKWISKRILEVTVTDQQWIYHLRMLNLPKLKPMSLASSDCPAREEKAS
LISIEECQKFTSLVRDKNPFHQGEAAIVPAALLLEKIMEVRKGKIKEIHLTFLSPVRVNQEFSVQVVDNTVIIFQHQILW

SEQ ID 177

TTGTTTAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTCACATTGTAGAAGTAGCAGGAGATCCCAA
GCT

SEQ ID 178

MFNARCCCISNASESENRIPDCSHCRSSRRSQA

SEQ ID 179

ATGAAGAATAGAGATGTTTATATTGGTTTTGGGCTACGAACACCTATCGGTATAAAAGGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGA
GCACACCTTTTAAATCAAATAAAAAAAATAGAATCAGAATCTAACATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGT
CGTTTGATGACTCTTTTTTCTGATTATGAATCCTATATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTTTTTTGGT
TATCTAAAAATCAGTACCGGTATTAATGAAAAAGTTCTTGTTGGGGGGGATTGAAAGTAGTTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGAT
AATCGTAACGGAGAATATACAGTTGCTCAGTTTTCTCCTGACTCTTATGCTGAAACTGTAATGTTAGAAGGGGCCCAGAGAGTCTGTCAAAAATAT
GGTTTTAGAAGAGAAATGTTAGATAAATTGGCATTCTTGAGCCATAAACGCGCCTTAACAGCTAAACAAGGTGGCTATTTAGAAGAGGTAATCTTA
CCAATGGAAGGGATGCGAGATCAAGGCGTTAGAAAACTAAAAGAAACATTTTTTCAAAAATTACCAAGATTGATGGAAAATTCACCTTTGCTCACT
ATTGGAAATGTTTGTTTAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTCACATTGTAGAAGTAGCA
GGAGATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAAACTATTAACAGAAACTCATACTAAAATATCGGATTATGATGCAATTGAA
TGGAATGAACCATTTGCAGCGATTGATGCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTTGGAGGGACATTAGCTTAC
GGACACCCTTATGCCTGCTCAGGAATTATTAATATCCTTCATCTTATGCAGGCATTAAAATATAAAAATAAACCTATGGGTCTAACTGCCATTGCA
GGGGCAGGAGGAGTCGGAATGGCCATATCAATAGAGTACTTAGGAGTTAAGAATGCT

SEQ ID 180

MKNRDVYIGFGLRTPIGIKGKQFKHYRPELLGAHLLNQIKKIESESNIDSIICGNTVGTGGNIGRLMTLFSDYESYIPVQTIDMQCASSSSALFFG
YLKISTGINEKVLVGGIESSSLQPMRRYAKEDNRNGEYTVAQFSPDSYAETVMLEGAQRVCQKYGFRREMLDKLAFLSHKRALTAKQGGYLEEVIL
PMEGMRDQGVRKLKETFFQKLPRLMENSPLLTIGNVCLMHDAAAFLTLQSQKTEFRIVHIVEVAGDPKLSPELVHTATEKLLTETHTKISDYDAIE
WNEPFAAIDALFNHYYPEEREKFNIFGGTLAYGHPYACSGIINILHLMQALKYKNKPMGLTAIAGAGGVGMAISIEYLGVKNA

SEQ ID 181

ATGACGGATGTTTATATTGCTGCAGGCCTTAGAACCCCTATCGGTTTAGTAGGGAAACAATTTGCTAAAGAACAACCAGAAATCCTTGGAGCAAAG
CTCATCAACGCTTTACAAAATAAGTATCCAGTTCCCATTGACCAAGTGATTTGTGGCAATACCGTCGGAACGGGTGGTAATATTGGGCGCTTGATG
ACCCTGTATTCTCATTTAGGAGAATCTGTCTCTGCTTTGACGGTTGATATGCAGTGTGCATCAGCTGGTGCAGCTCTTTCCGTGGGTTATGCTAAA
ATCAAGGCAGGTATGGCAAGCAACCTTTTAGTGGGAGGGATTGAAAGCAGCTCCTTACAACCTGAATCGGTATATGCTTCAGCTGATTGGCGCCAA
GGAGCCTACAAGGTAGCTCAGTTTTCTCCAGATAGTATCAGCCCTTTTGCGATGATTGAAGGGGCAGAACGAGTGGCAAGAGAGCATGGCTTTACA
AAGGAGTATTTGAATCACTGGACATTGAGAAGTCATCAAAAGGCTAGTTATTGCCAGGAGCAAGCCCTGTTAGCTGATCTTATTCTAGACCTGTCA
GGAGCCAGTGATCAAGGTATTCGACCGCGCTTGTCAAGTAAGGTGTTGTCAAAGGTACCCCCTATCTTAGGAGAAGGTCACGTGATTAGTGCAGCC
AATGCCTGCCTAACCCATGATGCTGCTGCCTTTTTACAGCTAAGTAGTCAGCCTTCAGCTTTAAACTGATTGATGTGGTAGAAGTAGCAGGAGAC
CCACAGCGTAGCCCTTTAATGGTGATTAAGGCTAGTCAAGTCCTTTTGGAAAAACATGGTCTAGGGATGGCAGATATGACAGCGATTGAATGGAAC
GAAGCCTTTGCCGTTATTGATGGTCTATTTGAAACCCATTATCCAGATTTATTGGACCGCTATAATATATTTGGTGGTGCATTAGCTTATGGTCAT
CCCTATGGTGCCTCAGCAGCCATTATAATATTGCACTTAATGAGGGCTTTAGAGATTAAAAATGGACGCTATGGAATAGCTGCTATAGCAGCAGCT
GGTGGCCAAGGGTTTGCTGTTTTACTAAAATATCATAAGGAGTTTAGTCATGCTGACAAAGCTAGAATATTGGGCAAAGCAATGCCCAAA

SEQ ID 182

MTDVYIAAGLRTPIGLVGKQFAKEQPEILGAKLINALQNKYPVPIDQVICGNTVGTGGNIGRLMTLYSHLGESVSALTVDMQCASAGAALSVGYAK
IKAGMASNLLVGGIESSSLQPESVYASADWRQGAYKVAQFSPDSISPFAMIEGAERVAREHGFTKEYLNHWTLRSHQKASYCQEQALLADLILDLS
GASDQGIRPRLSSKVLSKVPPILGEGHVISAANACLTHDAAAFLQLSSQPSAFKLIDVVEVAGDPQRSPLMVIKASQVLLEKHGLGMADMTAIEWN
EAFAVIDGLFETHYPDLLDRYNIFGGALAYGHPYGASAAIIILHLMRALEIKNGRYGIAAIAAAGGQGFAVLLKYHKEFSHADKARILGKAMPK

SEQ ID 183

ATGCTTGAATCATTGAAAACGATAGTTAAAACCAATAGCGATAAAAAGTTATTTGATGGTGATTTACAGGTCAGTTATGGAGAATTTTATAACTTA
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CAAAAAGCTCTTCCTATTATTTGTAAACCTAACCTTACTCATAATGAAATAAGTCGATTAGAAAAAGAAGTGCAGTATGCTCCTCAACTAGCTGAT
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TTTTCGGTCACTTCCAATAGCAAACTGTTTATTCAAGGTGATTTTTCATTTACTGGTAACTTAAATTTAGCGCTATCCCTTTTATTACTGGGGGGA
ACACTTGTTGTCACACAGAAAAATTCTGTAAAATACTGGCAGACTTTATGGGAAAAAACTGGTGTAACGCATCTATATCTGCTCCCTAGTTATCTC
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TATAGAAAGCATCCTAAAGTGTCAGTGAAAATCTTCTATGGTGCTAGTGAGCTCAATTATGTGTCATGGTACGATGGTCGTGATATCCGAGATAAG
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AGTGAATATTGTGCTGGTGATTATGGTGAACTGATAGATGGCAAATTATATCTATTTGGCCGTGGTGGTGATTGGTGCAATCAATCGGGCATTAAG
CTCTATTTACCTAGATTAATCGAAAAAATAAAAACATGCCCTTATATCAAGGATGCAGTAGCATTTACAAAAGAGAGTCAAAGTCATGGACAAGAG
TCACATTGCTGTATTGTTTTAATTGAAAATCAGATGCAACAAGAGTGTTTGAAGTGGTTATCGGAACATTTTGAAAAGAAGTATGGGTTTAAGCAT
TATCATATTGTATCTAAAATTCCTTTGATGCCATCTGGAAAAATTGATTATCAACAACTCAAAAGACAGTTAGCA

SEQ ID 184

MLESLKTIVKTNSDKKLFDGDLQVSYGEFYNLVRQDMASQDNRKHVISTHSLLNQLVRFVSKLCQKALPIICKPNLTHNEISRLEKEVQYAPQLAD
FGVLSSGTTADAKLLWRSFTSWSDFFSIQNAYFSVTSNSKLFIQGDFSFTGNLNLALSLLLLGGTLVVTQKNSVKYWQTLWEKTGVTHLYLLPSYL

KLVEQYSKETALDNKTIITSSQYVSDSLLEGLYRKHPKVSVKIFYGASELNYVSWYDGRDIRDKPQYVGEIVPNVAVRIKEGRIFVKTPYSICGLS
SEYCAGDYGELIDGKLYLFGRGGDWCNQSGIKLYLPRLIEKIKTCPYIKDAVAFTKESQSHGQESHCCIVLIENQMQQECLKWLSEHFEKKYGFKH
YHIVSKIPLMPSGKIDYQQLKRQLA

SEQ ID 185

ATGCTGACAAAGCTAGAATATTGGGCAAAGCAATGCCCAAATAAAAAAGCTATCGTAGCCGATCAGATAAGCTTGACTTATCAAGAGCTATGGCAA
GCGGTTTTAATAAAGGATCAGACAATAAAAGACAGTGTACCATATATCATCAGTCATAGTCGCTATCTTAATCAGTTACTCTCTTTTTTACGAGGA
TTAAAAGAAGGCAGTTGTCCTATCATTTTACACCCTAATATCTCAGGTACATTTCAGCAGCAAATAAAACACGTCGATGGTGAGCTTCTTAAAAAA
GCTGATTTTGCTGTTTTGAGTTCGGGAACAACTGGCAAAGCAAAATTATTTTGGCGTCGTCTATCAACTTGGACGAGACTTTTTGATTATCAAAAT
AAGGTGTTTGGTATGACTGGTAATAGTTGTCTATTCTTACATGGTAGTTTTAGTTTTACTGGCAATCTTAACTTAGCATTAGCTCAACTATGGGCC
GGGGGATGTCTGGTTTTAAGCCAAAAGCTGTCTTTGAAAACGTGGTTAAGCTTATGGCAAGCAAAAAAGGTGAGTCACCTTTACCTTTTACCGACC
TACCTAAATCGCTTGCTACCTTATTTGACTAAGAACAACATGACTGCGACTCACTTATTGACCTCTTCGCAAATGATATCACAAGAATTACTAAGA
CATTATTACAAAAAATTTCCTCAGCTTGAAATTGTCATTTTCTACGGGGCTAGTGAATTATCTTTTATAACGTGGTGTAATGGCAGAGCTGCTGTC
AAAATTAATGGTTTGGTAGGACAGCCCTTTCCTGATGTGTCTATCAGTTTCAAAGATAAGGAAATTTTTGTAGAGACTCCTTATAGTGTAGAAGGA
ATGTCACAACCATACAGTGTTTCAGACTTAGGAAAAATGAGCCCAGCGGGTTTAATTTTAGAAGGGCGACAAGATGACTGGGTTAATCAACGAGGA
GTGAAATGCCACCTGCCTAGCCTAGTTGAACTCGCTCACCAAGCGCCAAACGTCAAAGAAGCGCACGCTTTAAAGATAGGAAAAGGAGAAAACGAA
ACCCTAATATTAGTATTAGTTTTGACTAAGAAGGATTGCCTAGCACCTATTAAAGACTTTTTAGCTCTTTATTTAAACTCTGGACAACTTCCCAAG
TACTATCTTGTGATTGATTGTTTGCCTTTAAAAGATAATGGTAAAATTAATCGAGAAGTTCTTTTAAATAAAATACCCAAACAGTGGCTTAGT

SEQ ID 186

MLTKLEYWAKQCPNKKAIVADQISLTYQELWQAVLIKDQTIKDSVPYIISHSRYLNQLLSFLRGLKEGSCPIILHPNISGTFQQQIKHVDGELLKK
ADFAVLSSGTTGKAKLFWRRLSTWTRLFDYQNKVFGMTGNSCLFLHGSFSFTGNLNLALAQLWAGGCLVLSQKLSLKTWLSLWQAKKVSHLYLLPT
YLNRLLPYLTKNNMTATHLLTSSQMISQELLRHYYKKFPQLEIVIFYGASELSFITWCNGRAAVKINGLVGQPFPDVSISFKDKEIFVETPYSVEG
MSQPYSVSDLGKMSPAGLILEGRQDDWVNQRGVKCHLPSLVELAHQAPNVKEAHALKIGKGENETLILVLVLTKKDCLAPIKDFLALYLNSGQLPK
YYLVIDCLPLKDNGKINREVLLNKIPKQWLS

SEQ ID 187

ATGTTATCAAAAGCAAAATCACGATATATTATCCGTGAGATTATTAAGTTATTTCCAGATGCTAAACCTAGCTTAGACTTTACTAATGTCTTTGAG
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TTGGCACAAGCTGATCCCAAAGAGATTGAACCCTATATTTCTAAAATTGGGCTTTACCGTAATAAAGCTCGATTCTTAAATCAATGCGCTAAACAA
TTGATAGAGCATTTTGATGGAAAAGTCCCCCGAACTCGTCAAGAGCTAGAAAGTTTGGCTGGCGTTGGAAGGAAAACGGCTAACGTGGTCATGAGT
GTTGGATTTGGTATTCCGGCTTTTGCCGTAGATACTCATGTCACTCGGATTTGTAAACACCACCAGATTTGCAAACAGTCGGCTTCTCCACTGGAA
ATTGAGAAACGAGTCATGGAGGTTTTACCACCAGAAGAGTGGCTAGCTGCACATCAATCCATGATTTATTTTGGTCGTGCAATTTGTCATCCTAAA
AATCCAAAATGCGACCAGTACCCACAACTTTATCACTTTCCTGATAATTTAAAG

SEQ ID 188

MLSKAKSRYIIREIIKLFPDAKPSLDFTNVFELLVAVMLSAQTTDAAVNKVTPALFERFPNPLVLAQADPKEIEPYISKIGLYRNKARFLNQCAKQ
LIEHFDGKVPRTRQELESLAGVGRKTANVVMSVGFGIPAFAVDTHVTRICKHHQICKQSASPLEIEKRVMEVLPPEEWLAAHQSMIYFGRAICHPK
NPKCDQYPQLYHFPDNLK

SEQ ID 189

ATGAGAATTGGAAAAGCAAGATTAGCAAAAGTCCTGACCATCATTGGTCAAATGTTTCCTGAGGCTAAGGGAGAGTTAGACTGGGAAACACCTTTT
CAATTGTTGATTGCGGTGATTTTATCAGCTCAAACGACAGATAAGGCCGTCAATAAGGTAACTCCTGGACTATGGCAGTCTTATCCAGAAATAGAA
GACTTAGCTTTTGCTGAACTTTCTGATGTTGAAAATGCTCTGAGAACGATTGGACTCTATAAAAATAAGGCCAAAAATATCATTAAAACTGCTCAG
GCTATTCGTGATGATTTTAAGGGTCAAGTGCCAAAAACCCACAAAGAGCTTGAAAGTTTACCGGGTGTTGGCCGAAAAACAGCCAATGTGGTGCTG
GCAGAGGTTTATGGTGTTCCAGCTATTGCGGTTGATACTCATGTGGCTAGAGTCTCAAAGAGGCTCAATATTTCATCGCCAGATGCCGATGTCAAG
CAGATTGAAGCAGATTTGATGGCTAAAATTCCAAAGAAAGATTGGATTATTACTCACCATCGATTGATTTTTTTTGGACGCTACCATTGTTTAGCC
AAAAAACCAAAATGTGAGATTTGTCCCGTTCAGTCTTACTGCAAGTACTATCAAGATACTTATGGAAAATCGAAAGCC

SEQ ID 190

MRIGKARLAKVLTIIGQMFPEAKGELDWETPFQLLIAVILSAQTTDKAVNKVTPGLWQSYPEIEDLAFAELSDVENALRTIGLYKNKAKNIIKTAQ
AIRDDFKGQVPKTHKELESLPGVGRKTANVVLAEVYGVPAIAVDTHVARVSKRLNISSPDADVKQIEADLMAKIPKKDWIITHHRLIFFGRYHCLA
KKPKCEICPVQSYCKYYQDTYGKSKA

SEQ ID 191

ATGAAAGTTTTATTCGATGTGCAGAATCTTTTGAAAAAATTTGGTATTTATGTTTATATTGGTAAACGTCTTTATGATATCGAAGTTATGAAGATT
GAATTGCAACGTCTCTACGATAATGGTCTGATAAGTAGAGATGATTATTTAAAAGCAGAACTGATTTTAAGAAGAGAGCACAGACTAGAATTGGAG
AAGGAAAATAAAAAA

SEQ ID 192

MKVLFDVQNLLKKFGIYVYIGKRLYDIEVMKIELQRLYDNGLISRDDYLKAELILRREHRLELEKENKK

SEQ ID 193

TTGCTAAAATCTACTTATATGAAAACACTATATGATGTGCAACAATTGCTAAAAAACTTTGGCATTTTTGTTTACCTTGGCAAACGTCTTTATGAT
ATTGAAATGATGAAGATTGAACTTCAGCGTCTCTATGATAGCGGCTTATTGGATAAGAGGGATTACTTAAATGCGGAGTTAATTTTGCGACGTGAG
CATAGATTAGAATTGGAAAAAGAAGGA

SEQ ID 194

LLKSTYMKTLYDVQQLLKNFGIFVYLGKRLYDIEMMKIELQRLYDSGLLDKRDYLNAELILRREHRLELEKEG

SEQ ID 195

ATGAGTAAGAAATTATTGGGAATTGACCTCGGAGGAACGACCATTAAATTTGGTATCTTGACGCTTGAGGGAGAAGTACAAGAAAAATGGGCAATT
GAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAAACATCGTTTGAGCCTCTATGGATTAACAAAAGATGAC
TTTCTCGGTATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAACAGGTGCTTTTAATCTAAATTGGGCTGATACTCAAGAA
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GCCAATAATCCCGACGTTGTTTTCGTAACCCTCGGAACAGGAGTAGGTGGAGGTGTTATCGCAGATGGTAACCTCATCCATGGTGTTGCAGGAGCA
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GGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAATATGAGGGTTCGTCTGCCATTAAAGCAGCGATTGACAACGGTGATACTGTTACAAGTAAA
GATATTTTTATAGCAGCAGAAGATGGGGATAAATTTGCTAATTCTGTTGTTGAACGTGTATCACGTTACCTTGGACTGGCAGCAGCTAATATTTCA
AATATTTTAAACCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTTACGTAGTCGCGTTGAGAAATACTTTGTCACATTT
GCTTTCCCACAAGTTAAAAAGTCAACTAAAATTAAGATTGCTGAACTAGGTAATGATGCTGGTATTATTGGTGCAGCAAGCTTAGCCAATCAACAA
GCAAGT

SEQ ID 196

MSKKLLGIDLGGTTIKFGILTLEGEVQEKWAIETNTLENGRHIVSDIVESLKHRLSLYGLTKDDFLGIGMGSPGAVDRTSKTVTGAFNLNWADTQE
VGSVIEKEVGIPFFIDNDANVAALGERWVGAGANNPDVVFVTLGTGVGGGVIADGNLIHGVAGAGGEIGHMIVDPENGFTCTCGNKGCLETVASAT

GVVRVARQLAEQYEGSSAIKAAIDNGDTVTSKDIFIAAEDGDKFANSVVERVSRYLGLAAANISNILNPDSVVIGGGVSAAGEFLRSRVEKYFVTF
AFPQVKKSTKIKIAELGNDAGIIGAASLANQQAS

SEQ ID 197

ATGAGTCAAAAATTACTGGGGATTGATTTAGGTGGTACCACCATTAAATTTGGAATTTTAACAGCAGCAGGAGAAGTCCAAGAAAAATGGGCAATT
GAGACTAATATTTTAGAAGGAGGCAAACATATTGTCCCTGATATCATCGCTTCCATCAAACATCGCTTAGACTTGTATGGTCTAAGCAGTGCTGAC
TTTGTGGGAATTGGTATGGGATCACCAGGAGCGGTTGACCGTGATACTAATACAGTTACTGGGGCATTCAACCTTAATTGGAAAGAAACCCAAGAA
GTCGGTTCCGTTGTTGAAAAAGAATTGGGCATTCCTTTTGCCATTGACAATGATGCCAATGTGGCTGCCCTTGGTGAACGTTGGGTAGGTGCTGGT
GAAAATAACCCAGATGTCGTCTTCATGACACTTGGAACAGGTGTCGGTGGAGGCATTATTGCTGATGGTAACTTGATTCATGGTGTTGCAGGAGCA
GGTGGTGAAATCGGCCACATGATTGTTGAGCCAGAAAATGGCTTTGCTTGTACTTGTGGCTCACACGGCTGTTTGGAAACAGTAGCTTCAGCAACA
GGAGTTGTCAAAGTGGCACGTTTACTGGCAGAAGCCTACGAAGGGGATTCAGCCATCAAAGCAGCTATTGACAATGGTGAAGGTGTTACCAGTAAA
GACATTTTCATGGCGGCTGAAGCAGGGGATTCCTTTGCTGATTCTGTTGTGGAAAAGGTTGGTTACTACCTTGGCCTTGCTTCAGCAAATATTTCC
AATATCTTGAATCCAGACTCAGTGGTTATCGGTGGGGGTGTGTCAGCAGCAGGAGAATTTCTACGCTCACGTATTGAAAAATACTTTGTGACCTTC
ACTTTCCCACAAGTGAGGTATTCAACTAAAATTAAGATTGCAGAACTTGGCAATGATGCTGGAATTATCGGTGCAGCTAGCCTTGCTCGACAATTT
ATCACAAAA

SEQ ID 198

MSQKLLGIDLGGTTIKFGILTAAGEVQEKWAIETNILEGGKHIVPDIIASIKHRLDLYGLSSADFVGIGMGSPGAVDRDTNTVTGAFNLNWKETQE
VGSVVEKELGIPFAIDNDANVAALGERWVGAGENNPDVVFMTLGTGVGGGIIADGNLIHGVAGAGGEIGHMIVEPENGFACTCGSHGCLETVASAT
GVVKVARLLAEAYEGDSAIKAAIDNGEGVTSKDIFMAAEAGDSFADSVVEKVGYYLGLASANISNILNPDSVVIGGGVSAAGEFLRSRIEKYFVTF
TFPQVRYSTKIKIAELGNDAGIIGAASLARQFITK

SEQ ID 199

ATGGATATGTCTGTTATTTTAATTATTGTTATTCTTCTGGCTTTTGTTGCTTGGGCATCTTGGAATTATTGGAGGGTTCGTAGGGCAGCTAAATTT
TTAGATAACGAGTCTTTTCAAAAAGAAATGTCACGAGGACAGTTAATTGATATCCGAGAAGCTGGTGCTTTTCATAGAAAGCATATTCTCGGAGCA
CGTAACATTCCAGCAAGTCAATTTAAAGTTGCCTTATCGGCTTTGCGCAAAGATAAACCTGTCCTCTTATATGACGCAAGCCGTGGTCAATCTATT
CCAAGGATTGTTTTGTTACTCAGAAAAGAAGGTTTTAATCAACTTTACGTGTTAAAGGACGGTTTCAATTACTGGACGGGTAGAGTTAAG

SEQ ID 200

MDMSVILIIVILLAFVAWASWNYWRVRRAAKFLDNESFQKEMSRGQLIDIREAGAFHRKHILGARNIPASQFKVALSALRKDKPVLLYDASRGQSI
PRIVLLLRKEGFNQLYVLKDGFNYWTGRVK

SEQ ID 201

ATGTCTCCAATCACACTTATCTTATGGTTACTTCTTGTCGGCATTGTTGGTTATTATACATGGAACTATTTCTCTTTTCGAAAAATGGCAAAGCAG
GTTGATAACGAGACTTTTAAAGACGTGATGCGTCAAGGTCAATTGATTGATTTACGAGAGCCAGCGGCTTTTAGAACTAAGCATATTTTAGGAGCT
CGAAATTTTCCAGCGCAACAATTTGATGCTGCTATTAAGGGACTACGCAAGGACAAACCTGTTCTTATTTACGAAAATATGCGTCCCCAGTACCGT
GTGCCTGCGGTCAAAAAACTTAAAAAAGCTGGCTTTGAAGACGTTTATGTCTTAAAAGACGGTATTGATTATTGGGATGGCAAAGTTAAACAAACA
ACC

SEQ ID 202

MSPITLILWLLLVGIVGYYTWNYFSFRKMAKQVDNETFKDVMRQGQLIDLREPAAFRTKHILGARNFPAQQFDAAIKGLRKDKPVLIYENMRPQYR
VPAVKKLKKAGFEDVYVLKDGIDYWDGKVKQTT

SEQ ID 203

ATGACAAATTTAAGAACAGATATCCGTAACGTTGCGATCATTGCCCACGTTGACCACGGTAAAACAACTCTCGTTGATGAATTATTAAAACAATCA
CATACTCTTGATGAGCGTAAAGAGCTTGAAGAACGTGCAATGGATTCAAATGATATCGAAAAAGAACGTGGTATCACCATTCTTGCAAAAAATACA
GCCGTAGCATACAACGATGTTCGTATCAATATTATGGACACACCTGGTCACGCGGACTTTGGTGGTGAAGTTGAGCGTATTATGAAAATGGTTGAT
GGTGTTGTTTTAGTCGTTGATGCCTACGAAGGAACAATGCCACAAACACGTTTTGTTTTGAAGAAAGCTCTTGAACAAAACTTAATTCCAATCGTT
GTTGTAAATAAAATTGATAAGCCGTCAGCTCGTCCATCAGAGGTTGTTGATGAAGTTCTTGAACTATTTATTGAGCTCGGTGCTGATGATGATCAA
CTAGATTTCCCTGTTGTTTATGCTTCAGCTATCAATGGAACATCTTCAATGTCAGATGATCCTTCAGATCAAGAAAAAACAATGGCACCGATTTTT
GATACTATCATTGATCACATTCCAGCCCCAGTTGACAACTCGGAAGAACCACTTCAATTCCAAGTTTCTCTTCTTGATTACAATGATTTTGTAGGA
CGTATTGGTATTGGACGTGTTTTCCGCGGGACTGTCAAAGTTGGAGATCAAGTTACTCTTTCAAAACTTGATGGTACAACTAAAAACTTCCGCGTA
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CAGGGTGCTATTATCCAAAGTTTGTCAGAGCGTAAAGGTGATATGCTTGATATGCAGATGGTTGGTAATGGTCAAACGCGTTTGATTTTCTTGATT
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GCTAAACAAATGACAAATGTCCGTTCAGCAACTAAAGATCAAACTGCAGTCATCAAGACGCCTCGTATCCTTACTTTAGAAGAGTCACTTGAATTT
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AAAAAATCAGCTGAA

SEQ ID 204

MTNLRTDIRNVAIIAHVDHGKTTLVDELLKQSHTLDERKELEERAMDSNDIEKERGITILAKNTAVAYNDVRINIMDTPGHADFGGEVERIMKMVD
GVVLVVDAYEGTMPQTRFVLKKALEQNLIPIVVVNKIDKPSARPSEVVDEVLELFIELGADDDQLDFPVVYASAINGTSSMSDDPSDQEKTMAPIF
DTIIDHIPAPVDNSEEPLQFQVSLLDYNDFVGRIGIGRVFRGTVKVGDQVTLSKLDGTTKNFRVTKLFGFFGLERKEIQEAKAGDLIAVSGMEDIF
VGETVTPTDAIEPLPVLRIDEPTLQMTFLVNNSPFAGREGKWITSRKVEERLLAELQTDVSLRVDPTDSPDKWTVSGRGELHLSILIETMRREGYE
LQVSRPEVIIKEIDGVQCEPFERVQIDTPEEYQGAIIQSLSERKGDMLDMQMVGNGQTRLIFLIPARGLIGYSTEFLSMTRGYGIMNHTFDQYLPV
VQGEIGGRHRGALVSIENGKATTYSIMRIEERGTIFVNPGIEVYEGMIVGENSRDNDLGVNITTAKQMTNVRSATKDQTAVIKTPRILTLEESLEF
LADDEYMEVTPESIRLRKQILNKAARDKANKKKKSAE

SEQ ID 205

ATGACTAACTTAAGAAACGATATCCGTAACGTAGCGATTATTGCCCACGTTGACCACGGAAAAACAACACTTGTAGATGAATTATTAAAACAATCC
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GCAGTAGCCTATAACGATGTTCGTATTAACATCATGGATACCCCAGGACACGCGGACTTCGGTGGTGAAGTTGAACGTATCATGAAAATGGTTGAC
GGGGTTGTTCTTGTTGTGGATGCCTACGAAGGAACAATGCCCCAGACGCGTTTCGTATTGAAAAAAGCACTTGAGCAAAACCTTATCCCGATCGTT
GTGGTGAACAAGATTGACAAACCTTCAGCTCGTCCAGCAGAAGTTGTAGATGAAGTGCTTGAATTATTCATCGAACTTGGTGCCGATGATGAGCAA
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GATACGATTATTGATCATATTCCAGCGCCAGTTGATAATTCAGATGAGCCTTTGCAATTCCAAGTGTCACTTTTGGACTACAACGATTTCGTAGGT
CGTATCGGTATCGGTCGTGTTTTCCGTGGTACTGTTAAAGTGGGTGACCAAGTAACTCTTTCAAAACTTGATGGTACCACTAAAAACTTCCGTGTT
ACAAAACTGTTTGGTTTCTTCGGTTTGGAACGTCGTGAAATTCAAGAAGCTAAAGCAGGTGACTTGATTGCTGTTTCAGGTATGGAAGATATCTTT

GTTGGAGAAACCATTACACCAACTGACTGTGTGGAAGCTCTGCCAATTCTTCGTATTGATGAGCCAACACTTCAGATGACTTTCTTGGTCAATAAC
TCTCCTTTTGCAGGTCGTGAAGGTAAATGGATCACGTCACGTAAGGTTGAAGAACGTCTTTTAGCAGAATTGCAAACAGACGTGTCACTTCGTGTT
GACCCAACAGATTCGCCAGATAAATGGACGGTTTCAGGGCGTGGAGAATTGCATTTATCTATCCTCATTGAAACCATGCGCCGTGAAGGCTATGAA
CTTCAAGTATCACGTCCAGAAGTTATCATCAAAGAAATTGATGGTGTCAAATGTGAACCGTTTGAGCGTGTTCAAATTGATACACCAGAAGAATAT
CAGGGTGCAATCATCCAGTCTCTTTCAGAACGTAAAGGGGATATGCTTGATATGCAGATGGTTGGTAATGGTCAAACGCGTTTGATTTTCTTGATT
CCTGCACGTGGTTTGATTGGTTATTCAACAGAGTTTCTTTCAATGACACGTGGATATGGTATCATGAATCATACTTTTGATCAGTATCTACCGGTT
GTTCAAGGAGAAATCGGTGGCCGTCATCGTGGTGCCTTGGTTTCTATTGAAAATGGGAAAGCAACGACATATTCAATCATGCGTATTGAAGAACGT
GGAACTATCTTTGTCAATCCAGGTACAGAAGTTTACGAAGGGATGATTGTTGGTGAAAACTCACGTGATAACGACCTTGGTGTTAACATTACAACA
GCTAAGCAAATGACAAATGTCCGTTCAGCGACTAAAGATCAAACTGCAGTTATCAAGACGCCTCGTATCCTAACGCTTGAAGAATCATTAGAGTTC
TTGAATGACGACGAATACATGGAAGTAACGCCAGAATCTATCCGCTTGCGTAAACAAATCTTGAATAAAGCTGCGCGTGATAAAGCTAATAAAAAG
AAAAAATCAGCCGAA

SEQ ID 206

MTNLRNDIRNVAIIAHVDHGKTTLVDELLKQSHTLDERKELQERAMDSNDLEKERGITILAKNTAVAYNDVRINIMDTPGHADFGGEVERIMKMVD
GVVLVVDAYEGTMPQTRFVLKKALEQNLIPIVVVNKIDKPSARPAEVVDEVLELFIELGADDEQLEFPVVYASAINGTSSLSDDPADQEHTMAPIF
DTIIDHIPAPVDNSDEPLQFQVSLLDYNDFVGRIGIGRVFRGTVKVGDQVTLSKLDGTTKNFRVTKLFGFFGLERREIQEAKAGDLIAVSGMEDIF
VGETITPTDCVEALPILRIDEPTLQMTFLVNNSPFAGREGKWITSRKVEERLLAELQTDVSLRVDPTDSPDKWTVSGRGELHLSILIETMRREGYE
LQVSRPEVIIKEIDGVKCEPFERVQIDTPEEYQGAIIQSLSERKGDMLDMQMVGNGQTRLIFLIPARGLIGYSTEFLSMTRGYGIMNHTFDQYLPV
VQGEIGGRHRGALVSIENGKATTYSIMRIEERGTIFVNPGTEVYEGMIVGENSRDNDLGVNITTAKQMTNVRSATKDQTAVIKTPRILTLEESLEF
LNDDEYMEVTPESIRLRKQILNKAARDKANKKKKSAE

SEQ ID 207

ATGGGACGAGTAATGAAAACAATAACAACATTTGAAAATAAAAAAGTTTTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACGTTTGTTA
GCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAAAGTGGTT
TGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTTGTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGCA
TTAGAAAAACAAATCCCTGTTTTGACTGAAGTGGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACG
ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTCAGAGAGGTTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAG
GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGAGTTAAGGAATTTCGTCCTCATATTGCAGTAATTACTAAT
TTAATGCCAACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGAATATCCAAAATCAAATGTCTTCATCTGATTTTTTG
GTACTTAATTTTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTTCCTTTCTCTACTACGGAAAAAGTTGATGGTGCT
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GCAACTATTGCGGTTGCTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTGCAATCA
CTCGGTAAGGTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCATTATCTGGCTTTGATAATACTAAA
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GCACAACAGGGCGATGTTATCTTGCTAAGTCCTGCAAATGCATCATGGGACATGTATAAGAATTTCGAAGTCCGTGGTGATGAATTCATTGATACT
TTCGAAAGTCTTAGAGGAGAG

SEQ ID 208

MGRVMKTITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGIKVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKA
LEKQIPVLTEVELAYLVSESQLIGITGSNGKTTTTMIAEVLNAGGQRGLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHIAVITN
LMPTHLDYHGSFEDYVAAKWNIQNQMSSSDFLVLNFNQGISKELAKTTKATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENAL
ATIAVAKLAGISNQVIRETLSNFGGVKHRLQSLGKVHGISFYNDSKSTNILATQKALSGFDNTKVILIAGGLDRGNEFDELIPDITGLKHMVVLGE
SASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID 209

ATGAAAGTGATAAGTAATTTTCAAAACAAAAAAATATTAATATTGGGGTTAGCCAAATCGGGCGAAGCAGCAGCAAAATTATTGACCAAACTTGGT
GCTTTAGTGACTGTTAATGATAGTAAACCATTTGACCAAAATCCAGCGGCACAAGCCTTGTTGGAAGAGGGGATTAAGGTCATTTGTGGTAGCCAC
CCAGTAGAATTATTAGATGAGAACTTTGAGTACATGGTTAAAAACCCTGGGATTCCTTATGATAATCCTATGGTTAAACGCGCCCTTGCAAAGGAA
ATTCCCATCTTGACTGAAGTAGAATTGGCTTATTTCGTATCTGAAGCGCCTATTATCGGGATTACAGGATCAAACGGGAAGACAACCACAACGACA
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AATCAAGAGATTTCAGCAACTCTAGCTAAGACCACCAAAGCAACAGTGATTCCTTTTTCAACTCAAAAAGTGGTTGATGGAGCTTATCTGAAGGAT
GGAATACTCTATTTTAAAGAACAGGCGATTATAGCTGCAACTGACTTAGGTGTCCCAGGTAGCCACAACATTGAAAATGCCCTAGCAACTATTGCA
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AAAGATATTACCTTCTACAATGACAGTAAGTCAACCAATATTTTAGCCACTCAAAAAGCTTTATCAGGTTTTGATAACAGTCGCTTGATTTTGATT
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GATACTATCTTGCTTAGCCCAGCCAATGCTAGCTGGGATATGTATCCTAATTTTGAGGTTCGTGGGGATGAATTTTTGGCAACCTTTGATTGTTTA
AGAGGAGATGCC

SEQ ID 210

MKVISNFQNKKILILGLAKSGEAAAKLLTKLGALVTVNDSKPFDQNPAAQALLEEGIKVICGSHPVELLDENFEYMVKNPGIPYDNPMVKRALAKE
IPILTEVELAYFVSEAPIIGITGSNGKTTTTMIADVLNAGGQSALLSGNIGYPASKVVQKAIAGDTLVMELSSFQLVGVNAFRPHIAVITNLMPT
HLDYHGSFEDYVAAKWMIQAQMTESDYLILNANQEISATLAKTTKATVIPFSTQKVVDGAYLKDGILYFKEQAIIAATDLGVPGSHNIENALATIA
VAKLSGIADDIIAQCLSHFGGVKHRLQRVGQIKDITFYNDSKSTNILATQKALSGFDNSRLILIAGGLDRGNEFDDLVPDLLGLKQMIILGESAER
MKRAANKAEVSYLEARNVAEATELAFKLAQTGDTILLSPANASWDMYPNFEVRGDEFLATFDCLRGDA

SEQ ID 211

ATGGGGAAAAAAATTGTTTTTACAGGTGGTGGTACGGTAGGTCATGTAACACTAAACCTAATATTAATCCCCAAATTTATCAAAGATGGTTGGGAA
GTACATTATATTGGTGATAAAAATGGCATAGAACATGAACAAATTAATCAGTCTGGACTTGATATCACATTTCACTCTATAGCTACTGGGAAACTA
CGTCGCTATTTTTCATGGCAAAATATGTTAGATGTCTTTAAAGTAGGGGTTGGCGTTCTTCAATCGATTGCTATTATTGCTAAACTTAGACCCCAA
GCCTTATTTTCAAAAGGGGGATTTGTTTCAGTACCTCCTGTAGTAGCTGCACGCCTATTAAAAGTTCCTGTTTTTGTTCATGAATCAGATTTATCA
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GATTCTTCTCTCAATCGATTGAAGAAGAACCTTTATCGCGTGGATTATGTTACAGACCTTTATCAGCCTTTAATGAATTTAGCAGATGTGGTTGTT
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TTAGAGAATGCTGCTTATTTTGAAGAAAAGGGCTACGCATTGCAGTTACCAGAATCTGAATTAAACATAAATACACTTGAGAAACAGATAAATTTA
TTAATTTCTAACAGTGAGAGTTACGAAAAAAACATGTCACAATCATCTGAAATAAAATCTCAAGATGAATTTTATCAATTATTAATTGATGATATG
GCAAAAGTAACAAAAGGA

SEQ ID 212
MGKKIVFTGGGTVGHVTLNLILIPKFIKDGWEVHYIGDKNGIEHEQINQSGLDITFHSIATGKLRRYFSWQNMLDVFKVGVGVLQSIAIIAKLRPQ
ALFSKGGFVSVPPVVAARLLKVPVFVHESDLSMGLANKIAYKFATIMYTTFEQSKDLIKTKHIGAVTKVMDCKKSFENTDLTSIKEAFDPNLKTLL
FIGGSAGAKVFNDFITQTPELEEKYNVINISGDSSLNRLKKNLYRVDYVTDLYQPLMNLADVVVTRGGSNTIFELVAMKKLHLIIPLGREASRGDQ
LENAAYFEEKGYALQLPESELNINTLEKQINLLISNSESYEKNMSQSSEIKSQDEFYQLLIDDMAKVTKG
SEQ ID 213
TTGTTTAAGAGGAGATGCCTAATGCCTAAGAAGATTTTATTTACAGGTGGTGGAACTGTAGGTCATGTCACCTTGAACCTCATTCTCATACCAAAA
TTTATCAAGGACGGTTGGGAAGTACATTATATTGGTGATAAAAATGGCATTGAACATACAGAAATTGAAAAGTCAGGCCTTGACGTGACCTTTCAT
GCTATCGCCACAGGCAAGCTTAGACGCTATTTTTCATGGCAAAATCTAGCTGATGTTTTTAAGGTTGCACTTGGCCTCCTACAGTCTCTCTTTATT
GTTGCCAAGCTTCGCCCTCAAGCCCTTTTTTCCAAAGGTGGTTTTGTCTCAGTACCGCCAGTTGTGGCTGCTAAATTGCTTGGTAAACCAGTCTTT
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AATTTTGATCAGGCAATGGCTGATTTGTTTGAACATCAGGCTGATTATGAGGCTACTATGTTGGCAACTAAGGAGATTCAGTCACCGGACTTCTTT
TATGACCTTTTGAGAGCTGATATTAGCTCCGCGATTAAGGAGAAG
SEQ ID 214
LFKRRCLMPKKILFTGGGTVGHVTLNLILIPKFIKDGWEVHYIGDKNGIEHTEIEKSGLDVTFHAIATGKLRRYFSWQNLADVFKVALGLLQSLFI
VAKLRPQALFSKGGFVSVPPVVAAKLLGKPVFIHESDRSMGLANKIAYKFATTMYTTFEQEDQLSKVKHLGAVTKVFKDANQMPESTQLEAVKEYF
SRDLKTLLFIGGSAGAHVFNQFISDHPELKQRYNIINITGDPHLNELSSHLYRVDYVTDLYQPLMAMADLVVTRGGSNTLFELLAMAKLHLIVPLG
KEASRGDQLENATYFEKRGYAKQLQEPDLTLHNFDQAMADLFEHQADYEATMLATKEIQSPDFFYDLLRADISSAIKEK
SEQ ID 215
ATGCCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTTAAAAAAACGCAAAGAA
GATGAAGAAGAACAAAAACGTATTAACGAAAAATTACGCTTAGATAAAAGAAGTAAATTAAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
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GCTATTGAACAACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATTTCCCAATAAGTTTCATATTCAAGTTCAAGAA
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ATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGCGGAAAATAGTCAAGGA
CAAACAAATAACTCAAATACTAATCAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCCTCAAAATGTTAAT
SEQ ID 216
MPKKKSDTPEKEEVVLTEWQKRNLEFLKKRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQNTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTN
RIRTAPIFVVAFLVILVSVFLLTPFSKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQFPNKFHIQVQE
NKIIAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLLIKDLKALDPDLISEIQVISLADSKTTPDLLLLDMHDGNSIRIPLSKF
KERLPFYKQIKKNLKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNSNTNQQGQQIATEQAPNPQNVN
SEQ ID 217
ATGGCAAAAGATAAAGAGAAACAAAGTGATGACAAGCTCGTTTTGACAGAGTGGCAAAAGCGTAACATTGAATTTTTAAAGAAAAAGAAGCAGCAA
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GATGAGAAAACTGATAGTCAGGAAATTGAGTCAGAAACGACGTCAAAACCTAAAAAAACCAAAAAAGTTAGACAACCCAAGGAAAAAAGCGCGACA
CAAATCGCTTTTCAAAAATCCTTGCCTGTTCTTTTGGGGGCGCTCTTACTCATGGCGGTGTCTATTTTTATGATCACTCCTTATAGCAAAAAGAAA
GAGTTTTCTGTAAGAGGAAACCATCAAACGAACCTTGACGAATTAATCAAAGCTAGCAAAGTCAAAGCATCTGACTATTGGTTAACGCTGTTAACT
TCGCCTGGTCAGTATGAACGACCGATTCTTCGTACTATTCCATGGGTGAAATCTGTACATCTCTCTTACCAATTTCCTAATCACTTTCTATTTAAC
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GAACTACCGAAATCTTTCTTGATTCTTAATTTAAAAGATGAGAAAGCGATCCAACAGTTAGTTAAGCAATTAACGACATTACCTAAAAAATTAGTC
AAGAATATCAAGTCAGTGTCTCTTGCAAATTCCAAAACGACAGCGGATTTACTACTTATTGAAATGCATGACGGTAATGTAGTTAGAGTACCGCAG
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ACACAGGAGATTGAAAATCAACCTGAAGTTCCTCTTACGCCTGAACAAAACGCAGCTGATAAAGAAGGAGATAAGCCTGGTGAACATCAGGAACAG
ACAGACAATGATTCAGAAACGCCAGCAAATCAGAGTAGTCCTCAGCAAACACCACCATCCCCAGAAACGGTCCTCGAACAGGCCCATGGC
SEQ ID 218
MAKDKEKQSDDKLVLTEWQKRNIEFLKKKKQQAEEEKKLKEKLLSDKKAQQQAQNASEAVELKTDEKTDSQEIESETTSKPKKTKKVRQPKEKSAT
QIAFQKSLPVLLGALLLMAVSIFMITPYSKKKEFSVRGNHQTNLDELIKASKVKASDYWLTLLTSPGQYERPILRTIPWVKSVHLSYQFPNHFLFN
VIEFEIIAYAQVENGFQFILENGKRVDKVRASELPKSFLILNLKDEKAIQQLVKQLTTLPKKLVKNIKSVSLANSKTTADLLLIEMHDGNVVRVPQ
SQLTLKLPYYQKLKKNLENDSIVDMEVGIYTTTQEIENQPEVPLTPEQNAADKEGDKPGEHQEQTDNDSETPANQSSPQQTPPSPETVLEQAHG
SEQ ID 219
ATGGCTAGAAATGGCTTTTTTACTGGTTTGGATATAGGAACAAGCTCGATTAAAGTTTTAGTTGCAGAATTTATTGCAAATGAAATGAATGTAATT
GGGGTTAGCAACGTCCCTAGTTCCGGTGTAAAAGATGGTATAATTATTGATATTGAGGCAGCAGCAACTGCAATCAAAGAGGCGGTAAAACAAGCT
GAGGAGAAAGCAGGCATCACCATTGACAAAATCAATGTTGGATTACCAGCAAATCTTCTCCAAATTGAACCAACTCAAGGAATGATTCCTGTTCCT
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TCAGTTCTAAACGAAGGTGAACGTGAGTTTGGTGCAACTGTGATTGATATGGGAGGCGGACAAACAACAGTCGCTTCTATGCGTAATCAAGAATTG
CAATATACTAATATTTATTCTGAAGGTAGCGATTATGTTACCAAAGATATTTCTAAAGTGCTACGTACAACAGTAGAAATCGCCGAAGCATTGAAA
TTCAACTTTGGACAAGCTAATGTTGAAGAAGCAAGTACTTCTGATACAGTTCAAGTTAATGTTGTTGGTAACGAGGAACCTGTTGAAATTACAGAA
AGCTATCTTTCGCAAATTATTTCAGGACGTATTCGTCAAATTTTAGAACATGTCAAACAAGACTTGGGTAGAGGTCGTTTACTTGATTTACCTGGT
GGTATTATTCTTGTTGGAGGTGGTGCAATTATGCCAGGAGTTGTCGAGGTTGCTCAACAAATTTTTGGAACTAGAGTTAAATTGCACGTTCCAAAC
CAAGTAGGTATTCGCAATCCAATGTTTGCTAATGTTATTAGTATCGTTGATTATGTAGGAATGATGTCAGAAGTTGACATTATCGCACAACATGCT
GTAACTGGCGACGAAATGCTAAGACATAAACCAGTCGACTTTGATTATAAAGAAAAAACAAATACAATGTCGACAATGCCTTATTCTGAGCCGTTA
ACCTCTTCTATGGAAGATTCTAATTTAGAACCAATCCGAGCAAGAGAAAACGCTCAAGAGCCTACTGAGCCTAAAGCTAATATTGGTGAGCGCATC
AGAGGAATTTTTGGAAGTATGTTTGAC

SEQ ID 220

MARNGFFTGLDIGTSSIKVLVAEFIANEMNVIGVSNVPSSGVKDGIIIDIEAAATAIKEAVKQAEEKAGITIDKINVGLPANLLQIEPTQGMIPVP
NESKEIKDEDVESVVKSALTKSITPEREVISLIPLEFIVDGFQGIRDPRGMMGIRLEMRGLIYTGPTTILHNLRKTVERAGIKVEHVVIAPLALAK
SVLNEGEREFGATVIDMGGGQTTVASMRNQELQYTNIYSEGSDYVTKDISKVLRTTVEIAEALKFNFGQANVEEASTSDTVQVNVVGNEEPVEITE
SYLSQIISGRIRQILEHVKQDLGRGRLLDLPGGIILVGGGAIMPGVVEVAQQIFGTRVKLHVPNQVGIRNPMFANVISIVDYVGMMSEVDIIAQHA
VTGDEMLRHKPVDFDYKEKTNTMSTMPYSEPLTSSMEDSNLEPIRARENAQEPTEPKANIGERIRGIFGSMFD

SEQ ID 221

TTGGACATTGGAACAAGCTCGATAAAAGTTTTAGTAGCAGAATTTATTTCTGGTGAGATGAACGTCATTGGTGTTAGTAATGTTCCAAGTACCGGC
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AAGGTTAATGTTGGGCTACCGGCAAACCTTCTTCAAATTGAACCAACACAAGGAATGATTCCTGTCCCAAGTGAGTCTAAAGAGATAAAAGATGAG
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TTTCAGGGCATTCGAGATCCACGTGGTATGATGGGGATTAGATTAGAGATGCGCGGGCTTATTTATACTGGACCAAGCACCATTTTACATAATCTG
CGTAAAACGGTAGAAAGAGCAGGCATTAAAGTTGAAAACATCATTATTTCTCCGTTAGCTATGGCTAAAACCATTTTAAACGAAGGTGAGCGCGAG
TTTGGAGCTACTGTAATTGATATGGGAGGTGGACAGACAACTGTCGCTTCTATGCGAGCACAAGAATTGCAGTATACCAATATATATGCCGAAGGC
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GAAGCTAGTATAACTGAAACAGTAAAAGTTGATGTGGTAGGTAGTGAAGAGCCTGTTGAGGTAACTGAACGTTATTTATCTGAAATTATTTCAGCG
CGTATTCGTCATATTTTAGATCGTGTGAAGCAAGATTTGGAAAGAGGTCGTTTACTAGACTTACCAGGAGGCATTGTTTTGATTGGTGGCGGTGCA
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AAGCCTATCGATTTCAGTGGCCAAGAATCTTATTTACCAGATTATGATGATTCAAGAAGACCAGAATCGACCATTGGCTATGAACAACAAGCGTCA
CAAACAGCATATGATTCACAAGTTCCGAGTGATCCTAAACAAAAAATTTCAGAACGTGTTCGTGGCATATTTGGGAGTATGTTTGAT

SEQ ID 222

LDIGTSSIKVLVAEFISGEMNVIGVSNVPSTGVKDGIIIDIEAAATAIKTAVEQAEEKAGMTIEKVNVGLPANLLQIEPTQGMIPVPSESKEIKDE
DVDSVVKSALTKSITPEREVISLVPEEFIVDGFQGIRDPRGMMGIRLEMRGLIYTGPSTILHNLRKTVERAGIKVENIIISPLAMAKTILNEGERE
FGATVIDMGGGQTTVASMRAQELQYTNIYAEGGEYITKDISKVLKTSLAIAEALKFNFGQAEISEASITETVKVDVVGSEEPVEVTERYLSEIISA
RIRHILDRVKQDLERGRLLDLPGGIVLIGGGAIMPGVVEIAQEIFGVTVKLHVPNQVGIRNPMFSNVISLVEYVGMMSEVDVLAQTAVSGEELLRR
KPIDFSGQESYLPDYDDSRRPESTIGYEQQASQTAYDSQVPSDPKQKISERVRGIFGSMFD

SEQ ID 223

ATGGTATTTTCATTTGATACAGCATCAGTACAAGGTGCAGTTATTAAAGTTATTGGTGTTGGAGGCGGTGGCGGTAACGCTATTAACCGCATGATT
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AAATTAACTCGCGGACTTGGTGCAGGAGGACAACCTGAAGTTGGTCGTAAAGCAGCTGAAGAAAGTGAAGAAGTTTTAACAGAAGCACTTACTGGC
GCTGATATGGTATTTATCACAGCAGGTATGGGGGGCGGATCTGGTACAGGTGCGGCTCCAGTTATTGCACGTATTGCAAAGAGTTTAGGAGCACTT
ACAGTAGCGGTCATCACACGTCCTTTTGGCTTTGAGGGTAATAAACGTTCTAACTTCGCTATCGAAGGTATTCAAGAATTAAGAGAACAAGTTGAT
ACACTGCTTATCATTTCAAATAATAATCTTCTTGAAATTGTAGATAAGAAGACACCATTGCTTGAAGCTCTTAGTGAAGCAGATAATGTTTTACGT
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GCACTGATGGGAATTGGTATCGGTTCTGGTGAGGAACGTATTACTGAAGCTGCTCGAAAAGCAATTTATTCACCACTTCTTGAAACAACGATTGAT
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CTTCGTCGTGATAATATTTCACGTCCGACAGAAGGTGAACTTGATAGCAAGTTGTCTATGTCAACGTTTTCAGAAAATGATGATATGGATGATGAA
CTTGAAACACCTCCATTCTTTAAAAACCGT

SEQ ID 224

MVFSFDTASVQGAVIKVIGVGGGGGNAINRMIDEGVAGVEFIAANTDIQALSSSKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEEVLTEALTG
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QGVQGITDLITNPGLINLDFADVKTVMANKGNALMGIGIGSGEERITEAARKAIYSPLLETTIDGAEDVIVNVTGGMDMTLTEAEEASEIVSQAAG
KGVNIWLGTSIDMDMKDEIRVTVVATGVRKDKTNQVSGFTTSAPTNQAPSERQSTSNSNFDRRGNFDMTESREMPTQQNQPHAQNQQQSSAFGNWD
LRRDNISRPTEGELDSKLSMSTFSENDDMDDELETPPFFKNR

SEQ ID 225

ATGGCATTTTCATTTGATACTGCATCAATTCAAGGTGCAATTATAAAAGTAATTGGAGTCGGCGGAGGTGGCGGAAATGCCATTAATCGTATGATT
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AAATTAACTCGTGGACTTGGTGCTGGAGGACAACCTGAAGTAGGACGTAAAGCTGCTGAAGAAAGCGAAGAAATTTTAACAGAAGCTCTTACAGGA
GCGGACATGGTATTTATTACTGCCGGTATGGGTGGTGGCTCTGGGACAGGGGCTGCACCGGTTATTGCTCGTATCGCTAAAAGTTTGGGAGCCTTG
ACAGTAGCTGTTGTTACTCGCCCGTTTGGTTTTGAAGGTAACAAACGTGGTAATTTTGCTATTGAAGGTATCGAAGAACTACGTGAACAAGTTGAT
ACTTTGTTAATTATTTCAAATAATAACCTTCTTGAGATTGTTGATAAAAAGACACCTTTATTAGAAGCACTTAGTGAAGCTGATAATGTTTTACGC
CAGGGAGTTCAAGGGATAACCGACTTAATTACTAGTCCTGGCCTTATCAATCTCGATTTTGCCGACGTGAAAACAGTTATGGCAAATAAAGGGAAT
GCCTTGATGGGGATTGGGATTGGCTCTGGAGAAGAGCGCATTGTTGAGGCGGCGCGTAAGGCAATCTATTCACCCCTATTAGAAACGACTATTGAT
GGTGCACAAGACGTTATTGTGAACGTTACAGGAGGTCTCGACATGACACTTACAGAAGCTGAAGAAGCCTCTGAAATTGTTGGGCAAGCTGCTGGT
CAAGGCGTTAACATTTGGTTAGGAACATCTATTGATGATACTATGAAAGATGACATCCGTGTGACTGTTGTAGCAACTGGAGTGCGCCAAGAAAAA
GCCGAACAAGTTTCAGGTTTTCGTCAGCCTAGGACTTTTACCCAAACCAACGCGCAGCAAGTAGCGGGTGCACAATATGCATCAGATCAAGCAAAA
CAGTCGGTTCAACCAGGGTTTGATCGTCGCTCAAATTTTGATTTTGACATGGGGGAGTCTCGCGAGATACCAAGTGCACAAAAGGTAATTTCTAAT
CATAATCAAAATCAAGGTTCTGCTTTTGGAAATTGGGATTTGAGACGTGATAATATTTCTCGTCCAACAGAAGGTGAATTGGATAACCATCTTAAT
ATGTCAACGTTCTCAGCTAACGATGACAGTGATGATGAATTAGAAACGCCTCCATTCTTTAAAAACCGT

SEQ ID 226

MAFSFDTASIQGAIIKVIGVGGGGGNAINRMIDEGVAGVEFIAANTDIQALSSSKAETVIQLGPKLTRGLGAGGQPEVGRKAAEESEEILTEALTG
ADMVFITAGMGGGSGTGAAPVIARIAKSLGALTVAVVTRPFGFEGNKRGNFAIEGIEELREQVDTLLIISNNNLLEIVDKKTPLLEALSEADNVLR
QGVQGITDLITSPGLINLDFADVKTVMANKGNALMGIGIGSGEERIVEAARKAIYSPLLETTIDGAQDVIVNVTGGLDMTLTEAEEASEIVGQAAG
QGVNIWLGTSIDDTMKDDIRVTVVATGVRQEKAEQVSGFRQPRTFTQTNAQQVAGAQYASDQAKQSVQPGFDRRSNFDFDMGESREIPSAQKVISN
HNQNQGSAFGNWDLRRDNISRPTEGELDNHLNMSTFSANDDSDDELETPPFFKNR

SEQ ID 227

ATGATGAATTTACAAGAAAATAAAACAGCGATTTTTGACAATGTTAGTAAATTAGCACTAAAAGCAGGTCGCGCTCATGAATCAGTTCATATCGTA
GCTGTAACAAAATATGTTAACTGTCAAACAACAGAAGCGCTTATTAGAACAGGTGTTAATCATATCGGTGAAAATCGTGTTGATAAATTTCTTGAA
AAATATCAAGCATTAAAAGATGAAAAGCTTACATGGCATCTCATTGGTAGTTTACAACGTCGAAAAGTTAAAGATGTCATTAATTATGTTGATTAT
TTTCATGCTTTAGATTCTGTTAAGTTAGCAGCTGAGATTCAAAAACATGCTCAAAAACTAATTAAATGTTTTCTACAAGTTAATATATCACGAGAA
GACAGTAAGCATGGTTTTACTATTGAGCAAATAGATGATGCACTGAACTTAATTTCTCGGTACGATAAAATTGAACTTATCGGCATCATGACTATG

GCTCCCTTAAAAGCAACTAAAGAGGAAATATCATCAATTTTTGAAGAGACTGAGAGTCTTAGGAAAAGGCTTCAAGCTAGGAACATAGAACGAATG
CCGTTTACAGAATTAAGCATGGGCATGAGTAGAGATTATGATATTGCTATTCAAAATGGATCAACATTTGTAAGGATAGGAACTTCATTCTTTAAA

SEQ ID 228

MMNLQENKTAIFDNVSKLALKAGRAHESVHIVAVTKYVNCQTTEALIRTGVNHIGENRVDKFLEKYQALKDEKLTWHLIGSLQRRKVKDVINYVDY
FHALDSVKLAAEIQKHAQKLIKCFLQVNISREDSKHGFTIEQIDDALNLISRYDKIELIGIMTMAPLKATKEEISSIFEETESLRKRLQARNIERM
PFTELSMGMSRDYDIAIQNGSTFVRIGTSFFK

SEQ ID 229

ATGGATTTACTGACAAATAAAAAGAAAATTTTTGAGACTATCCGCTTATCTACAGAGGCAGCAAATAGGACTAATGATAGTGTTTCAGTTATTGCT
GTAACAAAATATGTGGATAGTACAATTGCAGGTCAGCTTATCGAAGCAGGAATTGAGCACATTGCCGAAAACCGTGTTGATAAATTTCTTGAAAAG
TATGATGCGTTAAAGTATATGCCAGTAAAGTGGCATTTAATTGGTACCTTACAACGTCGTAAAGTCAAGGAAGTTATCAATTATGTTGATTATTTT
CACGCTCTAGATTCTGTGAGATTAGCTTTGGAAATCAACAAGAGAGCTGACCATCCTGTGAAGTGTTTTCTACAAGTTAATATTTCTAAAGAAGAG
AGTAAACATGGTTTTAACATTTCTGAGATTGATGAAGCGATTGGAGAAATAGGTAAGATGGAGAAGATACAGTTAGTTGGTTTAATGACTATGGCA
CCAGCAAATGCCAGTAAAGAAAGTATTATAACTATTTTTCGACAAGCAAATCAATTAAGAAAAAACTTGCAGTTAAAAAAAAGAAAGAATATGCCT
TTTACAGAATTGAGCATGGGCATGAGTAACGATTATCCAATTGCTATTCAAGAAGGCTCAACTTTTATTCGGATTGGTAGAGCTTTCTTTCAC

SEQ ID 230

MDLLTNKKKIFETIRLSTEAANRTNDSVSVIAVTKYVDSTIAGQLIEAGIEHIAENRVDKFLEKYDALKYMPVKWHLIGTLQRRKVKEVINYVDYF
HALDSVRLALEINKRADHPVKCFLQVNISKEESKHGFNISEIDEAIGEIGKMEKIQLVGLMTMAPANASKESIITIFRQANQLRKNLQLKKRKNMP
FTELSMGMSNDYPIAIQEGSTFIRIGRAFFH

SEQ ID 231

ATGGAGGGGAATATGGCATTAAAAGATAGATTTGACAAAATTATTTCTTATTTTGACACTGACGATGTAAGTGAAAATGAAGTACACGAAGTACAA
GAGAGAACTTCAGTGCAAAGAGATTCCAGAGCAGCTACAGCACAGGAAGCTTCTCAGCGTAGTCATATGACTAACTCCGCAGAGGAAGAGATGATT
GGTAGTCGTCCGAGAACTTATACCTATGATCCTAATCGTCAGGAGAGACAAAGGGTACAGAGAGACAATGCTTATCAGCAAGCTACTCCTAGGGTT
CAAAATAAAGACTCAGTTCGACAACAGAGAGAACAAGTAACAATTGCTCTGAAGTATCCCCGTAAGTATGAGGATGCACAAGAAATTGTTGATTTA
CTTATCGTTAATGAATGTGTCTTGATTGATTTTCAATATATGCTTGATGCGCAAGCACGACGTTGCTTGGATTATATTGATGGTGCAAGTAGAGTA
TTATATGGTTCATTACAAAAGGTTGGGAGTTCAATGTTTCTATTAACACCAGCCAATGTTATGGTTGATATTGAGGAGATGAATATTCCAAAGACT
GGTCAAGAGACGAGTTTTGATTTTGATATGAAGAGACGA

SEQ ID 232

MEGNMALKDRFDKIISYFDTDDVSENEVHEVQERTSVQRDSRAATAQEASQRSHMTNSAEEEMIGSRPRTYTYDPNRQERQRVQRDNAYQQATPRV
QNKDSVRQQREQVTIALKYPRKYEDAQEIVDLLIVNECVLIDFQYMLDAQARRCLDYIDGASRVLYGSLQKVGSSMFLLTPANVMVDIEEMNIPKT
GQETSFDFDMKRR

SEQ ID 233

ATGGAGAATAAGATGGCTTTTAAAGATACATTTAACAAGATGATTTCTTATTTTGACACGGATGAGGTTAACGAAGTTGAAGAAGATGTTGCAGCA
TCAACTGATAACGTTATTCCAAGATCACAACAATCAGTCAGAGCAAGTAGTCATCCAAAACAAGAACCTAGAAACAATCACGTACAACAAGATCAT
CAAGCGAGATCCCAAGAACAGACAAGGTCACAAATGCATCCAAAACATGGCACTTCTGAACGCTATTATCAGCAGTCTCAGCCAAAAGAAGGCCAT
GAAATGGTTGACAGAAGAAAACGGATGAGCACTTCTAGTATTGCAAATCGCCGTGAGCAGTATCAACAATCAACTTGTTCAGATCAAACAACTATT
GCCTTAAAGTATCCTCGTAAATATGAGGATGCTCAAGAAATTGTGGATCTTTTAATAGTTAATGAATGCGTTTTGATTGATTTTCAGTTTATGCTA
GATGCTCAGGCTAGACGGTGTTTAGATTTTATTGATGGTGCTAGTAAAGTGCTCTATGGTAGCTTACAAAAGGTCGGCTCTTCAATGTACTTACTG
GCTCCGTCAAATGTATCCGTCAATATAGAAGAAATGACTATCCCACATACTACACAAGATATTGGCTTTGATTTTGATATGAAAAGGCGG

SEQ ID 234

MENKMAFKDTFNKMISYFDTDEVNEVEEDVAASTDNVIPRSQQSVRASSHPKQEPRNNHVQQDHQARSQEQTRSQMHPKHGTSERYYQQSQPKEGH
EMVDRRKRMSTSSIANRREQYQQSTCSDQTTIALKYPRKYEDAQEIVDLLIVNECVLIDFQFMLDAQARRCLDFIDGASKVLYGSLQKVGSSMYLL
APSNVSVNIEEMTIPHTTQDIGFDFDMKRR

SEQ ID 235

ATGACGTTAGATGATATTTATCAGCATTTTCGACCAGAAGAGTATGCGTTTATCCATAAAATAGACCATTTAGCTCAATATGTCGAAAACACCTAT
TCGTTTATTACCACTGAATTTCTAAATCCTAGGGAATTTAAAATACTCGAAAGTGTTCTAGAGAGGCGAGGTAGTCATTATTACACTTCTGGTCAG
TATTTTCAAACAGAATATGTTAAAGTAATAATAGCACCGGAATACTATCAGTTAGATATGGCTGATTTTAACCTTAGCCTAATTGAAATAAAGTAT
AATGCTAAATTTAATCACCTTACCCATGCTAAAATTATGGGAACTTTACTGAATTACTTAGGTGTAAAACGATCAATTTTAGGGGATATCCTAGTT
GAAGAAGGCTGTGCTCAGGTTTTGGTCGATAGTCAAATGACAAATCACCTTGTTCATTCAGTTACAAAAATTGGAACTGCTAGTGTACAATTAGCT
GAAGTTCCCTTGTCCAAACTTCTAACTCCCAAACAAGATATTCAAAAACTAACTGTTATTGCTTCCAGTTTACGTCTTGATAAAATTTTAGCAACG
ATTTTAAAGATTTCACGAACACAGTCGACGAAATTGATTGAGGCAGATAAAGTCAAGGTCAATTATGCAACCGTCAATCGAGTTTCTGAACAATTA
GTAGAGGGGATTTGATTAGTGTTAGAGGATATGGTCGATTTACGTTGAACCATAACCTAGGGTTAACTAAAAATCAAAAATATAAGTTAGAAGTA
GACAAAATGATACATAAC

SEQ ID 236

MTLDDIYQHFRPEEYAFIHKIDHLAQYVENTYSFITTEFLNPREFKILESVLERRGSHYYTSGQYFQTEYVKVIIAPEYYQLDMADFNLSLIEIKY
NAKFNHLTHAKIMGTLLNYLGVKRSILGDILVEEGCAQVLVDSQMTNHLVHSVTKIGTASVQLAEVPLSKLLTPKQDIQKLTVIASSLRLDKILAT
ILKISRTQSTKLIEADKVKVNYATVNRVSEQLVEGDLISVRGYGRFTLNHNLGLTKNQKYKLEVDKMIHN

SEQ ID 237

ATGGTTAGTCATAGTAAGATTTATCAGCATTTTCACCAAGAAGAATATCCTTTTATTGATAGAATGTCTGATATGATTAATAGAGTTGAAGATTAC
TATCTTTTAGAAGTTACTGAGTTTTTAAATCCTAGAGAAGTGATGATTTTAAAAAGTTTGATTGCTTTAACAGATCTAAAAATGTTCGTATCAACA
GATTACTACCCAAGCGAATATGGTCGTGTCATTATTGCACCTGGTTACTATGACTTAGAACAAAGTGATTTTCAAATAGCTTTAGTAGAGATAAGT
TATCAGGCAAAGTTTAATCAGTTGACACATAGTCAAATTTTAGGAACTTTAATTAATGAATTAGGAGTAAAGCGAAATTTATTTGGAGATGTTTTT
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AGAGAAGTTAACTTTGATCAGTTAATTAGGTCTATTGATAACAGCCAGACCCTGGATATTCTAGTTTCTAGTTTTCGATTAGATGGTGTAGTTGCT
ACTATCTTAAAAAAATCTCGAACGCAAGTTATAGCATTAATTGAAGCAAATAAGATTAAGGTAAACTATCGAGTTGCTAATAAAGCTTCAGATAAT
CTAGTCATAGGGGATATGGTGAGTATCAGAGGTCACGGGCGTTTTACTCTTTTAGCAGATAATGGAGTGACCAAACATGGCAAACAAAAAATAACA
CTAAGTAAAATGATACATAAA

SEQ ID 238

MVSHSKIYQHFHQEEYPFIDRMSDMINRVEDYYLLEVTEFLNPREVMILKSLIALTDLKMFVSTDYYPSEYGRVIIAPGYYDLEQSDFQIALVEIS
YQAKFNQLTHSQILGTLINELGVKRNLFGDVFVEMGYAQLMIKRELLDYFLGTITKIAKTSVKLREVNFDQLIRSIDNSQTLDILVSSFRLDGVVA
TILKKSRTQVIALIEANKIKVNYRVANKASDNLVIGDMVSIRGHGRFTLLADNGVTKHGKQKITLSKMIHK

SEQ ID 239

ATGCCACTTACAGCACTTGAAATTAAAGATAAAACATTTTCATCAAAATTTCGCGGTTATAGCGAAGAAGAAGTTAATGAATTTTTAGAGATTGTT
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GAATCGTTAAGTCAATCAGTTATTTTAGCTCAAGAAACTGCTGAGCGTGTGAAAATTTCAGCACAGGATGAAGCATCTAACCTAATGGGGAAAGCT
ACATTTGATGCTCAACATTTAATTGATGAGGCTAAATTAAAAGCAAATCAAATCCTTCGAGATGCGACAGATGATGCTAAGCGTGTTGCTATAGAA

ACAGAAGATTTGAAACGTCAATCACGTGTTTTCCACCAACGTTTGCTTTCTGAGTTAGAAGGGCAGCTAAAATTAGCTAACTCATCTGCTTGGGAA
GAATTGTTGAAACCAACAGCTATTTATCTTCAAAATTCTGATGCTTCTTTCAAAGAAGTTGTTGAAAAAGTTCTTGATGAAGATGATGCTTTACCA
GTGGTGGATGACACTGAGTCATTTGATGCTACTCGTCAATTCTCACCAGATGAAATGGAAGAATTACAGCGTCGTGTTGAAGAAAGTAACAAACAA
CTTGAAGAGTCAGGTTTATTAGATACTAATAATTTCCAAATGGAAGAACCGATCAATTTAGGTGAAACTCAAACTTTTAAATTAAATATTGAAGAT

SEQ ID 240

MPLTALEIKDKTFSSKFRGYSEEEVNEFLEIVVDDYEDLIRRNREQEQYIKDLEEKIAYFNEMKESLSQSVILAQETAERVKISAQDEASNLMGKA
TFDAQHLIDEAKLKANQILRDATDDAKRVAIETEDLKRQSRVFHQRLLSELEGQLKLANSSAWEELLKPTAIYLQNSDASFKEVVEKVLDEDDALP
VVDDTESFDATRQFSPDEMEELQRRVEESNKQLEESGLLDTNNFQMEEPINLGETQTFKLNIED

SEQ ID 241

ATGGCACTTACAACGCTAGAAATTAAAGATAAAACTTTTAAGACAAAATTCCGAGGATACTGTGAAGAAGAAGTCAATGAATTCCTTGATATTGTT
GTTGATGATTACGAAGCTCTTGTACGTAAAAATCGTGATAACGAAGCAAGAATTAAAGATCTTGAAGAAAAATTATCTTACTTTGATGAAATGAAA
GAGTCACTTAGCCAGTCTGTAATCTTAGCTCAAGAAACAGCTGAAAAAGTGAAAGCAACGGCTAATGCGGAAGCAACAAACTTGGTTAGTAAAGCG
ACTTATGATGCTCAGCATTTATTAGATGAATCTAAAGCTAAAGCCAATCAAATGTTGCGTGATGCAACTGATGAGGCTAAGCGAGTTGCGATTGAA
ACAGAAGAACTAAAGCGTCAAACACGTGTGTTCCACCAACGTTTAATCTCATCTATTGAGTCACAATTAAGCTTATCAAATTCACCTGAATGGGAT
GAACTGCTACAACCGACTGCAATCTATCTTCAAAATTCTGACGATGCTTTTAAGGAAGTCGTGAAGACCGTTCTTAATGAAGACATTCCTGAATCT
GATGATAGTGCCTCTTTTGATGCAACACGTCAGTTTACTCCAGAAGAGTTAGAAGAATTGCAACGTCGTGTTGATGAAAGCAATAAGGAGTTAGAG
GCTTACCAACTTGACTCTCAATCTGATTCTACGACTGAGCCAGAGGTAAATCTCAGTGAAACACAAACGTTTAAATTAAATATC

SEQ ID 242

MALTTLEIKDKTFKTKFRGYCEEEVNEFLDIVVDDYEALVRKNRDNEARIKDLEEKLSYFDEMKESLSQSVILAQETAEKVKATANAEATNLVSKA
TYDAQHLLDESKAKANQMLRDATDEAKRVAIETEELKRQTRVFHQRLISSIESQLSLSNSPEWDELLQPTAIYLQNSDDAFKEVVKTVLNEDIPES
DDSASFDATRQFTPEELEELQRRVDESNKELEAYQLDSQSDSTTEPEVNLSETQTFKLNI

SEQ ID 243

ATGAAATTAAAAGAAACCTTGAATTTAGGACAAACAGCTTTTCCAATGCGTGCAGGGCTTCCAAATAAGGAACCTCAATGGCAAGAAGCATGGGAT
CAAGCTGACATTTATAAAAAACGTCAAGCATTGAATGAAGGAAAACCAGCCTTTCACCTTCATGACGGACCTCCCTATGCTAATGGGAATATTCAT
GTAGGACATGCACTAAATAAAATTTCGAAAGACATTATTGTACGTTCAAAATCAATGTCAGGTTTTCGAGCTCCTTATGTGCCTGGTTGGGATACT
CATGGACTCCCAATTGAGCAAGTATTAGCTAAAAAAGGGGTTAAACGTAAAGAAATGGACTTGGCTGAATACCTTGAAATGTGTCGTGATTATGCT
CTCAGCCAAGTTGACAAACAACGTGATGATTTAAACGTCTGGGCGTTTCTGCCGATTGGGAAAATCCTTATATTACACTAACACCAGATTATGAA
GCAGATCAAGTACGTGTTTTCGGTGCTATGGCAGATAAAGGATATATCTATCGTGGTGCTAAACCAGTGTATTGGTCATGGTCATCAGAGTCTGCC
CTTGCTGAGGCTGAAATCGAATATCATGATATTGATTCGACATCACTCTACTATGCCAATAAAGTTAAAGATGGTAAGGGAATTCTTGATACAGAT
ACCTATATCGTCGTTTGGACGACAACACCATTTACTGTAACAGCTTCACGCGGTTTAACAGTAGGACCAGATATGGAGTATGTTGTAGTTGTACCA
GTAGGTAGTGAGCGTAAATACCTTCTTGCAGAGGTTCTTGTAGATAGTCTCGCTGCTAAGTTTGGCTGGGAAAACTTTGAAATTGTGACTCATCAC
ACTGGTAAAGAACTTAATCACATTGTTACAGAACATCCATGGGATACAGAAGTAGAAGAGTTGGTTATCCTTGGAGACCATGTTACAACAGATTCT
GGTACAGGTATTGTCCACACGGCTCCTGGTTTTGGTGAAGATGACTATAACGTTGGTATTGCTAATGGACTTGATGTTGTAGTTACCGTAGATAGT
CGTGGTTTGATGATGGAAAATGCTGGTCCTGATTTTGAAGGTCAATTCTATGACAAAGTAACACCACTTGTAAAAGAAAAATTGGGAGATCTTCTT
TTAGCCAGCGAAGTTATCAACCACTCATATCCATTTGACTGGCGTACGAAAAAGCCAATCATTTGGCGTGCGGTTCCACAATGGTTTGCCTCTGTT
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GGCGACTGGGTAATCTCACGTCAACGTGCTTGGGGTGTTCCACTTCCAATTTTTTATGCAGAAGATGGTACAGCTATCATGACAAAAGAAGTGACT
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CTTTCCTATCCAGCAGATCTTTATCTTGAAGGTTCTGATCAATACCGTGGTTGGTTCAACTCATCACTAATTACATCAGTTGCTGTTAATGGTCAC
GCTCCATACAAAGCAGTCTTATCTCAAGGTTTTGTACTTGATGGTAAAGGTGAGAAAATGTCTAAATCTCTAGGAAATACAATTCTTCCTAGTGAT
GTTGAAAAACAATTTGGTGCGGAAATCTTGCGTCTGTGGGTAACTTCTGTTGACTCAAGTAATGATGTTCGTATTTCAATGGATATCTTAAAACAA
ACATCAGAAACTTATCGTAAGATCAGGAATACATTGCGTTTCTTGATTGCAAATACTTCCGATTTTAATCCTAAACAAGATGCAGTAGCCTATGAA
AATTTAGGTGCCGTTGATCGTTATATGACTATTAAATTTAATCAAGTTGTGGATACAATCAACAAAGCTTATGCTGCTTATGATTTTATGGCAATT
TATAAAGCTGTCGTTAACTTCGTAACAGTTGATCTATCAGCATTTTACCTTGATTTTGCAAAAGATGTGGTTTACATTGAAGCGGCTAACAGTCCA
GAACGACGTCGTATGCAAACTGTTTTCTATGATATTTTAGTTAAACTTACAAAACTTTTGACTCCGATTCTACCACATACTGCTGAAGAAATTTGG
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GCAGACAAACCAGCTGACTCAGTATCATTTGAAGGTGTTGCATTTACTGTTGAACACGCTGAAGGTGAAGTCTGCGAACGCTCACGCCGTATTGAT
CCAACCACAAAGATGCGTTCGTATGGTGTAGCTGTTTGTGATGCTAGTGCAGCAATTATTGAGCAATATTATCCTGAAGCAGTAGCTCAAGGTTTT
GAAGCT

SEQ ID 244

MKLKETLNLGQTAFPMRAGLPNKEPQWQEAWDQADIYKKRQALNEGKPAFHLHDGPPYANGNIHVGHALNKISKDIIVRSKSMSGFRAPYVPGWDT
HGLPIEQVLAKKGVKRKEMDLAEYLEMCRDYALSQVDKQRDDFKRLGVSADWENPYITLTPDYEADQVRVFGAMADKGYIYRGAKPVYWSWSSESA
LAEAEIEYHDIDSTSLYYANKVKDGKGILDTDTYIVVWTTTPFTVTASRGLTVGPDMEYVVVVPVGSERKYLLAEVLVDSLAAKFGWENFEIVTHH
TGKELNHIVTEHPWDTEVEELVILGDHVTTDSGTGIVHTAPGFGEDDYNVGIANGLDVVVTVDSRGLMMENAGPDFEGQFYDKVTPLVKEKLGDLL
LASEVINHSYPFDWRTKKPIIWRAVPQWFASVSKFRQEILDEIEKTNFQPEWGKKRLYNMIRDRGDWVISRQRAWGVPLPIFYAEDGTAIMTKEVT
DHVADLFAEYGSIVWWQRDAKDLLPAGYTHPGSPNGLFEKETDIMDVWFDSGSSWNGVMNARENLSYPADLYLEGSDQYRGWFNSSLITSVAVNGH
APYKAVLSQGFVLDGKGEKMSKSLGNTILPSDVEKQFGAEILRLWVTSVDSSNDVRISMDILKQTSETYRKIRNTLRFLIANTSDFNPKQDAVAYE
NLGAVDRYMTIKFNQVVDTINKAYAAYDFMAIYKAVVNFVTVDLSAFYLDFAKDVVYIEAANSPERRRMQTVFYDILVKLTKLLTPILPHTAEEIW
SYLEHEEEEFVQLAEMPVAQTFSGQEEILEEWSAFMTLRTQAQKALEEARNAKVIGKSLEAHLTIYASQEVKTLLTALNSDIALLMIVSQLTIADE
ADKPADSVSFEGVAFTVEHAEGEVCERSRRIDPTTKMRSYGVAVCDASAAIIEQYYPEAVAQGFEA

SEQ ID 245

ATGAAATTAAAAGAGACACTTAATCTAGGAAAAACAGCCTTTCCAATGCGCGCAGGTCTTCCTAATAAAGAGCCACAATGGCAAGCAGCTTGGGAA
CAAGCAGAGCTTTACAAAAAACGTCAAGAATTGAATGCAGGTAAGCCTGCCTTTCATCTTCATGATGGACCTCCATACGCTAACGGCAATATTCAC
GTTGGGCATGCCCTTAATAAAATTTCAAAAGATATCATTGTGCGTTCTAAGTCCATGTCTGGCTTTCAAGCGCCTTATGTACCTGGTTGGGACACA
CACGGCCTTCCAATCGAACAAGTCTTGGCTAAGCAAGGAATCAAACGTAAGGAGATGGATTTAGCAGAATACCTTGAGATGTGTCGTCAATACGCT
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GCTGATCAAATTCGTGTTTTTGGAGCGATGGCTGAAAAAGGTTACATCTATCGTGGTGCTAAACCTGTTTATTGGTCATGGTCTTCAGAATCGGCC
TTGGCAGAGGCTGAAATTGAATACCATGACATCGATTCAACCTCTTTATACTACGCCAATAAAGTTAAAGATGGTAAAGGTATCCTTGATACTAAT
ACGTATATCGTTGTTTGGACCACAACACCATTTACCGTTACAGCATCACGCGGTTTGACTGTTGGTCCTGATATGGATTATCTTGTGGTGAAACCT
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AAAGGAGCTGATTTAGAGTACATTGTGACAGAACACCCATGGGATACTGACGTAGAAGAATTGGTTATCCTTGGTGACCATGTTACCCTTGAGTCA
GGGACAGGGATTGTCCACACAGCACCAGGTTTTGGTGAGGATGACTACAATGTTGGGACAAAATACAAACTGGAAGTTGCTGTGACTGTTGATGAA
CGTGGCCTAATGATGGAAAATGCAGGTCCAGATTTCCACGGACAATTTTATAACAAGGTAACGCCGATTGTCATTGATAAACTTGGTGATCTTTTA

TTGGCACAAGAAGTGATCAATCACTCTTACCCATTTGACTGGCGGACGAAAAAACCAATCATCTGGCGTGCTGTACCGCAATGGTTTGCTTCTGTT
TCTGATTTCCGTCAAGATATTTTGGATGAAATTGAAAAAACAACCTTTCATCCATCATGGGGTGAAACACGCCTTTACAATATGATTCGTGATCGT
GGCGACTGGGTTATTTCTCGTCAACGTGCTTGGGGAGTTCCGCTTCCTATCTTCTATGCCGAAGATGGCACAGCTATTATGACTAAAGAAGTGACA
GATCATGTGGCTGATTTGTTCCAAGAAAATGGATCAATCATTTGGTGGCAAAAAGAAGCTAAAGACCTATTACCAGAGGGCTTCACTCATCCAGGG
TCACCAAATGGCGAGTTTACAAAAGAAACTGATATCATGGACGTTTGGTTTGACTCTGGTTCTTCTTGGAATGGAGTCATGAATACTAAAGAAAAT
CTTTCCTATCCAGCGGATCTATACTTAGAAGGCTCTGACCAGTATCGTGGTTGGTTCAATTCATCCTTAATTACATCTGTGGCTGTTAATGGGCAT
GCTCCATATAAGGCTATTTTATCGCAAGGCTTTGTTCTTGATGGTAAGGGCGAAAAAATGTCTAAATCAAAAGGCAATATCATTTCTCCTAATGAT
GTGGCTAAACAATATGGTGCAGATATTCTTCGACTTTGGGTAGCTTCTGTGGATACCGATAATGATGTCCGTGTTTCTATGGAGATCCTTGGTCAA
GTCTCTGAAACTTACCGTAAAATCCGTAACACCCTTCGCTTCTTGATTGCTAATACATCTGATTTCAACCCTGCTACGGATACAGTAGCTTATGCA
GATTTAGGAACTGTTGATAAGTACATGACAATTGTCTTTAATCAGTTGGTAGCAACGATTACTGACGCTTATGAGCGTTATGACTTTATGGCTATT
TACAAAGCAGTGGTGAACTTTGTTACGGTTGATTTATCAGCCTTCTATCTTGATTTTGCTAAAGACGTTGTCTATATTGAAGCTGCCAATAGCTTA
GAACGTCGTCGCATGCAGACAGTCTTCTATGATATCTTGGTTAAGATTACCAAGTTATTGACGCCAATCTTGCCTCACACTACTGAAGAAATCTGG
TCTTATCTAGAGCATGAGTCAGAAGCATTTGTTCAATTGGCAGAAATGCCTGTGGCAGAAACCTTCTCGGCTCAAGAGGATATTTTAGAAGCTTGG
TCAGCTTTCATGACTTTGCGTACTCAAGCTCAAAAAGCTTTGGAAGAAGCGCGAAATGCTAAGATTATCGGTAAATCATTGGAAGCCCATTTGACC
ATCTACGCTAGTGAAGAAGTGAAAACCTTATTGACTGCTTTAGACAGCGATATTGCTTTGCTTTTGATCGTGTCTCAATTAACCATTGCTGACTTG
GCAGATGCGCCTGCGGATGCAGTGGCATTTGAAGGTGTTGCCTTTATAGTAGAACATGCCATAGGTGAAGTTTGTGAGCGTTCACGTCGCATCGAC
CCAACTACTCGCATGCGTTCTTACAATGCATTTGTCTGTGATCACAGCGCTAAAATCATTGAAGAAAATTTCCCAGAAGCTGTGGCTGAAGGGTTT
GAAGAGAGTGGCAAA

SEQ ID 246

MKLKETLNLGKTAFPMRAGLPNKEPQWQAAWEQAELYKKRQELNAGKPAFHLHDGPPYANGNIHVGHALNKISKDIIVRSKSMSGFQAPYVPGWDT
HGLPIEQVLAKQGIKRKEMDLAEYLEMCRQYALSQVDKQRDDFKRLGVSADWENPYVTLDPQFEADQIRVFGAMAEKGYIYRGAKPVYWSWSSESA
LAEAEIEYHDIDSTSLYYANKVKDGKGILDTNTYIVVWTTTPFTVTASRGLTVGPDMDYLVVKPAGSDRQYVVAEGLLDSLAGKFGWESFETLASH
KGADLEYIVTEHPWDTDVEELVILGDHVTLESGTGIVHTAPGFGEDDYNVGTKYKLEVAVTVDERGLMMENAGPDFHGQFYNKVTPIVIDKLGDLL
LAQEVINHSYPFDWRTKKPIIWRAVPQWFASVSDFRQDILDEIEKTTFHPSWGETRLYNMIRDRGDWVISRQRAWGVPLPIFYAEDGTAIMTKEVT
DHVADLFQENGSIIWWQKEAKDLLPEGFTHPGSPNGEFTKETDIMDVWFDSGSSWNGVMNTKENLSYPADLYLEGSDQYRGWFNSSLITSVAVNGH
APYKAILSQGFVLDGKGEKMSKSKGNIISPNDVAKQYGADILRLWVASVDTDNDVRVSMEILGQVSETYRKIRNTLRFLIANTSDFNPATDTVAYA
DLGTVDKYMTIVFNQLVATITDAYERYDFMAIYKAVVNFVTVDLSAFYLDFAKDVVYIEAANSLERRRMQTVFYDILVKITKLLTPILPHTTEEIW
SYLEHESEAFVQLAEMPVAETFSAQEDILEAWSAFMTLRTQAQKALEEARNAKIIGKSLEAHLTIYASEEVKTLLTALDSDIALLLIVSQLTIADL
ADAPADAVAFEGVAFIVEHAIGEVCERSRRIDPTTRMRSYNAFVCDHSAKIIEENFPEAVAEGFEESGK

SEQ ID 247

ATGAGACTAATTAATACAACCAGTAGTCATCCTGAACTAGTTCGAAATCAACTCCAAAATACAGATGCAAAATTAGTGGAAGTCTATTCAGCTGGC
AACACCGATGTCGTTTTTACAAAAGCACCTAAACATTATGAATTATTAATTTCAAACAAATATCGTGCTATCAAAGATGAAGAATTAGAAGCTATT
CGTGAGTTCTTCTTAAAGCGTAAAATAGATCAATCTATTATTATTCAAGAGCAGATGAAATCACTCCATACTGCCAAGTTAATTGAAATTTCATAT
CCAACAACAGCA

SEQ ID 248

MRLINTTSSHPELVRNQLQNTDAKLVEVYSAGNTDVVFTKAPKHYELLISNKYRAIKDEELEAIREFFLKRKIDQSIIIQEQMKSLHTAKLIEISY
PTTA

SEQ ID 249

ATGAGACTCATCAATACCACTAGCAGTCACCCAGAACTCATCAAAAATCAGCTAAAAAACACCGATGCCTATTTAGTCGAAGTATACTCAGCAGGA
AATACAGATGTCATTTTTACCCAAGCACCAAAACATTACGAACTACTTATTTCAAATAAATACCGTGCCATCAAGGAGGATGAACTTGATATCATT
CGCGAATTTTTTTTAAAACGTAAAATTGATCCTAAAATTGTTATTCCTGGACAATCAAAAACACTTCACACGAATAACCTTATTGAAATTTCATTT
CAAACTTCTGTA

SEQ ID 250

MRLINTTSSHPELIKNQLKNTDAYLVEVYSAGNTDVIFTQAPKHYELLISNKYRAIKEDELDIIREFFLKRKIDPKIVIPGQSKTLHTNNLIEISF
QTSV

SEQ ID 251

ATGACTAATCCTACTTTCGGTGAAAAAATAGATAATGTAAACTATAGGTCACGATTTGGTGTCTATGCTATTATTCCAAATCCAACTCATGATAAA
ATTATTTTAGTACAGGCACCTAATGGTGCTTGGTTTCTTCCAGGTGGGGAAATTGAAGAAAATGAAAATCACCTAGAAGCTTTAACTCGTGAGTTA
ATTGAAGAATTAGGTTATTCCGCAACAATTGGCCATTACTATGGTCAAGCTGATGAATATTTTTACTCTAGACACCGTGATACTTACTACTATAAT
CCCGCCTATATTTATGAAGTTACTGCCTATCATAAGGATCAAGCGCCACTAGAAGATTTCAACCATCTAGCCTGGTTTCCTATCCAAGAAGCTAAA
GAAAAGCTAAAACGAGGAAGCCATAGATGGGGTGTCCAAGCTTGGGAAAAAAATCACCATTCTAGGAAA

SEQ ID 252

MTNPTFGEKIDNVNYRSRFGVYAIIPNPTHDKIILVQAPNGAWFLPGGEIEENENHLEALTRELIEELGYSATIGHYYGQADEYFYSRHRDTYYYN
PAYIYEVTAYHKDQAPLEDFNHLAWFPIQEAKRKLKRGSHRWGVQAWEKNHHSRK

SEQ ID 253

ATGATGATTCCAACATTTGGACATAAAAATGCACATAAAGACTATGTCACACGTTACGGTGTCTATGCTATCATTCCCAATCACGAACAAACAAAA
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ATTGAAGAACTTGGTTTTTCTGCTACTATTGGTTCATATTACGGTCAGGCAGATGAATATTTCTACTCTCGCCATCGTGATACCCACTTCTACCAT
CCTGCCTATCTTTATGAAGTAACTGCATTTCAAGCCGTTTCTAAGCCCTTAGAAGATTTTAATAACTTAGGTTGGTTTTCTCCTATCGAGGCAATT
GCTAAATTAAAACGAGAGAGCCATCAATGGGGAGTCAAGGAATGGCAAAAAAAGCATCATTCTACTAAC

SEQ ID 254

MMIPTFGHKNAHKDYVTRYGVYAIIPNHEQTKIILVQAPNGSWFLPGGEIEAGEGQLQALERELIEELGFSATIGSYYGQADEYFYSRHRDTHFYH
PAYLYEVTAFQAVSKPLEDFNNLGWFSPIEAIAKLKRESHQWGVKEWQKKHHSTN

SEQ ID 255

ATGCTCTGTCAAAACTGCAAACTAAACGAATCAACTATTCATTTGTATACAAATGTTAATGGAAAACAAAAGCAAGTTGATCTTTGTCAAAATTGC
TACCAAATTATTAAAACTGACCCTAATAATCCACTTTTTTCAGGTTTAAATCATGTTTCACATGCGCCTGGTGGCATCAATCCTTTCTTTGATGAT
TTCTTTGGAGATTTAAATAATTTCAGAGCCTTTAATGGCCAAGATTTACCAAACACTCCTCCTACACAATCAGGAGGAAACCGAGGTGGAGGAAAC
GGTAATGGACGAAATAATAATCGCAACCAAACTGCAACTCCTTCTCAAGCCAAAGGGATTCTAGAAGAATTTGGTATCAATGTCACTGAAATAGCC
CGCCATGGTGATATTGACCCTGTTATTGGACGTGACTCAGAAATTATTCGTGTTATCGAAATCCTTAATCGTCGTACAAAAAATAATCCTGTACTT
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GTTATTCGTTTGGATGTTGTGAGTCTAGTACAAGGAACGGGCATTCGTGGTCAATTTGAAGAACGCATGCAAAAGTTGATGGAAGAAATTCGTCAA
CGTCAAGATGTTATTCTATTCATAGATGAAATTCACGAAATAGTTGGAGCTGGTACAGCTGGCGAAGGTAGTATGGATGCAGGTAATATTTTAAAA
CCTGCCCTTGCACGTGGAGAATTACAACTAGTAGGTGCTACTACTCTCAATGAATATCGTATTATCGAAAAGGACGCTGCCTTAGAACGCCGTATG
CAACCTGTAAAAGTCGATGAGCCTTCTGTTGAAGAAACCATTACTATTTTGAAAGGTATCCAAAAAAAATACGAAGATTATCATCATGTAAAATAT
AATAATGATGCCATAGAAGCAGCTGCAGTACTATCTAATCGTTATATCCAGGACCGCTTTTTACCTGATAAAGCAATAGACTTATTAGATGAAGCT

GGTTCTAAAATGAACCTAACACTAAATTTTGTTGATCCAAAAGAAATTGATCAACGTCTCATTGAAGCAGAAAATTTAAAAGCGCAAGCGACTCGT
GAAGAAGATTACGAACGTGCAGCTTACTTCCGTGACCAGATTGCAAAATATAAAGAAATGCAACAACAAAAGGTCGACGATCAAGATACACCTATT
ATTACCGAAAAAACAATTGAGCACATCATTGAAGAAAAAACGAATATCCCTGTTGGTGATTTAAAAGAAAAAGAACAATCTCAATTAATTAATCTC
GCAGATGACTTGAAACAACATGTGATCGGCCAGGATGACGCTGTCGTTAAGATTGCAAAAGCTATTCGTCGTAATCGAGTTGGTCTTGGTAGCCCA
AACCGTCCTATTGGTTCCTTTTTATTTGTAGGACCAACCGGCGTTGGTAAAACTGAACTTTCTAAACAACTAGCAATTGAGCTCTTTGGTTCAGCT
GATAGTATGATTCGTTTTGATATGTCAGAGTACATGGAAAAGCATGCTGTTGCTAAATTAGTCGGAGCGCCTCCAGGATACGTGGGATACGAGGAA
GCTGGACAATTAACTGAAAAGGTTCGTCGAAATCCTTACTCGCTCATCCTTCTAGATGAAATTGAAAAAGCTCATCCTGATGTCATGCATATGTTC
TTGCAGGTCCTTGATGACGGTCGATTAACAGATGGACAAGGAAGAACTGTTAGTTTTAAAGATACCATTATCATCATGACCTCAAATGCTGGTTCT
GGTAAAACTGAAGCAAGCGTTGGCTTTGGTGCCTCACGAGAAGGTAGAACGAATTCCGTACTAGGTCAACTAGGTAACTTCTTCAGCCCTGAATTT
ATGAACCGCTTTGACGGTATTATTGAATTCAAGGCTTTAGATAAAGAGAATCTCCTCAATATCGTTGATATTATGTTATCTGACGTTAATGCACGT
CTCGCCATCAATGGTATTCATCTAGATGTCACTGATAAAGTGAAAGAAAAATTGGTTGATTTAGGTTACGATCCCAAAATGGGAGCACGTCCATTA
CGTCGTACCATTCAAGAACATATTGAAGATGCTATCACAGATTACTATCTTGAGAATCCAAGCGAAAAAGAACTTCGTGCTATTATGACTAGCAAT
GGAAATATCATAATAAAATCTTCTAAAAAAACTGAAGAAAGTACAAAAGGT

SEQ ID 256

MLCQNCKLNESTIHLYTNVNGKQKQVDLCQNCYQIIKTDPNNPLFSGLNHVSHAPGGINPFFDDFFGDLNNFRAFNGQDLPNTPPTQSGGNRGGGN
GNGRNNNRNQTATPSQAKGILEEFGINVTEIARHGDIDPVIGRDSEIIRVIEILNRRTKNNPVLIGEPGVGKTAVVEGLAQKIVDGNVPHKLQGKQ
VIRLDVVSLVQGTGIRGQFEERMQKLMEEIRQRQDVILFIDEIHEIVGAGTAGEGSMDAGNILKPALARGELQLVGATTLNEYRIIEKDAALERRM
QPVKVDEPSVEETITILKGIQKKYEDYHHVKYNNDAIEAAAVLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFVDFKEIDQRLIEAENLKAQATR
EEDYERAAYFRDQIAKYKEMQQQKVDDQDTPIITEKTIEHIIEEKTNIPVGDLKEKEQSQLINLADDLKQHVIGQDDAVVKIAKAIRRNRVGLGSP
NRPIGSFLFVGPTGVGKTELSKQLAIELFGSADSMIRFDMSEYMEKHAVAKLVGAPPGYVGYEEAGQLTEKVRRNPYSLILLDEIEKAHPDVMHMF
LQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGSGKTEASVGFGASREGRTNSVLGQLGNFFSPEFMNRFDGIIEFKALDKENLLNIVDIMLSDVNAR
LAINGIHLDVTDKVKEKLVDLGYDPKMGARPLRRTIQEHIEDAITDYYLENPSEKELRAIMTSNGNIIIKSSKKTEESTKG

SEQ ID 257

ATGCTGTGTCAAAATTGTAATTTAAACGAATCTACTATTCATCTTTATACAAGTGTTAATGGAAAACAAAGACAGGTTGATCTCTGTCAAAATTGT
TATCAAATCATGAAATCCGATCCTGCCAATTCTATTTTAAATGGCCTAACCCCAGGATATAGAGCACAAGATAGATCCACAAGTCCTTTCTTTGAT
GACTTTTTTGGTGATTTGAATAATTTTAGAGCTTTTGGTAATCTTCCAAATACCCCACCTACTCAGGCAGGGCAAAATGGAAATGGCGGAGGACGC
TATGGTGGTAACTACAACGGACAACGACCTGCTCAGCCACAAACACCAAATCAGCAAGCAAAGGGCTTGTTAGAAGAGTTTGGGATTAATGTCACA
GATATTGCAAGAAATGGTAATATTGATCCTGTTATTGGTCGTGACGAAGAGATTACACGCGTTATCGAGATCCTCAACCGCCGTACTAAAAATAAT
CCTGTGCTAATTGGTGAGCCTGGAGTTGGTAAAACTGCTGTTGTAGAAGGTTTGGCTCAAAAAATTATTGATGGTACTGTTCCTCAAAAACTCCAA
GGCAAGCAAGTGATTCGTCTTGATGTGGTTAGCCTCGTTCAGGGAACAGGTATCCGTGGTCAGTTTGAAGAGCGCATGCAAAAATTAATGGAAGAA
ATTCGCAATCGCAAGGATGTGATTCTCTTTATTGATGAAATTCATGAGATTGTCGGTGCTGGTTCTGCAGGAGACGGCAATATGGATGCTGGTAAT
ATTTTAAAACCAGCCTTGGCCCGTGGTGAGTTGCAACTCGTTGGTGCTACTACATTAAATGAATACCGTATTATTGAAAAAGACGCTGCCTTAGAA
CGACGTATGCAACCCGTTAAAGTTGATGAACCTTCTGTTGAGGAAACCATCACGATTTTAAAAGGTATCCAACCGAAATACGAAGACTATCATCAT
GTCAAATATAGCCCAGCCGCTATTGAAGCTGCCGCTCATTTATCTAACCGCTATATTCAAGACCGTTTTCTTCCTGATAAGGCTATTGACCTTCTG
GACGAAGCTGGTTCCAAAATGAATCTAACCCTCAACTTTGTTGATCCTAAAGAAATTGACAAACGTCTTATTGAAGCTGAGAATCTCAAGGCGCAA
GCTACTCGAGACGAAGACTATGAACGCGCAGCTTATTTCCGCGATCAAATTACAAAATACAAAGAAATGCAGGCTCAAAAAGTCGATGAGCAAGAT
ATTCCCATCATTACTGAAAAAACCATTGAAGCTATTGTAGAGCAAAAAACTAATATTCCAGTTGGGGACTTAAAAGAAAAGGAACAGTCTCAACTC
GTAAACTTAGCCAATGATCTGAAAGCACACGTGATCGGGCAAGACGATGCTGTTGATAAAATCGCTAAGGCTATTCGTCGTAACCGTGTGGGATTA
GGAACTCCAAATCGCCCTATTGGTTCTTTCTTATTCGTTGGACCGACTGGGGTTGGTAAAACTGAATTGTCTAAACAACTAGCCATTGAACTCTTT
GGTTCGACAAACAATATGATTCGCTTTGACATGTCCGAATACATGGAAAAACACGCTGTCGCCAAATTAGTCGGGGCTCCTCCAGGTTATATCGGC
TATGAAGAAGCTGGACAGCTAACCGAACAAGTTCGTCGCAATCCATATTCACTTATTCTCTTAGATGAGGTGGAAAAAGCCCATCCTGACGTCATG
CACATGTTCTTACAAGTTCTTGATGATGGCCGTTTAACAGATGGTCAAGGACGAACAGTCAGCTTCAAGGACACCATTATTATCATGACCTCTAAT
GCCGGAACAGGTAAAAGCGAAGCTTCTGTCGGATTTGGTGCTGCTAGAGAAGGACGGACAAGTTCTGTCCTTGGTGAATTAAGCAACTTCTTCAGC
CCAGAGTTTATGAATCGTTTCGATGGTATTATTGAATTCAAAGCTTTATCTAAAGAGCATTTGCTGCATATCGTTGATTTAATGCTGGAAGATGTT
AATGAGCGCTTAGGCTATAATGGGATTCATCTTGATGTGACACAAAAGGTCAAAGAAAAATTAGTAGATTTAGGCTATGATCCTAAAATGGGCGCT
CGGCCGCTCCGTCGTACTATTCAAGATTATATCGAAGATGCCATTACAGACTATTATTTAGAACACCCAACTGAAAAACAGTTACGTGCACTGATG
ACAAACAGTGAAAATATCACGATTAAAGCTGTTAAAGAGGGAGATTCTTTTCTTAACGAAGAGTCTCTCGAT

SEQ ID 258

MLCQNCNLNESTIHLYTSVNGKQRQVDLCQNCYQIMKSDPANSILNGLTPGYRAQDRSTSPFFDDFFGDLNNFRAFGNLPNTPPTQAGQNGNGGGR
YGGNYNGQRPAQPQTPNQQAKGLLEEFGINVTDIARNGNIDPVIGRDEEITRVIEILNRRTKNNPVLIGEPGVGKTAVVEGLAQKIIDGTVPQKLQ
GKQVIRLDVVSLVQGTGIRGQFEERMQKLMEEIRNRKDVILFIDEIHEIVGAGSAGDGNMDAGNILKPALARGELQLVGATTLNEYRIIEKDAALE
RRMQPVKVDEPSVEETITILKGIQPKYEDYHHVKYSPAAIEAAAHLSNRYIQDRFLPDKAIDLLDEAGSKMNLTLNFVDPKEIDKRLIEAENLKAQ
ATRDEDYERAAYFRDQITKYKEMQAQKVDEQDIPIITEKTIEAIVEQKTNIPVGDLKEKEQSQLVNLANDLKAHVIGQDDAVDKIAKAIRRNRVGL
GTPNRPIGSFLFVGPTGVGKTELSKQLAIELFGSTNNMIRFDMSEYMEKHAVAKLVGAPPGYIGYEEAGQLTEQVRRNPYSLILLDEVEKAHPDVM
HMFLQVLDDGRLTDGQGRTVSFKDTIIIMTSNAGTGKSEASVGFGAAREGRTSSVLGELSNFFSPEFMNRFDGIIEFKALSKEHLLHIVDLMLEDV
NERLGYNGIHLDVTQKVKEKLVDLGYDPKMGARPLRRTIQDYIEDAITDYYLEHPTEKQLRALMTNSENITIKAVKEGDSFLNEESLD

SEQ ID 259

ATGTCAATGAATTTTTCATTTTTACCACAATATTGGTCCTATTTTAATTATGGTGTGATGGTAACCATTATGATTTCAACATGTGTTGTTTTTTTT
GGAACTATTATAGGTGTGTTAATTGCTTTAGTAAAGCGTACTAATTTACATTTTCTCACAATATTAGCTAATTTCTATGTATGGGTATTTCGTGGG
ACACCGATGGTAGTTCAAATTATGATTGCTTTCGCATGGATGCATTTTAACAATTTACCAACGATTAGCTTTGGTGTTTTAGATTTAGATTTTACA
CGACTTTTACCTGGTATCATTATCATTTCCTTAAATAGTGGTGCCTATATTTCGGAAATTGTACGTGCAGGGATTGAGGCTGTACCATCTGGACAA
ATAGAAGCAGCTTACTCGTTGGGGATTCGACCTAAAAATACACTTCGCTATGTTATCTTACCCCAAGCTTTTAAAAATATTTTACCTGCTCTAGGG
AATGAATTTATTACAATTATTAAAGATAGTGCTCTCCTTCAAACTATTGGTGTCATGGAATTATGGAACGGAGCACAATCAGTTGTAACGGCTACT
TACTCACCAGTTGCACCGTTATTATTTGCAGCATTTTACTATTTAATGTTGACAACGATTCTCTCAGCTTTGTTAAAACAAATGGAGAAATATCTT
GGGAAAGGGGTAAAAATAGATGGT

SEQ ID 260

MSMNFSFLPQYWSYFNYGVMVTIMISTCVVFFGTIIGVLIALVKRTNLHFLTILANFYVWVFRGTPMVVQIMIAFAWMHFNNLPTISFGVLDLDFT
RLLPGIIIISLNSGAYISEIVRAGIEAVPSGQIEAAYSLGIRPKNTLRYVILPQAFKNILPALGNEFITIIKDSALLQTIGVMELWNGAQSVVTAT
YSPVAPLLFAAFYYLMLTTILSALLKQMEKYLGKGVKIDG

SEQ ID 261

ATGGATTTGTCATTTTTGCCCAAATACTGGGCCTACTTTAACTACGGTGTACTTGTCACCATTATGATTTCAGTCAGCGTTGTCTTTTTTGGAACC
CTTATTGGTGTCTTGGTAACCCTGATTAAGCGTAGTCATGTGAAGCCGTTGACCTGGGTCGTTAATCTTTACGTTTGGATCTTTCGGGGAACACCT
ATGGTGGTTCAAATCATGATTGCCTTTGCTTGGATGCATTTTAACAATATGCCTACTATTGGTTTTGGGGTTTTAGACTTGGACTTTTCAAGACTA
CTTCCTGGAATTATTATCATTTCATTGAATAGCGGTGCTTATATTTCAGAAATTGTTAGAGCAGGTATTGAGGCTGTACCAAAAGGGCAATTAGAA
GCAGCTTATTCACTAGGTATTCGTCCTCAAAATGCCATGCGTTATGTGATTTTGCCTCAGGCCTTTAAAAATATTTTGCCAGCCTTAGGAAATGAA
TTTATTACCATTATTAAGGATAGTGCTCTTTTACAAACCATTGGAGTGATGGAACTTTGGAATGGTGCCCAATCGGTGGTAACGGCTACTTATTCT

CCAATTTCCCCTTTACTGGTGGCTGCTTTTTACTACTTAATGGTCACAACAGTGATGGCACAGTTATTGGCAGTCTTAGAACGTCACATGGCGCAA
GGAGGTAATCAT

SEQ ID 262

MDLSFLPKYWAYFNYGVLVTIMISVSVVFFGTLIGVLVTLIKRSHVKPLTWVVNLYVWIFRGTPMVVQIMIAFAWMHFNNMPTIGFGVLDLDFSRL
LPGIIIISLNSGAYISEIVRAGIEAVPKGQLEAAYSLGIRPQNAMRYVILPQAFKNILPALGNEFITIIKDSALLQTIGVMELWNGAQSVVTATYS
PISPLLVAAFYYLMVTTVMAQLLAVLERHMAQGGNH

SEQ ID 263

ATGTCTCATATGAATTATAAAGAGATTTATCAAGAGTGGTTAGAAAACGACTCACTCGGTAAAGATATTAAGTCAGATTTAGAAGCTATTAAAGGC
GATGAATCTGAAATTCAGGATCGTTTTTACAAAACATTAGAATTTGGAACGGCGGGATTGAGAGGTAAACTTGGAGCAGGAACCAATCGTATGAAT
ACTTATATGGTGGGGAAAGCAGCACAAGCATTAGCTAATACGATTATTGATCATGGCCCTGAAGCTATTGCACGTGGAATTGCAGTTAGTTATGAT
GTCCGTTATCAATCTAAGGAATTTGCAGAATTAACTTGTTCCATTATGGCAGCAAATGGTATTAAGTCTTATATTTATAAAGGGATTCGCCCAACA
CCAATGTGCTCATATGCTATTCGTGCTCTAGGATGTGTTTCGGGTGTGATGATTACTGCTAGTCATAATCCTCAAGCTTATAATGGTTATAAGGCA
TATTGGAAAGAAGGATCTCAGATTTTAGATGATATTGCTGATCAAATTGCCAATCATATGGATGCTATAACCGATTATCAGCAAATTAAGCAAATA
CCCTTTGAAGAGGCTCTGGCAAGTGGTTCGGCAAGTTATATCGATGAGAGTATTGAAGAAGCATATAAAAAAGAAGTGCTTGGTTTAACTATTAAT
GATACTAATATTGATAAGTCAGTCCGGGTAGTTTATACTCCTTTAAATGGCGTAGGAAATTTACCTGTGCGCGAAGTTTTAAGACGCCGTGGTTTT
GAAAATGTTTATGTGGTACCTGAGCAGGAAATGCCCGATCCTGATTTTACAACGGTTGGCTATCCAAACCCTGAAGTTCCTAAAGCATTTGCCTAT
TCAGAATCTCTAGGAAAGTCAGTTGATGCAGATATCTTACTTGCCACAGATCCAGATTGTGACCGAGTAGCATTGGAAGTCAAAGATAGTAAGGGA
GAATATATTTTCTTAAATGGTAATAAGATAGGGGCACTTCTTTCCTATTATATTTTTTCACAACGATGTGCCTTAGGGAATTTGCCACATCATCCT
GTATTGGTAAAATCCATTGTAACTGGTGATCTATCAAAAGTTATTGCAGATAAATATAATATTGAAACTGTTGAAACTTTAACAGGATTTAAAAAT
ATTTGTGGAAAAGCTAATGAATATGATATCTCAAAGGATAAAACTTATCTCTTTGGCTATGAAGAAAGTATTGGTTTTTGCTATGGCACTTTTGTA
CGTGATAAAGATGCTGTGAGTGCTTCAATGATGGTAGTAGAAATGACTGCCTATTATAAAGAACGAGGGCAAACACTTTTAGACGTTTTGCAAACC
ATTTACGATAAATTTGGCTATTACAACGAGCGCCAATTTTCTCTTGAGTTAGAGGGTGCTGAGGGGCAAGAACGTATTAGTCGTATTATGGAGGAT
TTTAGACAGGACCCAATATTACAAGTAGGTGAGATGACATTGGAGAATTCTATTGATTTCAAGGATGGTTATAAGGATTTTCCAAAGCAAAATTGT
TTAAAATATTATTTTAATGAGGGTTCATGGTATGCTTTAAGGCCGTCAGGGACGGAACCTAAGATAAAATGTTACCTTTATACGATTGGTTGTACA
GAAGCAGATAGTTTATCGAAACTTAATGCAATTGAGTCGGCTTGTCGTGCTAAAATGAATAGTACTAAA

SEQ ID 264

MSHMNYKEIYQEWLENDSLGKDIKSDLEAIKGDESEIQDRFYKTLEFGTAGLRGKLGAGTNRMNTYMVGKAAQALANTIIDHGPEAIARGIAVSYD
VRYQSKEFAELTCSIMAANGIKSYIYKGIRPTPMCSYAIRALGCVSGVMITASHNPQAYNGYKAYWKEGSQILDDIADQIANHMDAITDYQQIKQI
PFEEALASGSASYIDESIEEAYKKEVLGLTINDTNIDKSVRVVYTPLNGVGNLPVREVLRRRGFENVYVVPEQEMPDPDFTTVGYPNPEVPKAFAY
SESLGKSVDADILLATDPDCDRVALEVKDSKGEYIFLNGNKIGALLSYYIFSQRCALGNLPHHPVLVKSIVTGDLSKVIADKYNIETVETLTGFKN
ICGKANEYDISKDKTYLFGYEESIGFCYGTFVRDKDAVSASMMVVEMTAYYKERGQTLLDVLQTIYDKFGYYNERQFSLELEGAEGQERISRIMED
FRQDPILQVGEMTLENSIDFKDGYKDFPKQNCLKYYFNEGSWYALRPSGTEPKIKCYLYTIGCTEADSLSKLNAIESACRAKMNSTK

SEQ ID 265

ATGAGTAATATGACTTACAACGAGGTATATCAAGAATGGTTGCACAATAATGATCTTAGTGATGATATTAAAGCAGATTTAGCAGCCATAAAAGAC
AATGAGGCTGAGATTCAAGATCGTTTTTACAAAACACTTGAATTTGGAACAGCAGGGCTAAGAGGAAAACTTGGAGCAGGCACCAATCGCATGAAT
ACCTATATGGTTGGTAAGGCAGCACAAGCTTTAGCTAATACTATTATTGATCATGGACCTGAAGCGGTTAAAAAGGGCATTGCGGTTAGTTATGAT
GTTCGCTATCAATCTAGAACATTTGCAGAATTAACATGCTCTATTATGGCAGCTAACGGTATTAAGGCGTACCTTTATAAAGGGATTCGGCCAACA
CCAATGTGTTCGTACGCTATTCGTGCTTTGGGATGTATTTCTGGTGTTATGATTACGGCTAGTCACAATCCCCAAGCTTACAATGGTTACAAAGCT
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CCTTTTGAAAAGGCTCTGGACAGTGGACTTGTTACTTATATTGATGAGAGTATTGAAGAAGCATATAAAAAAGAAGTGCTTGGTTTAACGATTAAT
GATACTGACATTGATAAGTCAGTCCGAGTAGTCTATACCCCTTTAAATGGTGTTGGGAATCTACCAGTGCGTGAGGTTTTAAGACGCCGCGGTTTT
GAAAATGTTTATGTGGTACCTGAGCAGGAAATGCCCGATCCTGATTTTACAACAGTTGGCTATCCTAATCCCGAAGTCCCTAAAACTTTTGCATAT
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GACTATGTTTTTCTCAATGGCAATAAAATCGGAGCGCTTTTATCTTACTATATCTTTTCACAACGATTTGACTTAGGCAATTTACCGGCTAATCCT
GTTTTAGTGAAATCCATTGTAACAGGAGACTTGTCACGGGCTATTGCTAGCCATTATGGTATTGAAACCGTTGAAACATTGACTGGTTTTAAGAAT
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CGTGACAAAGACGCTGTTAGCGCCTCTATGATGATTGTAGAAATGGCAGCTTACTACAAGAAAAAAGGGCAGAATTTACTAGATGTTTTGCAGACT
ATTTATGCGACATTTGGGTATTATAATGAACGTCAAATTGCCTTGGAGCTTGAGGGGATAGAAGGACAAAAACGCATTGCGAGGATAATGGAAGAT
TTCAGACAGACACCAATAGCTAGTGTTGCAGAGATGGCGTTAGACAAGACAATTGATTTTATTGATGGCTATCAAGATTTTCCAAAGCAAAACTGT
CTCAAATTTTATTTGGATGATGGTTCTTGGTATGCACTTAGACCATCAGGAACAGAGCCTAAAATAAAATTTTATTTATATACTATTGGCCAAACA
CAAGAAAATAGTGCAACAAAATTAGATGCTATTGAAGCAGCGTGTCGCACAAAAATAAATCAGGTTAAT

SEQ ID 266

MSNMTYNEVYQEWLHNNDLSDDIKADLAAIKDNEAEIQDRFYKTLEFGTAGLRGKLGAGTNRMNTYMVGKAAQALANTIIDHGPEAVKKGIAVSYD
VRYQSRTFAELTCSIMAANGIKAYLYKGIRPTPMCSYAIRALGCISGVMITASHNPQAYNGYKAYWQEGSQILDDIADQIAQHMAALTQYQEIKQM
PFEKALDSGLVTYIDESIEEAYKKEVLGLTINDTDIDKSVRVVYTPLNGVGNLPVREVLRRRGFENVYVVPEQEMPDPDFTTVGYPNPEVPKTFAY
SEKLGKAVDADILIATDPDCDRVALEVKNAVGDYVFLNGNKIGALLSYYIFSQRFDLGNLPANPVLVKSIVTGDLSRAIASHYGIETVETLTGFKN
ICGKANEYDVTKQKNYLFGYEESIGFCYGTFVRDKDAVSASMMIVEMAAYYKKKGQNLLDVLQTIYATFGYYNERQIALELEGIEGQKRIARIMED
FRQTPIASVAEMALDKTIDFIDGYQDFPKQNCLKFYLDDGSWYALRPSGTEPKIKFYLYTIGQTQENSATKLDAIEAACRTKINQVN

SEQ ID 267

ATGACTGAATTAATAGATGGTAAAGCCTTATCACAAAAAATGCAGGCTGAGTTAGGGCGAAAAGTTGAAAGGTTAAAGGAACAGCATGGTATCATA
CCTGGTTTAGCTGTAATCCTTGTTGGGGATAATCCAGCTAGCCAAGTGTACGTTCGAAATAAAGAACGCTCTGCATTAGAAGCTGGTTTTAAAAGT
GAGACTCTACGATTATCTGAATCCATTTCTCAAGAAGAACTGATTGATATTATCCATCAATACAATGAAGATAAAAGTATCCATGGTATTTTAGTT
CAACTTCCGTTACCACAACATATTAACGATAAAAAAATTATTTTAGCAATAGATCCTAAGAAAGATGTTGATGGTTTCCACCCAATGAATACGGGT
CATCTTTGGTCAGGACGACCGATGATGGTACCTTGTACGCCAGCTGGTATTATGGAGATGTTTAGAGAGTACCATGTGGATTTAGAGGGAAAACAT
GCTGTTATCATCGGAAGGTCCAATATTGTTGGTAAGCCAATGGCACAACTTCTCCTTGATAAAAACGCAACAGTTACTTTGACACATTCAAGAACT
CGAAACCTTTCTGAGGTAACAAAGGAGGCTGATATCCTTATTGTTGCGATTGGTCAGGGGCACTTTGTTACAAAAGACTTCGTTAAAGAAGGTGCT
GTGGTGATTGATGTTGGTATGAATCGCGATGAAAATGGTAAATTGATTGGAGACGTTGTATTTGAACAAGTGGCAGAAGTTGCTAGTATGATAACA
CCTGTTCCTGGGGGCGTAGGACCTATGACGATTACAATGCTTTTGGAACAAACTTATCAAGCAGCTCTTAGAAGTGTGAGTCTA

SEQ ID 268

MTELIDGKALSQKMQAELGRKVERLKEQHGIIPGLAVILVGDNPASQVYVRNKERSALEAGFKSETLRLSESISQEELIDIIHQYNEDKSIHGILV
QLPLPQHINDKKIILAIDPKKDVDGFHPMNTGHLWSGRPMMVPCTPAGIMEMFREYHVDLEGKHAVIIGRSNIVGKPMAQLLLDKNATVTLTHSRT
RNLSEVTKEADILIVAIGQGHFVTKDFVKEGAVVIDVGMNRDENGKLIGDVVFEQVAEVASMITPVPGGVGPMTITMLLEQTYQAALRSVSL

SEQ ID 269

ATGTCAATGACAGAACTAATTGATGGTAAAGCCTTAGCTCAAAAGATGCAACAAGAGTTAGCAGCTAAAGTCAACAATCTAAAACAAAAAAAAGGA
ATTGTACCAGGCTTAGCCGTTATTCTTGTAGGTGATGATCCTGCTAGTCAGGTGTATGTCCGTAATAAAGAGCGTGCAGCTCTTACTGTAGGTTTT
AAAAGTGAGACCGTTAGATTATCAGAATTCATTTGTCAAGAAGAGCTTATTGCAGTAATCGAACGTTACAATGCAGATAACACTATTCATGGTATT

TTAGTGCAGCTACCCCTGCCAAATCATATTAATGATAAAAAAATTATTCTCGCCATTGATCCCAAAAAAGATGTGGATGGTTTTCACCCGATGAAT
ACAGGTCACCTTTGGTCAGGACGTCCCTTGATGGTTCCTTGTACTCCATCAGGGATTATGGAATTGCTTCGAGAATATAATGTTAACCTTGAAGGT
AAACATGCCGTCATTATTGGCAGATCGAATATCGTTGGAAAACCAATGGCACAGCTCTTACTGGACAAAAATGCAACAGTCACGTTGACACATTCA
AGAACACGTCAATTAGAAGAAGTATGTCGCTGTGCAGATGTGTTGATTGTGGCAATCGGACAAGGTCATTTCATAACAAAACAATATATAAAAGAT
GGTGCGATAGTGATTGATGTAGGAATGAACCGTGATGATAATGGCAAGCTAATTGGAGATGTGGCCTTTGATGAGGTGGCAGAAGTTGCAGCGAAA
ATCACCCCTGTACCAGGAGGTGTCGGTCCTATGACGATTGCTATGTTGCTAGAGCAAACTTATCAATCTGCTCTCCGTAGTACTCATAAA

SEQ ID 270

MSMTELIDGKALAQKMQQELAAKVNNLKQKKGIVPGLAVILVGDDPASQVYVRNKERAALTVGPKSETVRLSEFICQEELIAVIERYNADNTIHGI
LVQLPLPNHINDKKIILAIDPKKDVDGFHPMNTGHLWSGRPLMVPCTPSGIMELLREYNVNLEGKHAVIIGRSNIVGKPMAQLLLDKNATVTLTHS
RTRQLEEVCRCADVLIVAIGQGHFITKQYIKDGAIVIDVGMNRDDNGKLIGDVAFDEVAEVAAKITPVPGGVGPMTIAMLLEQTYQSALRSTHK

SEQ ID 271

ATGATTGTTGGTGAACAAGAAGCGAGGGCGTTAATTAAGCCACGCCCTAAATCAAGCCATAAAGGTGATTATGGTAGTGTTCTTCTGATAGGAGGT
TTTTATCCCTATGGAGGTGCTATTATAATGGCAGCTTTGGCCTGTGTCAAAACTGGTGCAGGATTAGTTACTGTAGCAACCCAAAGTTGCAATATC
CCCTCTTTGCATAGTCAACTACCAGAGGTAATGGCGTTTGATAGTGATGATTACAAATGGTTGGAAAAATCAATTGTTCAAAGTGATGTTATTGTA
ATTGGTCCTGGATTAGGAGTATCAGAATCATCTCGAAAAATTTTGAACCAGACCATGGAGAAGATTCAATCACATCAAAGTGTCATCCTTGACGGA
TCAGCCTTGACTCTGTTATCAGAAGGTGCGTTTCCGCAAACAAAGGCTAAAAATTTAGTGTTGACACCTCATCAAAAAGAATGGGAGCGATTGTCA
GGTATCGCTGTATCGCAACAGACAAAAGAAAATACCCAAACCGCTCTTAAATCTTTTCCCAAAGGGACGATTTTAGTCGCTAAGAGTTCGCATACG
CGTATTTTTCAAGATTTAGACGAAAAAGAAATTATAGTAGGAGGTCCTTACCAGGCGACTGGAGGGATGGGGGATACTTTGTGTGGTATGATTGCA
GGTATGTTAGCGCAATTTAAAGAAGCCTCTCCTCTAGATAAGGTATCAGTGGGAGTTTATCTACATTCGGCAATTGCTCAAGGATTATCTAAAGAA
GCCTATGTTGTTCTACCGACAACGATTAGTGATGAGATTCCAAAAGAAATGGCTAGACTATCTAAA

SEQ ID 272

MIVGEQEARALIKPRPKSSHKGDYGSVLLIGGFYPYGGAIIMAALACVKTGAGLVTVATQSCNIPSLHSQLPEVMAFDSDDYKWLEKSIVQSDVIV
IGPGLGVSESSRKILNQTMEKIQSHQSVILDGSALTLLSEGAFPQTKAKNLVLTPHQKEWERLSGIAVSQQTKENTQTALKSFPKGTILVAKSSHT
RIFQDLDEKEIIVGGPYQATGGMGDTLCGMIAGMLAQFKEASPLDKVSVGVYLHSAIAQGLSKEAYVVLPTTISDEIPKEMARLSK

SEQ ID 273

ATGTCAGACTATTTATCCGTGTCGACACTGACTAAGTATTTAAAATTAAAATTTGACAAAGACCCTTATTTAGAGAGGGTTTATTTAACTGGGCAA
GTGTCTAATTTTCGTCGTCGCCCAAACCATCAATATTTCTCTTTAAAAGATGATAAATCAGTCATTCAGGCGACAATGTGGTCAGGTCACTTCAAA
AAATTGGGTTTTGAATTAGAGGAAGGGATGAAGGTTAATGTAGTTGGCCGTGTTCAACTTTATGAACCAAGCGGCTCCTACTCTATTATTGTTGAA
AAAGCAGAACCGGATGGTATAGGAGCTCTTGCTATCCAATTTGAACAACTAAAGAAGAAACTCTCTCAAGCAGGTTATTTTGATGATCGTCATAAG
CAATTAATTCCTCAATTTGTTAGAAAAATAGGAGTTGTGACTAGTCCAAGTGGAGCCGTTATTCGGGATATTATTACAACAGTATCTCGTCGATTT
CCAGGAGTGGAAATATTACTTTTCCCCACAAAAGTTCAAGGAGAGGGCGCAGCTCAGGAAATAGCACAAACTATTGCTTTAGCTAACGAGAAAAAG
GATTTGGATCTATTAATTGTTGGCCGTGGGGGAGGTTCTATTGAGGACTTATGGGCATTTAATGAAGAATGTGTTGTAGAAGCTATTTTTGAATCT
CGTCTTCCCGTTATTTCTAGTGTCGGACATGAAACTGATACAACTTTAGCAGATTTTGTAGCCGATCGCAGAGCAGCAACTCCAACTGCAGCAGCT
GAGCTTGCTACACCGGTTACTAAAATTGATATCTTGTCTTGGATTACTGAACGTGAAAATAGAATGTATCAGTCTAGCCTTCGTCTTATCAGGACA
AAAGAGGAGAGGTTGCAAAAATCAAAGCAATCAGTTATTTTTAGGCAACCAGAGCGTCTATATGATGGTTTCCTTCAAAAATTAGATAACCTAAAT
CAGCAGTTAACATATTCTATGCGTGATAAACTACAAACAGTAAGACAAAAGCAAGGTTTGCTTCATCAAAAACTGCAAGGCATAGATTTAAAACAG
CGTATTCATATTTACCAAGAGCGTGTTGTGCAAAGTAGACGACTATTATCAAGTACAATGACTAGTCAGTATGACAGCAAGCTAGCACGTTTTGAA
AAGGCTCAAGATGCGCTTATATCATTGGATAGTTCTAGAATTGTAGCGCGTGGTTACGCTATTATCGAAAAAAACCATACTTTAGTATCTACTACT
AATGGAATAAATGAAGGAGATCATTTGCAAGTTAAGATGCAAGATGGTCTTTTAGAAGTTGAGGTGAAGGATGTCAGACAAGAAAACATT

SEQ ID 274

MSDYLSVSTLTKYLKLKFDKDPYLERVYLTGQVSNFRRRPNHQYFSLKDDKSVIQATMWSGHFKKLGFELEEGMKVNVVGRVQLYEPSGSYSIIVE
KAEPDGIGALAIQFEQLKKKLSQAGYFDDRHKQLIPQFVRKIGVVTSPSGAVIRDIITTVSRRFPGVEILLFPTKVQGEGAAQEIAQTIALANEKK
DLDLLIVGRGGGSIEDLWAFNEECVVEAIFESRLPVISSVGHETDTTLADFVADRRAATPTAAAELATPVTKIDILSWITERENRMYQSSLRLIRT
KEERLQKSKQSVIFRQPERLYDGFLQKLDNLNQQLTYSMRDKLQTVRQKQGLLHQKLQGIDLKQRIHIYQERVVQSRRLLSSTMTSQYDSKLARFE
KAQDALISLDSSRIVARGYAIIEKNHTLVSTTNGINEGDHLQVKMQDGLLEVEVKDVRQENI

SEQ ID 275

GTGAAAGGTGGCTTGATGGCAGATTATTTAACCGTCACTCATTTGACGAAATATTTAAAATTAAAATTTGACCGTGACCCTTATTTGGAACGGGTT
TATCTGACTGGTCAAGTGTCCAATTTTCGAAAACGACCAACTCATCAATATTTTTCCTTAAAAGATGAAAGTGCTGTGATTCAAGCCACCATGTGG
GCAGGAGTCTATAAAAAACTAGGATTCGACCTAGAAGAAGGCATGAAAATTAATGTAATTGGGCGAGTCCAACTTTATGAACCTAGTGGCTCTTAC
TCTATCGTGATTGAAAAGGCAGAGCCAGATGGTATAGGTGCCTTGGCTTTGCAGTTTGAACAATTAAAGAAAAAATTAACGGCAGAAGGTTATTTT
GAGCAAAAACACAAGCAGCCCTTGCCACAGTTTGTATCAAAAATTGGGGTCATTACAAGTCCTAGTGGTGCTGTGATTCGAGATATTATCACAACC
GTTTCACGGCGTTTTCCAGGGGTTGAGATTTTATTATTCCCAACTAAAGTACAAGGTGATGGAGCCGCCCAAGAAGTAGTGGCTAATATTCGAAGA
GCCAATCAAAGAGAGGATTTGGACTTGCTCATTGTCGGCCGTGGAGGTGGCTCGATAGAAGACCTTTGGGCCTTCAACGAGGAAATAGTGGTTCAG
GCTATCTTTGAATCGCAACTTCCAGTGATTTCGAGTGTGGGTCATGAAACAGACACGACTTTAGCGGATTTTGTGGCAGATCGCAGAGCAGCCACA
CCAACAGCAGCAGCAGAGTTAGCAACGCCTATTACAAAAACAGATCTTATGTCTTGGATAGTAGAGCGGCAAAATCGTTCCTATCAGGCCTGCTTG
AGGCGGATTAAGCAACGGCAAGAGTGGGTGGATAAACTCTCGCAATCTGTTATTTTTAGGCAACCAGAACGATTATATGATGCCTACCTGCAAAAA
ATTGATCGCCTTAGCATGACCCTGATGAATACGATGAAAGATCGTCTGAGTTCCGCCAAAGAAAACAAGGTTCAGTTGGACCATGCCTTGGCCAAT
AGTCAATTACAGACAAAAATCGAGCGATACCAAGACCGTGTTGCTACCGCTAAGCGTTTACTGATGGCTAATATGGCTAGTCAATATGATAGTCAG
CTGGCTCGCTTTGAAAAAGCACAGGATGCTTTGCTATCACTGGATGCCAGCCGAATTATCGCCCGTGGTTATGCAATGATTGAAAAAAATCAAGCA
CTGGTAGCCTCTGTAAGTCAGATAACAAAGGGTGATCAGTTAACCATTAAGATGCGTGATGGACAATTAGATGTAGAGGTAAAAGATGTCAAAAAC
GAAAACATT

SEQ ID 276

VKGGLMADYLTVTHLTKYLKLKFDRDPYLERVYLTGQVSNFRKRPTHQYFSLKDESAVIQATMWAGVYKKLGFDLEEGMKINVIGRVQLYEPSGSY
SIVIEKAEPDGIGALALQFEQLKKKLTAEGYFEQKHKQPLPQFVSKIGVITSPSGAVIRDIITTVSRRFPGVEILLFPTKVQGDGAAQEVVANIRR
ANQREDLDLLIVGRGGGSIEDLWAFNEEIVVQAIFESQLPVISSVGHETDTTLADFVADRRAATPTAAAELATPITKTDLMSWIVERQNRSYQACL
RRIKQRQEWVDKLSQSVIFRQPERLYDAYLQKIDRLSMTLMNTMKDRLSSAKENKVQLDHALANSQLQTKIERYQDRVATAKRLLMANMASQYDSQ
LARFEKAQDALLSLDASRIIARGYAMIEKNQALVASVSQITKGDQLTIKMRDGQLDVEVKDVKNENI

SEQ ID 277

ATGTCAGACAAGAAAACATTTGAAGAAAATTTACAGGAATTAGAGACAATTGTCTCACGTTTAGAAACAGGTGATGTTGCCTTAGAAGATGCCATT
GCTGAATTTCAAAAAGGAATGCTTATTTCAAAAGAGTTACAAAGAACTTTAAAAGAAGCTGAAGAGACGCTTGTAAAAGTGATGCAAGCTGACGGA
ACGGAAGTAGAAATGGATACT

SEQ ID 278

MSDKKTFEENLQELETIVSRLETGDVALEDAIAEFQKGMLISKELQRTLKEAEETLVKVMQADGTEVEMDT

SEQ ID 279

ATGTCAAAAACGAAAACATTTGAAGAAAATTTACAAGATTTAGAGACTATTGTGAACAAACTTGAAAATGGGGATGTCCCTTTGGAAGAAGCTATT
TCAGAATTTCAAAAAGGAATGCTTCTCTCAAAAGAACTTCAAAAGACCTTACAAGCGGCAGAAAAAACACTCGTCAAAGTGATGCAAGCTGATGGC
ACAGAAGTAGATATGGATGAT

SEQ ID 280

MSKTKTFEENLQDLETIVNKLENGDVPLEEAISEFQKGMLLSKELQKTLQAAEKTLVKVMQADGTEVDMDD

SEQ ID 281

TTGATGGTTACTATTGAAAAAATTGATGAAGCTATTCATCGTTATTACAAACAGACACATAGTGTCGTTTCTCCTGATTTGATTAAGGCTATCCTC
TACTCAGTTGATGGAGGTGGGAAACGTATTCGTCCACGCATCCTTTTAGAAATTTTAGAGGGATTTGGAGTTGAACTAATAGATGGTCATTATGAT
GTGGCTGCTGCTTTGGAGATGATTCACACCGGCTCATTAATCCATGATGATTTACCGGCGATGGATAATGATGATTTTCGTCGTGGCCGCTTAACA
AACCATAAAAAGTTTGATGAAGCTACAGCGGTTTTAGCTGGAGATTCCCTTTTTTTAGACCCATTTGATTTAGTTGTAAAAGCTGGTTTTAAAGCT
GATGTTACTGTTAGGTTAATAGAGTTATTGTCTATGTCTGCGGGTAGTTTTGGCATGGTTGGTGGACAAATGTTAGATATGAAGGGAGAAAACAAA
GTTTTATCTATTGACGATTTAAGCTTGATTCATATTAATAAAACGGGACGCCTGTTAGCTTATCCCTTTGTTGCAGCAGGTATTTTAGCTGAGAAG
TCGGAAGAAGTAAAAGGAAAACTGCATCAAGCTGGCCTTTTAATCGGTCATGCTTTTCAAGTACGTGATGATATTTTAGATGTGACTGCTAGTTTT
GAAGAATTGGGGAAGACACCAAATAAAGACATTGTAGCAGAAAAGACAACTTATCCAAATTTATTGGGTTTGGATAAGTCACAGGAAATACTTGAT
GATACTTTGAAAAAAGCTCAGGCAATTTTTCAAAATCTAGAGAAAAAAGCTAACTTTAATGCTAGAAAAATAATAGATATAATAGAGGGATTACGG
TTGAATGGC

SEQ ID 282

MMVTIEKIDEAIHRYYKQTHSVVSPDLIKAILYSVDGGGKRIRPRILLEILEGFGVELIDGHYDVAAALEMIHTGSLIHDDLPAMDNDDFRRGRLT
NHKKFDEATAVLAGDSLFLDPFDLVVKAGFKADVTVRLIELLSMSAGSFGMVGGQMLDMKGENKVLSIDDLSLIHINKTGRLLAYPFVAAGILAEK
SEEVKGKLHQAGLLIGHAFQVRDDILDVTASFEELGKTPNKDIVAEKTTYPNLLGLDKSQEILDDTLKKAQAIFQNLEKKANFNARKIIDIIEGLR
LNG

SEQ ID 283

ATGGACAAATTAGCTAGAATTGACGAAGCCATTCGTCGCTACTATAAGACGACTAGTAACGGTGTATCTGAAGAGTTGATTGATGCTATCTTGTAT
TCTGTTGACAGTGGTGGCAAGCGCATTCGCCCACTTATCTTATTAGAGATGATTGAGGGATTTGGGGTATCGTTACAGAATGCTCATTTTGATTTG
GCTGCAGCTCTTGAAATGATTCATACAGGAAGTCTGATTCACGATGATTTGCCAGCCATGGATAATGATGATTACCGACGTGGCAGACTGACCAAT
CACAAACAATTTGGAGAAGCCACGGCCATTTTGGCGGGAGACAGCTTATTTTTAGACCCCTTTGGGTTAATAGCTCAAGCTGAATTAAATAGTGAG
GTTAAAGTAGCCTTAATCCAAGAACTTTCCCTAGCTTCAGGAACTTTTGGCATGGTTGGTGGTCAGATGTTAGATATGAAAGGGGAAAATCAAGCA
TTAAGTCTTCCTCAGTTGTCACTGATTCACCTCAATAAAACCGGAAAATTATTAGCTTTTCCTTTTAAAGCAGCAGCTCTTATAACAGAACAGGCT
ATGACTGTTCGTCAACAACTAGAGCAAGCGGGAATGCTCATCGGGCACGCCTTTCAGATTAGGGATGATATTTTAGACGTGACAGCTAGCTTTGAA
GATCTTGGAAAAACGCCTAAAAAGGACTTATTCGCAGAAAAAGCTACTTATCCAAGTTTACTGGGGTTAGAAGCCTCTTACCAACTGCTGACAGAG
AGTTTAGATCAGGCTTTGACGATTTTTCAGACACTAGAAAGCGATGTAGGCTTTAAGCCTCAAATAATTACAAAACTGATAGAAGGGTTACGACTT
AATGCC

SEQ ID 284

MDKLARIDEAIRRYYKTTSNGVSEELIDAILYSVDSGGKRIRPLILLEMIEGFGVSLQNAHFDLAAALEMIHTGSLIHDDLPAMDNDDYRRGRLTN
HKQFGEATAILAGDSLFLDPFGLIAQAELNSEVKVALIQELSLASGTFGMVGGQMLDMKGENQALSLPQLSLIHLNKTGKLLAFPFKAAALITEQA
MTVRQQLEQAGMLIGHAFQIRDDILDVTASFEDLGKTPKKDLFAEKATYPSLLGLEASYQLLTESLDQALTIFQTLESDVGFKPQIITKLIEGLRL
NA

SEQ ID 285

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTTGATACACGAGAGCAAGCGAAACGTGGTGTTATGGCAGGAATGGTGATT
AACGTTATCAATGGAGAACGTTATGATAAACCAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAAACTAAAATATGTTAGT
AGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTT
ACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGTAGATGTAGGAACAAATCAATTAGTTTGGAAGTTACGTCAGGATCATCGTGTT
CGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAAGAAGATTTCAAGGAGGGACTGCCTGAATTTGCATCGATAGATGTCTCATTTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTGTAGTGGATGGTGGACAAGTAGTGGCATTAATTAAACCACAATTTGAAGCAGGTCGTGAGCAA
ATTGGTAAAAATGGTATTGTCAAAGACAAGTTGGTTCATGAAAAGGTTTTGACAACAGTGACCAATTTCACGAAAGATTATGGATATACGGTTAAA
CATCTTGATTTTTCGCCCATTCAAGGTGGACATGGAAATATTGAGTTTTTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGAC
CAAATACAAGATGTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID 286

MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTELKLKGEKLKYVSRGGLKLEKALQVFEISVADKLTIDIGASTGGF
TDVMLQSGARLVYAVDVGTNQLVWKLRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVALIKPQFEAGREQ
IGKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPIQGGHGNIEFLMHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID 287

ATGCCTAAAGAAAGAGTAGATGTGTTAGCCTATAAGCAAGGATTATTTGAGACCAGAGAGCAAGCTAAGCGTGGTGTCATGGCAGGCTTAGTGGTC
TCTGTGATTAATGGCCAACGCTATGACAAGCCAGGTGACAAAATTGACGATGGGACTGAGTTAAAACTTAAAGGTGAAAAACTCAAATACGTCAGT
CGTGGTGGATTAAAACTGGAAAAGGGGCTGCACGTTTTTGGTGTATCAGTTGCTAATCAAATTGGGATTGATATTGGCGCTTCAACAGGTGGTTTT
ACCGATGTTATGTTACAAGATGGGGCCAAACTAGTCTATGCCGTCGACGTTGGGACTAACCAGTTGGTATGGAAACTCAGACAAGATCCACGAGTA
AGAAGTATGGAACAGTATAACTTTCGTTATGCTCAGCCAGAAGACTTTAATGAGGGACAGCCTGTATTTGCCAGTATTGATGTGTCCTTTATTTCT
CTCAGCTTGATTTTGCCAGCCCTGCATAACGTTTTGTCAGATCAGGGACAGGTTATTGCTCTCATTAAACCGCAATTTGAAGCTGGGCGCGAGCAG
ATTGGTAAAAAAGGCATCGTCAAGGACAAACAGATTCATGAAAAAGTGATTCAAAAGGTCATGGATTTTGCCTCAGGTTACGGATTTACAGTTAAG
GGACTTGATTTTTCTCCTATTCAGGGTGGTCATGGCAATATCGAATTTTTAGCTCATCTTGCTAAGTCACAGACACCTGAAACGTTAGCCCCGCAT
TTGATTCAGAAAGTTGTTGCCAAGGCACATAAGGAGTTTGAGAAACATGAAAAAGAG

SEQ ID 288

MPKERVDVLAYKQGLFETREQAKRGVMAGLVVSVINGQRYDKPGDKIDDGTELKLKGEKLKYVSRGGLKLEKGLHVFGVSVANQIGIDIGASTGGF
TDVMLQDGAKLVYAVDVGTNQLVWKLRQDPRVRSMEQYNFRYAQPEDFNEGQPVFASIDVSFISLSLILPALHNVLSDQGQVIALIKPQFEAGREQ
IGKKGIVKDKQIHEKVIQKVMDFASGYGFTVKGLDFSPIQGGHGNIEFLAHLAKSQTPETLAPHLIQKVVAKAHKEFEKHEKE

SEQ ID 289

ATGAAGAAGAGTGAACGTTTAAATTTAATTAAGCAAATTGTTCTTAACCATGCTGTTGAAACACAACATGAGTTGTTACGCAGATTGGAAGCTTAT
GGGGTAACTCTAACTCAAGCAACTATTTCACGTGATATGAATGAAATTGGCATTATAAAAGTGCCATCAGCAAAAGGTCGCTATATTTACGGTTTG
TCAAATGAAAACGACCCTATCTTTACAACTGCTGTGGCAAAGCCTATTAAAACAAGTATTTTATCAATATCAGATAAGCTACTAGGTTTAGAGCAA
TTTATCAATATTAATGTCATACCAGGTAACAGTCAATTAATTAAAACCTTCATAATGTCACATTGTCAAGAACATATTTTTAGTTTGACAGCTGAC
GATAATAGTCTCCTTTTGATTGCAAAATCAGAAGCAGATGCTGATCACATTCGTCAATCAATGATTGCAATGTTGGAGAAAAAAGAT

SEQ ID 290

MKKSERLNLIKQIVLNHAVETQHELLRRLEAYGVTLTQATISRDMNEIGIIKVPSAKGRYIYGLSNENDPIFTTAVAKPIKTSILSISDKLLGLEQ
FININVIPGNSQLIKTFIMSHCQEHIFSLTADDNSLLLIAKSEADADHIRQSMIAMLEKKD

SEQ ID 291

TTGTTGCCAAGGCACATAAGGAGTTTGAGAAACATGAAAAAGAGTGAACGACTTGAATTAATCAAAAAAATGGTTTTGACGCATCCAATTGAGACG
CAACATGACCTCTTAAGATTATTGGCAGAGCATGGGTTAGAATTAACCCAGGCTACTATTTCAAGAGACATGAATGAAATTGGTATAGTAAAGATT
CCTTCTGGCAGTGGACGTTACATCTATGGTCTTTCTCAAGATAGTGGAAAAAAGATCGTTCAAGGACCTAGATCGATAAAGAGCACTATTTTAGCT
GTATCTGACAAAACAAAAGGTTTAGAACAACACCTCTATTTAAAAGTCGTACCTGGCAATAGTAAATTAATCAAACGTTATTTATTAGCAGATTTT
TCAAAAGCTATTTTTAGTCTTATTGCTGATGATGATAGTTTATTGTTAATTGCAAAGTCTCCTTCAGAAGCAGATATGATACGCCAAGAAATTTTG
CTTTGGATGCAGGGTATAACC

SEQ ID 292

LLPRHIRSLRNMKKSERLELIKKMVLTHPIETQHDLLRLLAEHGLELTQATISRDMNEIGIVKIPSGSGRYIYGLSQDSGKKIVQGPRSIKSTILA
VSDKTKGLEQHLYLKVVPGNSKLIKRYLLADFSKAIFSLIADDDSLLLIAKSPSEADMIRQEILLWMQGIT

SEQ ID 293

ATGGAAGTTTTATCTTCCTTACGTGAAAAAGCAGATTTAATAGCTAACATCAATCGAGATAACTCTCCTCCTGAAGCCACTTTTACCAATGGCTTA
AAGCCCTCTCCGGGATTCGTTGAAATA

SEQ ID 294

MEVLSSLREKADLIANINRDNSPPEATFTNGLKPSPGFVEI

SEQ ID 295

ATGCTTTTAGAAATTTCTATTAAGAATTTCGCTATTATCGAAGAAATTTCACTTAATTTTGAAACAGGAATGACTGTTTTAACTGGTGAGACTGGT
GCAGGGAAATCTATCATTATTGATGCTATGAATATGATGTTAGGATCCCGTGCTAGCGTTGAAGTGATTCGCCATGGTGCTAACAAAGCAGAAATT
GAAGGATTTTTCTCTGTTGAAAAAAATCAATCATTAGTCCAATTATTGGAAGAAAATGGCATTGAATTAGCAGATGAATTAATTATTCGCCGAGAA
ATCTTTCAAAATGGGCGCAGCGTTAGTCGAATTAATGGGCAAATGGTGAATTTGTCAACACTAAAAGCTGTGGGGCATTATTTGGTAGACATTTAT
GGTCAGCATGACCAAGAGGAACTAATGAAACCTAACATGCACATTCTGATGTTAGATGAATTTGGTAATACAGAATTTAATGTCATAAAAGAACGT
TATCAAAGTCTTTTTGATGCTTATCGTCAGCTTCGTAAACGCGTATTGGATAAGCAAAAAAATGAACAAGAGAATAAATCACGTATTGAAATGCTA
GAATTTCAAATAGCAGAAATTGAGTCTGTAGCCCTTAAATCAGATGAAGACCAAACGCTACTCAAGCAACGTGATAAATTAATGAATCATAAGAAT
ATTGCAGATACTTTGACAAATGCATATCTTATGTTAGATAACGAAGAGTTTTCAAGTTTATCGAATGTTCGTTCTGCAATGAATGACCTTATGGCT
TTAGAAGAATTTGATCGAGAATATAAAGATCTTTCCACCAATCTTTCAGAAGCTTACTACGTTATTGAAGAAGTTACTAAACGTTTAGGTGACGTT
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AATGATGTTTTAGACTATTTTGATAACATTACTAAAGAATATAGTCTATTGACAGGTAGTGAAGAGTCCTCAGATGCTTTAGAAAAAGAATTAAAG
ATTTTAGAACACGATTTGATTGAATCAGCAAATCAATTAAGTTTAGAGCGCCATAAGCTAGCTAAACAATTGGAAAATGAAATCAAACAAGAATTA
ACAGAGCTTTATATGGAGAAAGCTGATTTCCAAGTTCAATTTACAAAAGGAAAATTTAATAAAGAAGGGAACGAAATCGTTGAATTTTATATTTCA
ACGAATCCCGGAGAGGGCTTTAAGCCATTGGTAAAAGTGGCTTCAGGAGGAGAGTTATCTCGATTGATGTTAGCTATTAAATCTGCTTTTTCACGT
AAGGAAGATAAAACTTCCATTGTATTTGATGAGGTGGATACAGGAGTTTCTGGTCGCGTGGCCCAGGCTATCGCTCAAAAAATTCACAAGATTGGT
AGTCATGGACAAGTTTTAGCAATTTCTCATTTAGCTCAGGTTATTGCAATAGCGGATTACCAATATTTTATTGAAAAAATTTCCAGTGACTCTTCA
ACAGTTTCAACGGTAAGGCTTTTAAGCTATGAAGAACGTGTAGAAGAAATCGCTAAAATGTTGGCAGGAAACAATGTAACAGACACTGCACGTACT
CAAGCTAAAGAATTACTTGGTAGT

SEQ ID 296

MLLEISIKNFAIIEEISLNFETGMTVLTGETGAGKSIIIDAMNMMLGSRASVEVIRHGANKAEIEGFFSVEKNQSLVQLLEENGIELADELIIRRE
IFQNGRSVSRINGQMVNLSTLKAVGHYLVDIYGQHDQEELMKPNMHILMLDEFGNTEFNVIKERYQSLFDAYRQLRKRVLDKQKNEQENKSRIEML
EFQIAEIESVALKSDEDQTLLKQRDKLMNHKNIADTLTNAYLMLDNEEFSSLSNVRSAMNDLMALEEFDREYKDLSTNLSEAYYVIEEVTKRLGDV
IDDLDFDAGLLQEIENRLDVINTITRKYGGDVNDVLDYFDNITKEYSLLTGSEESSDALEKELKILEHDLIESANQLSLERHKLAKQLENEIKQEL
TELYMEKADFQVQFTKGKFNKEGNEIVEFYISTNPGEGFKPLVKVASGGELSRLMLAIKSAFSRKEDKTSIVFDEVDTGVSGRVAQAIAQKIHKIG
SHGQVLAISHLAQVIAIADYQYFIEKISSDSSTVSTVRLLSYEERVEEIAKMLAGNNVTDTARTQAKELLGS

SEQ ID 297

GTGATGTTATTAGAAATTTCTATTAAAAATTTTGCTATTATTGATGAAATTTCCCTAAATTTTGAAAATGGTATGACGGTTTTGACGGGTGAAACT
GGAGCAGGAAAGTCTATTATCATTGATGCTATGAATATGATGCTTGGTGCGCGTGCTAGTACAGAAGTGATTCGTCGTGGAGCTAATAAAGCAGAA
ATTGAGGGGTTCTTTTCGGTAGATGCTACCCCAGAACTGGTTGCGTGTCTGGAATCATCAGGTATTGCTATGGAAGAAGAACTGATTATTCGCCGA
GATATCTTTGCCAATGGCAGAAGCGTGAGCCGCATTAATGGTCAGATGGTTAACCTAGCCACCTTAAAACAGGTCGGACAGTTTTTGGTAGATATT
CATGGGCAACATGACCAAGAAGAATTAATGCGACCACAGCTCCACCAGCAAATTTTGGACGCTTTTGGTGATAAGGCTTTTGAGCAATTGAAAGAG
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SEQ ID 298

VMLLEISIKNFAIIDEISLNFENGMTVLTGETGAGKSIIIDAMNMMLGARASTEVIRRGANKAEIEGFFSVDATPELVACLESSGIAMEEELIIRR
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LAFQIAEIEAAALSRGEDDRLNQERDRLMNHKQIADTLTNAYVMLDNDDFSSLSNIRSSMNDLLSIEQFDSEYKGMSTSISEAYYILEEVSKQLSD
TIDQLDFDGGRLQEIEFRLDILNSLTRKYGGNVNDVLDYYDNIVKEYQLLTGDDLSSGDLEAELKSLEKQLVAAASELSVSRHQLAEQLEAEIKAE
LKELYMEKADFKVHFTTSKFNRDGNESLEFYISTNPGEGFKPLVKVASGGELSRLMLAIKAAISRKEDKTSIVFDEVDTGVSGRVAQAIAQKIYKI
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SEQ ID 299

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GAAACTGGCTCAATCATCCAAACTCATACTGGTGAGGATGCATTTGCTGTTATGGTTCGTTATGAA

SEQ ID 300
MSKIKIVTDSSITIEPELIKELDITVVPLSVMIDGTLYSDNDLKAQGEFLNLMRGSKELPKTSQPPVGVFAEIYEKLMNEGVEHIIAIHLTHTLSG
TIEASRQGANIAGADVTVIDSTFTDQCQKFQVVEAAKLAKEGADLDTILARVEEVRQKSELFIGVSTLENLVKGGRIGRVTGLLSSLLNIKVIMEL
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SEQ ID 301
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SEQ ID 302
MEKYMGTIKIVTDSSITIEPELIKALDITVVPLSVMIDSKLYSDNDLKEEGHFLSLMKASKSLPKTSQPPVGLFAETYENLVKKGVTDIVAIHLSP
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SEQ ID 303
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CCG
SEQ ID 304
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TSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPF
YLNFPQLTKMQTVIDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFHPNNIGYQIMSNAVMEKINETRKNW
P
SEQ ID 305
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SEQ ID 306
LRLWFVMNNRHLFSGIFFFVISLCLAFLLLNIIIPKSNSRLKKSDFLKKEQVAIQYVAIGDSLTEGVGDLTHQGGFVPLLTNDLSEYFKANVNHQN
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PELTDMQKVIDDWNTKTKEVVGEYDRVYFVPINDLLYKGINGQEGIVHSSGDQTTIVNDALFTGDHFHPNNTGYQIMSNAVMEKIKKHEKKIKP
SEQ ID 307
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SEQ ID 308
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FDIFKKKP
SEQ ID 309
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TATAAGAAA
SEQ ID 310
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YKK
SEQ ID 311
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GTAGCAGATTACCTTGCTGAAGGTGAAAAAGTACAATTAATCGGTTNNNNNTTAATTAAT

SEQ ID 312
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SEQ ID 313
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SEQ ID 314
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SEQ ID 315
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SEQ ID 316
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SEQ ID 317
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SEQ ID 318
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GSEVEKEMAKLGDEWKDVNLADAQDGFYNPEKAKAEFAKAKEALTAEGVTFPVQLDYPVDQANAATVQEAQSFKQSVEASLGKENVIVNVLETETS
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SEQ ID 319
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SEQ ID 320
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SEQ ID 321

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SEQ ID 322

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SEQ ID 323

ATGGAATCGATTGATAAATCTAAATTTCGATTTGTTGAGCGCGATAGTGAAGCCTCCGAAGTGATTGATACCCCTGCTTATTCTTACTGGAAATCA
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AACTACGACTTTAATGACGTTAGTAATATCAATGACTTTTCAAAGCGTTATATTTGGCCAAATGCAGAGTACTGGTTTGGAACCGACAAAAATGGG
CAATCTCTGTTTGATGGTGTTTGGTATGGGGCACGTAATTCTATTTTAATCTCAGTTATAGCGACACTAATTAATATCACCATTGGGGTAGTGTTA
GGAGCCATATGGGGAGTTTCTAAAGCATTTGATAAAGTTATGATTGAAATTTATAACATTATCTCAAATATCCCTTCTATTATCATTGTT
TTGACCTATTCATTAGGTGCAGGATTTTGGAATTTGATTCTAGCTTTCTGTATCACTGGATGGATTGGTGTCGCCTACTCCATCCGTGTTCAAATC
TTGCGTTACCGTGATTTAGAATACAACCTTGCTAGTCAAACTTTGGGAACACCAATGTACAAGATTGCTGTTAAGAACCTCCTGCCTCAATTGGTT
TCAGTTATCATGACTATGTTGTCACAAATGCTACCAGTTTATGTATCTTCTGAGGCCTTCTTATCCTTCTTTGGGATTGGTTTACCAACCACCACT
CCAAGTTTAGGACGTTTTATTGCTAATTATTCAAGCAACTTAACAACAAATGCCTACCTCTTTTGGATTCCCTTAGTAACATTGATTTTAGTATCG
TTACCACTATACATTGTCGGACAAAACTTGGCTGATGCCAGTGACCCACGTTCACATAGA

SEQ ID 324

MESIDKSKFRFVERDSEASEVIDTPAYSYWKSVFRQFFSKKSTVFMLVILVTVLMMSFIYPMFANYDPNDVSNINDFSKRYIWPNAEYWFGTDKNG
QSLFDGVWYGARNSILISVIATLINITIGVVLGAIWGVSKAFDKVMIEIYNIISNIPSMLIIIVLTYSLGAGFWNLILAFCITGWIGVAYSIRVQI
LRYRDLEYNLASQTLGTPMYKIAVKNLLPQLVSVIMTMLSQMLPVYVSSEAFLSFFGIGLPTTTPSLGRFIANYSSNLTTNAYLFWIPLVTLILVS
LPLYIVGQNLADASDPRSHR

SEQ ID 325

ATGGAAAAAGAAACTATTTTAAGTGTTAATAATCTTCATGTTGACTTCCACACATATGCTGGAGAAGTAAAAGCAATTCGTGATGTCAACTTTGAA
TTAAAAAAAGGTGAGACTCTTGCAATCGTTGGTGAATCTGGTTCAGGAAAATCTGTAACTACCAGAACTTTAATTGGTTTAAATGCTAAAAATTCA
GAGATATCAGGGAATGTTCAATTTAAGGGGCGTAACCTTGTTGAACTATCAGAAGAAGAGTGGACTAAGGTACGCGGGAATGAGATTTCTATGATT
TTCCAAGACCCTATGACTAGTTTGGATCCAACGATGAAAATTGGCATGCAAATAGCAGAACCAATGATGATTCATCAAAAAATTTCAAAAAAGGAT
GCTTTAAAATTAGCTCTTGAGCTAATGAAAGATGTAGGTATCCCAAATGCTGAAGAGCATATTAATGATTACCCACATCAGTGGTCTGGAGGAATG
CGCCAACGTGCGGTTATAGCGATTGCTTTAGCTGCTGATCCTGAAATTCTTATTGCTGATGAACCAACGACTGCTTTAGATGTAACAATTCAAGCA
CAAATTTTGAACTTAATGAAAAAAATTCAAGCAGAACGAGACTCCTCCATTGTTTTCATAACTCATGACTTAGGGGTCGTTGCAGGGATGGCAGAC
CGTGTAGCAGTTATGTATGCAGGGAAAATTGTTGAATTTGGAACTGTTGATGAAGTCTTTTATAATCCACAACATCCATATACTTGGGGATTATTG
AATTCAATGCCGACAACCGACACAGAATCAGGTAGTTTAGAGTCAATTCCGGGAACACCACCAGATTTGTTGAACCCACCTAAAGGAGATGCATTT
GCAGCTCGTAATGAATTTGCATTAGATATTGATCATGAAGAAGAACCACCGTACTTCAAAGTTTCAGAAACACATTTCGCTGCTACATGGCTTTTA
GATGAAAGATCACCTAAGGTGCTTCCTCCATTACCGATCCAAAAACGTTGGGAAAAATGGAACGAGATTGAAGGGAGGAAAGCC

SEQ ID 326

MEKETILSVNNLHVDFHTYAGEVKAIRDVNFELKKGETLAIVGESGSGKSVTTRTLIGLNAKNSEISGNVQFKGRNLVELSEEEWTKVRGNEISMI
FQDPMTSLDPTMKIGMQIAEPMMIHQKISKKDALKLALELMKDVGIPNAEEHINDYPHQWSGGMRQRAVIAIALAADPEILIADEPTTALDVTIQA
QILNLMKKIQAERDSSIVFITHDLGVVAGMADRVAVMYAGKIVEFGTVDEVFYNPQHPYTWGLLNSMPTTDTESGSLESIPGTPPDLLNPPKGDAF
AARNEFALDIDHEEEPPYFKVSETHFAATWLLDERSPKVLPPLPIQKRWEKWNEIEGRKA

SEQ ID 327

ATGACTGAAAATCGAAAAAAAATTAGTTGAAGTCAAAAATGTTTCTTTGACCTTCAATAAAGGAAAAGCTAATGAAGTGAGAGCAATTGATAATGTT
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ATTTCTGATGGAGAAATTACCTTTAATGGAGAAGTGATCTCACATCTGAAAGGTAAAGCATTACATAGTTTTCGTAAAGACGCTCAGATGATTTTT
CAGGATCCTCAGGCTAGCTTAAACGGCCGTATGAAGATTCGTGATATCGTAGCAGAAGGTTTAGATATACATAAATTAGCTAAATCAAAATCAGAT
CGTGATAGTAAAGTTCAGGCCCTATTAGATCTTGTAGGGTTAAATAAAGATCATTTAACACGTTATCCGCATGAATTTTCAGGTGGACAACGACAA
CGTATCGGGATTGCACGTGCTTTAGCAGTAGAGCCTAAATTTATCATTGCTGATGAACCAATATCTGCCTTAGATGTTTCAATCCAAGCACAAGTT
GTTAATTTAATGCAAAAATTGCAAAGAGAACAAGGATTGACTTATTTGTTTATCGCACATGATTTGTCTATGGTAAAATACATTTCAGATCGTATC
GGTGTTATGCATTGGGGGAAACTGTTAGAAGTTGGAACATCTGATGATGTTTATAACAATCCAATCCACCCTTATACGAAGAGTCTATTATCAGCT
ATTCCAGAACCAGATCCGGAGAGTGAACGTCAACGTGTTCACCAGCCGTATAATCCAGCTATTGAGCAAGACGGACAAGAACGTCAAATGCACGAG
ATTACCCCTGGTCATTTTGTTTTATCTACACCCCAAGAAGCTGAAGAATATAAAAAACAAATATTA

SEQ ID 328

MTENRKKLVEVKNVSLTFNKGKANEVRAIDNVSFDIYEGEVFGLVGESGSGKTTVGRSILKLYDISDGEITFNGEVISHLKGKALHSFRKDAQMIF
QDPQASLNGRMKIRDIVAEGLDIHKLAKSKSDRDSKVQALLDLVGLNKDHLTRYPHEFSGGQRQRIGIARALAVEPKFIIADEPISALDVSIQAQV
VNLMQKLQREQGLTYLFIAHDLSMVKYISDRIGVMHWGKLLEVGTSDDVYNNPIHPYTKSLLSAIPEPDPESERQRVHQPYNPAIEQDGQERQMHE
ITPGHFVLSTPQEAEEYKKQIL

SEQ ID 329

ATGTCTGAGAAATTAGTCGAAGTAAAAGACCTAGAAATTTCCTTCGGAGAAGGAAAGAAAAAATTTGTTGCAGTTAAAAATGCTAATTTCTTTATT
AAAAAAGGAGAAACCTTTTCTTTAGTTGGAGAATCTGGGAGTGGTAAAACAACAATTGGTCGTGCTATTATTGGTTTGAACGATACTAGTTCAGGT
CAAATTTTATACGATGGGAAAGTAATTAATGGCAGAAAATCAAAATCAGAAGCCAATGAGCTCATTCGTAAAATTCAAATGATTTTCCAAGATCCC
GCTGCTAGTTTGAATGAACGGGCAACCGTTGACTACATCATTTCAGAAGGTCTTTATAACTTTAATCTGTTTAAAACAGAGGAAGAACGTAAAGAA
AAAATTAAGAACATGATGGCCGAAGTTGGTTTGCTATCAGAGCATTTGACGCGCTACCCTCATGAATTTTCAGGAGGTCAACGTCAGCGGATCGGT
ATCGCTAGAGCCCTAGTAATGAACCCTGAATTCGTTATTGCTGATGAACCGATTTCAGCTTTGGACGTTTCCGTTCGCGCACAGGTCTTGAATCTT

CTTAAAAGAATGCAAGCCGAAAAAGGTTTGACTTATCTCTTCATTGCCCATGATCTTTCAGTCGTTCGCTTTATTTCAGATCGTATTGCGGTTATC
CATAAAGGGGTTATTGTAGAAGTTGCAGAAACAGAAGAACTGTTTAATAACCCAATTCATCCCTACACCCAATCTTTGTTATCAGCCGTGCCTATC
CCAGATCCAATTTTAGAGCGTCAAAAAGAACTTGTTGTCTATCATCCAGACCAACATGATTATACATTAGATAAGCCATCAATGGTTGAAATCAAA
CCAAATCACTTTGTTTGGGCAAACCAAGCAGAAATTGAAAAATATCAAAAAGAATTG

SEQ ID 330

MSEKLVEVKDLEISFGEGKKKFVAVKNANFFIKKGETFSLVGESGSGKTTIGRAIIGLNDTSSGQILYDGKVINGRKSKSEANELIRKIQMIFQDP
AASLNERATVDYIISEGLYNFNLFKTEEERKEKIKNMMAEVGLLSEHLTRYPHEFSGGQRQRIGIARALVMNPEFVIADEPISALDVSVRAQVLNL
LKRMQAEKGLTYLFIAHDLSVVRFISDRIAVIHKGVIVEVAETEELFNNPIHPYTQSLLSAVPIPDPILERQKELVVYHPDQHDYTLDKPSMVEIK
PNHFVWANQAEIEKYQKEL

SEQ ID 331

ATGACAAAAAACAATAAATCTGTCAGCGAGACAGAAAAGAGCAAAGCTCAAACTTTTAATGAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGG
CGTGCC

SEQ ID 332

MTKNNKSVSETEKSKAQTFNESLILAQDERWRRA

SEQ ID 333

GTGACGGTAACTAACCAGAAAGGGACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAA
GCGAGCGCAGGCGGTTCTTTAAGTCTGAAGTTAAAGGCAGTGGCT

SEQ ID 334

MTVTNQKGTANYVPAAAVIRRSRALSGFIGRKASAGGSLSLKLKAVA

SEQ ID 335

TTGTACGCTTTGGAAACTGGAGGACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGG
TGGCGAAAGCGGCTCTCTGGTCTG

SEQ ID 336

MYALETGGLECRRGEWNSMCSGEMRRYMEEHRWRKRLSGL

SEQ ID 337

GTGGCGAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAAC
GATGAGTGC

SEQ ID 338

MAKAALWSVTDAEARKRGEQTGLDTLVVHAVNDEC

SEQ ID 339

GTGCTAGGTGTTAGGCCCTTTCCGGGGCTTAGTGCCGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGG
AAT

SEQ ID 340

MLGVRPFPGLSAAANALSTPPGEYDRKVETQRN

SEQ ID 341

TTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCC
TTC

SEQ ID 342

MKLKGIDGGPHKRWSMWFNSKQREEPYQVLTSF

SEQ ID 343

TTGTTAGTTGCCATCATTAAGTTGGGCACTCTAGCGAGACTGCCGGTAATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTAT
GACCTGGGCTACACACGTGCTACAATGGTTGGTACAACGAGTCGCAAGCCGGTGACGGCAAGC

SEQ ID 344

MLVAIIKLGTLARLPVINRRKVGMTSNHHAPYDLGYTRATMVGTTSRKPVTAS

SEQ ID 345

TTGTTTAGTTTTGAGAGGTCTTGTGGGGCCTTAGCTCAGCTGGGAGAGCGCCTGCTTTGCACGCAGGAGGTCAGCGGTTCGATCCCGCTAGGCTCC
ATTGAATCGAAAGGTTCAAATTGTTCATTGAAAATTGAATATCTATATCAAATTCCACGATCTAGAAATAGATTG

SEQ ID 346

MFSFERSCGALAQLGERLLCTQEVSGSIPLGSIESKGSNCSLKIEYLYQIPRSRNRL

SEQ ID 347

ATGAAAATTTTTGAGAAAGCTCCTGCCAAACTTAATTTAGGATTAGATATTAAAGGACGATGTGACGATGGTTATCATGAATTAGCTATGATTATG
GTTAGTATTGATCTTAATGACTACGTTACCATTTCTGAGCTAAAGGAAGATTGTATTGTTATCGATTCTGATAGTAGCAAAATGCCTTTAAATAAT
GATAATGATGTGTTTAAAGCTGCAGATATAATCAAAAATCAATATGGTATTAATAAAGGTGTTCATATTAGATTAGAAAAATCCATTCCTGTCTGT
GCAGGACTGGGGGGTGGTTCTACTGATGCTGCTGCTACAATAAGAGCTCTTAATCGATTATGGAATCTTCAAATGGACTATGACGAAATGGTTGCT
ATTGGTTTTAAAATTGGTAGTGATGTTCCTTATTGTCTTGGTGGGGGATGTTCGTTAGTATTAGGTAAAGGTGAAATTGTTAAACCCTTACCGACA
TTGAGACCATGTTGGATAGTTCTGGTTAAGCCGGATTTTGGTATTTCAACTAAATCCATTTTTAGAGATATTGATTGTAAGTCTATAAGTAGAGTT
GATATTGATTTATTAAAGTCTGCTATTTTGTCATCAGATTATCAGTTAATGGTCAAATCTATGGGAAATTCACTCGAGGATATTACAATTACTAAA
AATCCAGTTATAAGTACAATAAAAGAACGTATGTTAAATTCTGGAGCCGATGTTGCATTAATGACAGGAAGTGGACCAACTGTTTTTTCAATGTGT
TCTACAGAGAAAAAAGCTGATCGTGTTTTTAATAGTATGAAAGGTTTTTGCAAAGAAGTTTATAAAGTTAGGTTGTTGAGA

SEQ ID 348

MKIFEKAPAKLNLGLDIKGRCDDGYHELAMIMVSIDLNDYVTISELKEDCIVIDSDSSKMPLNNDNDVFKAADIIKNQYGINKGVHIRLEKSIPVC
AGLGGGSTDAAATIRALNRLWNLQMDYDEMVAIGFKIGSDVPYCLGGGCSLVLGKGEIVKPLPTLRPCWIVLVKPDFGISTKSIFRDIDCKSISRV
DIDLLKSAILSSDYQLMVKSMGNSLEDITITKNPVISTIKERMLNSGADVALMTGSGPTVFSMCSTEKKADRVFNSMKGFCKEVYKVRLLR

SEQ ID 349

ATGATGGATATTGGTATACCGATTGGTAGTGATGTGCCTTATTGCTTGCTTTCAGGTTGTGCCCAAGTCACTGGTAAAGGTGAAGTGGTTTGTCGC
ATTTTGGGGCTGTTATCGTCTTGGGTGGTTTTGGTTAAACCAGATTTTGGTATCTCGACT

SEQ ID 350

MMDIGIPIGSDVPYCLLSGCAQVTGKGEVVCRILGLLSSWVVLVKPDFGIST

SEQ ID 351

ATGACAGTTTTAGAACAAAAATTAGACCATTTAGTGAGTCAAATCTTGCTTAAAGCAGAAAATCAACATGAATTATTGTTTGGTACTTGTCAAAGT
GATGTTAAATTGACTAATACGCAAGAACACATTCTGATGCTTTTATCACAAGAGCAGTTGACAAATTCTGATTTAGCTAAGAAGTTAAATATTAGT
CAGGCAGCTGTAACTAAAGCAGTAAAAAGTTTAATTTCTCAGGATATGTTGAAAGCGAATAAAGATTCTAAAGATGCTCGTATTACTTATTTTGAG
TTATCTGAACTTGCTAAACCCATTGCAGATGAACACACACATCATCATGACAATACGTTAGGGGTTTACGGAAGATTAGTAAATCATTTTTCAAAG
GACGAAAAGGTCGTTTTAGAACGTTTTCTTGATCTTTTCTCTAGAGAATTAGAAGGG

SEQ ID 352
MTVLEQKLDHLVSQILLKAENQHELLFGTCQSDVKLTNTQEHILMLLSQEQLTNSDLAKKLNISQAAVTKAVKSLISQDMLKANKDSKDARITYFE
LSELAKPIADEHTHHHDNTLGVYGRLVNHFSKDEKVVLERFLDLFSRELEG

SEQ ID 353
ATGGGGATTTTAGAAAAAAAACTTGATAACTTAGTAAATACTATTTTATTAAAAGCAGAAAATCAGCATGAGTTATTATTTGGAGCTTGTCAAAGT
GACGTTAAGCTTACTAATACGCAAGAACATATTTTAATGTTACTATCTCAGCAACGTCTCACTAATACAGATTTGGCTAAGGCATTAAATATTAGT
CAGGCGGCAGTAACTAAGGCTATCAAGAGTTTGGTCAAACAAGACATGTTAGCAGGAACTAAGGATACGGTTGATGCTAGGGTGACTTATTTTGAA
TTAACCGAGTTAGCTAAGCCTATTGCGTCAGAACATACCCATCATCATGATGAAACCTTAAATGTTTACAACCGTTTATTACAAAAATTCTCCGCG
AAAGAATTAGAGATTGTAGATAAGTTTGTAACAGTTTTTGCTGAGGAATTAGAAGGG

SEQ ID 354
MGILEKKLDNLVNTILLKAENQHELLFGACQSDVKLTNTQEHILMLLSQQRLTNTDLAKALNISQAAVTKAIKSLVKQDMLAGTKDTVDARVTYFE
LTELAKPIASEHTHHHDETLNVYNRLLQKFSAKELEIVDKFVTVFAEELEG

SEQ ID 355
ATGCGATATATTACAGTTAGTGGTCTTACTTTTCAGTACGATAGCGATCCTGTGCTGGAAGGGGTTAATTACCATTTAGACAGTGGGGAGTTTGTT
ACCTTAACAGGTGAAAATGGGGCTGCTAAATCAACTTTAATAAAGGCTACTTTAGGTATTTTAACGCCCAAAGTGGGTACAGTTAATATCTCTAAA
GAAAACAAAGAAGGAAAAAAATTACGTATTGCCTATTTACCTCAACAGATTGCAAGTTTTAACGCTGGCTTTCCATCGTCAGTTTATGAATTTGTG
AAATCTGGACGATACCCTAGAAATGGTTGGTTTAGAAGACTGACTAAACATGATGAAGAACATATTAGGGTTAGTTTAGAAGCTGTTGGTATGTGG
GATAATCGCCATAAAAAGATAGGAAGTTTATCTGGCGGTCAAAAGCAGAGGGCTGTCATTGCTAGGATGTTTGCTTCTGATCCAGATATTTTTGTA
TTGGATGAGCCAACAACTGGTATGGACGCAGGGACTACTGAGAAATTTTATGAGTTAATGCATCATAATGCTCATAAGCATGGTAAGTCTGTTTTG
ATGATTACTCACGATCCTGATGAAGTAAAGGGGTATGCTGACCGAAATATTCATCTTGTTAGGAACCAATCTTTACCATGGCGTTGTTTCAATGTC
CATACAAACGAAATGGAGGTTGAATCAGATGCTACT

SEQ ID 356
MRYITVSGLTFQYDSDPVLEGVNYHLDSGEFVTLTGENGAAKSTLIKATLGILTPKVGTVNISKENKEGKKLRIAYLPQQIASFNAGFPSSVYEFV
KSGRYPRNGWFRRLTKHDEEHIRVSLEAVGMWDNRHKKIGSLSGGQKQRAVIARMFASDPDIFVLDEPTTGMDAGTTEKFYELMHHNAHKHGKSVL
MITHDPDEVKGYADRNIHLVRNQSLPWRCFNVHTNEMEVESDAT

SEQ ID 357
ATGAGATACATATCAGTGAAAAATCTCTCCTTTCAATATGAAAGTGAGCCAGTTTTAGAAGGGATCACTTATCATTTAGATAGTGGAGAATTTGTC
ACCATGACCGGTGAAAATGGTGCTGCAAAGTCAACCTTAATAAAAGCAACCTTAGGAATTTTACAACCAAAGGCTGGACGAGTTACTATTGCTAAA
AAAAATAAAGACGGTAAACAATTAAGAATTGCTTACTTGCCGCAGCAAGTAGCTAGCTTTAACGCTGGTTTTCCATCCACCGTTTACGAGTTTGTC
AAATCAGGTCGCTACCCACGTAGTGGTTGGTTTAGACATTTGAACAAACACGATGAAGAGCATGTGCAAGCAAGCTTAGAAGCAGTCGGCATGTGG
GAAAACCGTCATAAGAGAATTGGTAGTTTATCAGGTGGTCAAAAACAACGTGTGGTTATTGCCCGTATGTTTGCTTCTGACCCTGATATTTTTGTG
CTAGACGAGCCAACAACGGGAATGGATAGCGGTACTACTGATACCTTTTATGAACTGATGCACCACAGTGCACATCAACATGGGAAATCCGTTCTG
ATGATTACCCATGACCCAGAAGAAGTGAAGGCTTATGCTGATCGGAACATTCATTTAGTCAGAAACCAAAAACTTCCTTGGCGTTGTTTCAACATT
CATGAAGCTGAAACAGATGACGAAAAAGGAGGTCATGGTCATGCT

SEQ ID 358
MRYISVKNLSFQYESEPVLEGITYHLDSGEFVTMTGENGAAKSTLIKATLGILQPKAGRVTIAKKNKDGKQLRIAYLPQQVASFNAGFPSTVYEFV
KSGRYPRSGWFRHLNKHDEEHVQASLEAVGMWENRHKRIGSLSGGQKQRVVIARMFASDPDIFVLDEPTTGMDSGTTDTFYELMHHSAHQHGKSVL
MITHDPEEVKAYADRNIHLVRNQKLPWRCFNIHEAETDDEKGGHGHA

SEQ ID 359
TTGTATACAGTACGCAAATACTCTAATACAACTGCCGCCAAAGTAACAACGAAAATAGTTGACCATGTAGGCGAGATACCTAAAACAACGCCTAAT
GCAACACCGGCTAAGGAAACG

SEQ ID 360
MYTVRKYSNTTAAKVTTKIVDHVGEIPKTTPNATPAKET

SEQ ID 361
ATGTCCATACAAACGAAATGGAGGTTGAATCAGATGCTACTTGATATGCTTTCCTATGATTTTATGCAACGAGCGCTCTTAGCAGTTGTGGCTATT
AGTATTTTTGCTCCAATTTTAGGCATCTTCCTAATTTTACGTCGTCAGAGTTTGATGAGTGATACTTTGAGTCACGTTTCCTTAGCCGGTGTTGCA
TTAGGCGTTGTTTTAGGTATCTCGCCTACATGGTCAACTATTTTCGTTGTTACTTTGGCGGCAGTTGTATTAGAGTATTTGCGTACTGTATACAAA
CATTATATGGAAATATCAACTGCTATCCTGATGTCGATGGGGTTGGCTATATCTTTAATCGTTATGAGTAAAGCTCATAATGTTGGTAATGTCAGT
CTTGAACAGTATTTATTTGGTTCTATTATTACTATTGGGAAGGAACAAGTGATTGCTTTGTTTGTTATTGCATTAATCACTTTTATTTTAACCATC
CTATTTATTAGACCAATGTATATATTAACGTTTGATGAGGATACAGCTTTTGTAGATGGATTGCCTGTGCGTACAATGTCTATTTTGTTCAATGTT
GTTACAGGTATTGCTATTGCATTAACAATTCCTGCCGCAGGTGCTCTATTGGTGTCAACTATTATGGTTTTACCAGCTAGTATTGCTATGCGGTTA
GGTCGAAATTTTAAAACTGTTATTTTTCTGGGTATGTTAATTGGATTTGTGGGAATGGTAGCTGGTATTTTCCTTTCGTATTATTGGGAGACACCT
GCTAGTGCAACAATAACGATGATTTTTATTGGCATTTTCCTATTAGTTAGCTTAGTAGGCTTGCTTCGCAAACGT

SEQ ID 362
MSIQTKWRLNQMLLDMLSYDFMQRALLAVVAISIFAPILGIFLILRRQSLMSDTLSHVSLAGVALGVVLGISPTWSTIFVVTLAAVVLEYLRTVYK
HYMEISTAILMSMGLAISLIVMSKAHNVGNVSLEQYLFGSIITIGKEQVIALFVIALITFILTILFIRPMYILTFDEDTAFVDGLPVRTMSILFNV
VTGIAIALTIPAAGALLVSTIMVLPASIAMRLGRNFKTVIFLGMLIGFVGMVAGIFLSYYWETPASATITMIFIGIFLLVSLVGLLRKR

SEQ ID 363
ATGGTCATGCTTGATATTTTATTCTATGATTTCATGCAACGGGCGGTAATGGCGGTAGTTGCCATTAGTATTTTTGCTCCGATTTTAGGTATTTTC
CTTATTTTACGTCGTCAAAGTTTGATGAGCGATACCCTTAGTCATGTTTCTTTGGCTGGGGTAGCGCTTGGGGTAGTCCTTGGTATTTCACCAACC
ATCACTACTATTATTGTTGTGGTTTTAGCTGCTATTTTGTTAGAATACCTGCGTGTAGTTTACAAACACTACATGGAGATTTCAACGGCGATTTTG
ATGTCACTTGGCTTGGCCCTATCTCTGATTATTATGAGTAAGTCGCATAGTTCATCAAGCATGAGTTTAGAACAATACCTTTTTGGATCGATCATC
ACGATTAGTATGGAACAAGTTGTCGCCTTGTTTGCTATTGCTGCGATTATTTTAATCTTGACCGTTCTCTTCATTAGACCGATGTACATTCTGACC
TTTGATGAAGATACTGCTTTTGTAGATGGTTTGCCCGTTCGCTTGATGTCTGTTCTATTCAATATCGTCACTGGGGTTGCTATTGCTTTGACCATT
CCAGCAGCAGGAGCACTTTTGGTTTCTACCATTATGGTCTTGCCAGCAAGTATCGCAATGAGATTGGGTAAAAACTTTAAAACAGTTATCTTACTG
GGAATTGTCATCGGTTTTAGCGGTATGTTATCTGGTATTTTCTTATCTTATTTCTTTGAAACGCCAGCTAGTGCCACTATTACCATGATTTTCATT
AGTATTTTCCTCTTAGTTAGTCTAGGTGGAATGCTTAAAAAACGGTTATTT

SEQ ID 364
MVMLDILFYDFMQRAVMAVVAISIFAPILGIFLILRRQSLMSDTLSHVSLAGVALGVVLGISPTITTIIVVVLAAILLEYLRVVYKHYMEISTAIL
MSLGLALSLIIMSKSHSSSSMSLEQYLFGSIITISMEQVVALFAIAAIILILTVLFIRPMYILTFDEDTAFVDGLPVRLMSVLFNIVTGVAIALTI
PAAGALLVSTIMVLPASIAMRLGKNFKTVILLGIVIGFSGMLSGIFLSYFFETPASATITMIFISIFLLVSLGGMLKKRLF

SEQ ID 365
GTGACTCCAATATACGAAGGAAATAATTTAGTACCTAGCCGAGTTGAACTTCAGTATGTTGGAATTGATAAACAAGGAAAACTTCTAGAAATCAAA
TTAGGCGGCGGCAAAGAACAAGTTGATGAATACGGCGTCACAACTGTTACATTAGAAAATACGTCTCCACTCGCAAAAATTGATTACAAAACTGGT
ATGCTAATCAAAGAAGATGGGAAACAGGCAGAAGAAGGTGAAGATCCAAATAGCGATGCTGATGAAAACGAAGCAGCTATTGAAAGTGCATCTGAT

ATAGAAGAAAATACTAACACTAATACTTCTGAATCAGATACAAATAATGTAGCTCCCCAAAATAGAATCGTCTACGTTGCAAATAAGGGTCGTTCA
AATACTTATTGGTATAGTTTAGAAAACATAAAAAATGCAAATACCGCTAATATCGTTCAAATGACTGAACAAGAAGCGTTAAATCAACACAAACAT
CACAGCACTACTGAAGCACAA

SEQ ID 366

MTPIYEGNNLVPSRVELQYVGIDKQGKLLEIKLGGGKEQVDEYGVTTVTLENTSPLAKIDYKTGMLIKEDGKQAEEGEDPNSDADENEAAIESASD
IEENTNTNTSESDTNNVAPQNRIVYVANKGRSNTYWYSLENIKNANTANIVQMTEQEALNQHKHHSTTEAQ

SEQ ID 367

ATGGATATGTCTAAATCAAATCGTCGTACTTGGCAAGGTTTAGTTGTTATTTTAATAGCTATTCTCACCACTTTTACCACAAGTACTGTTACGGCA
GCCAGAAAAATTAGAAATTTCCCTGATACCACGGAAATTTTGTTAGGAACGAAGGCGACTGAGACACCAGGAATCTTACCATTCACTGGTAGCTAC
CAATTAGTTTTGGGCGATCTTGACAATCTGCAAAGGCCAACCTTCGCACACATCCAGCTAAAAGATCAAGATGAGCCTAATATTAAACGAAAAGGA
CTTAAATTCAATCCTCCTGGCTGGCATAATTACAAATTGACTGACGCTAATGGAAAAACAACTTGGTTAATGGACCGTGGCCATTTAGTTGGTTAC
CAATTTAGCGGCTTAAATGACGAGCCTAAAAACCTAGTTACAATGACAAAATATCTTAATACTGGCTTTAGTGACAAAAATCCTTTAGGAATGCTC
TATTATGAAAATAGATTAGATAGCTGGTTAGCTCTACACCCTAACTTCTGGCTAGACTATAAAGTTACTCCTGTTTATCATAAAAATGAGTTAGTT
CCTCGCCAAGTAGTTCTACAGTATGTTGGAATTGATGAAAATGGAGATCTACTTCAAATTAAGTTAGGTAGTGAAAAAGAAAGTGTAGACAACTTT
GGAGTAACATCAGTTACATTAGATAACGTATCTCCTTTAGCTGAATTGGATTACCAAACAGGAATGATGCTAGATTCAACTCAAAACGAAGAAGAT
AGTAATTTAGAAACCGAAGAGTTTGAAGAAGCGGCT

SEQ ID 368

MDMSKSNRRTWQGLVVILIAILTTFTTSTVTAARKIRNFPDTTEILLGTKATETPGILPFTGSYQLVLGDLDNLQRPTFAHIQLKDQDEPNIKRKG
LKFNPPGWHNYKLTDANGKTTWLMDRGHLVGYQFSGLNDEPKNLVTMTKYLNTGFSDKNPLGMLYYENRLDSWLALHPNFWLDYKVTPVYHKNELV
PRQVVLQYVGIDENGDLLQIKLGSEKESVDNFGVTSVTLDNVSPLAELDYQTGMMLDSTQNEEDSNLETEEFEEAA

SEQ ID 369

ATGAATATTTTTGATGAACTCAAAGAACGTGGACTCGTTTTTCAGACAACTGACGAAGATGCTTTACGCAAAGCTCTTGAAGAAGGTTCTGTCTCT
TACTATACTGGCTACGATCCTACGGCTGACAGCCTTCATCTTGGACATTTAGTTGCTATTTTAACCTCTCGTCGCTTACAACTTGCTGGTCACAAG
CCTTATGCACTTGTGGGAGGCGCAACTGGACTTATTGGGGACCCTTCATTTAAAGATGTTGAGCGCAGTTTACAAACAAAGAAAACTGTAGTTAGT
TGGGGTAATAAAATCCGCGGTCAATTATCTAATTTTCTAGAGTTTGAAACAGGTGATAACAAAGCTGTATTGGTAAATAATTATGATTGGTTCAGC
AATATTAGTTTCATTGATTTCTTACGAGATGTTGGTAAATATTTTACTGTCAATTATATGATGAGTAAAGAATCTGTTAAAAAACGTATCGAAACA
GGGATTTCCTATACTGAATTTGCTTATCAAATTATGCAAGGATATGACTTTTACGAATTAAATAAGAACTATAATGTCACTTTGCAAATTGGTGGT
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TCTACAGGAAAAAAATTCGGAAAATCTGAAGGAAATGCTGTTTGGCTTGATGCTGACAAAACCTCTCCTTATGAAATGTACCAATTTTGGCTCAAT
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CTATTTGCTGGCAATATAAAAGGATTGTCTGTTAAAGAGCTCAAACAAGGTTTACGTGGAGTACCAAATTATCACGTTCAGACGGAAGATAACCTC
AATATCATAGACCTTCTAGTCACTTCAGGAGTTGTCAATTCTAAACGTCAAGCTCGAGAAGATGTCTCCAATGGAGCTATTTATATTAATGGAGAT
CGTATTCAAGATTTAGAATATACTATCTCAGAAAATGATAAGCTTGAAAATGAAATTACAGTCATTCGTCGTGGAAAGAAAAAATACTTTGTATTA
AACTTTAAA

SEQ ID 370

MNIFDELKERGLVFQTTDEDALRKALEEGSVSYYTGYDPTADSLHLGHLVAILTSRRLQLAGHKPYALVGGATGLIGDPSFKDVERSLQTKKTVVS
WGNKIRGQLSNFLEFETGDNKAVLVNNYDWFSNISFIDFLRDVGKYFTVNYMMSKESVKKRIETGISYTEFAYQIMQGYDFYELNKNYNVTLQIGG
SDQWGNMTAGTELIRRKSNGVSHVMTVPLITDSTGKKFGKSEGNAVWLDADKTSPYEMYQFWLNVMDADAVRFLKIFTFLSLKEIEDIRIQFEEAP
HQRLAQKTLAREVVTLVHGEKAYKEAVNITEQLFAGNIKGLSVKELKQGLRGVPNYHVQTEDNLNIIDLLVTSGVVNSKRQAREDVSNGAIYINGD
RIQDLEYTISENDKLENEITVIRRGKKKYFVLNFK

SEQ ID 371

ATGAATATTTTTGAAGAACTCAAAGCTCGTGGCTTGGTCTTTCAAACGACTGATGAACAAGCCCTTGTCAAAGCATTAACAGAAGGGCAAGTATCC
TATTATACCGGTTATGATCCAACCGCTGACAGCCTTCATCTGGGCCATCTAGTGGCTATCTTAACATCTCGTCGCTTGCAACTAGCAGGGCACAAA
CCTTACGCTCTTGTGGGGGGTGCCACAGGTTTAATTGGTGATCCTTCCTTTAAAGATGCAGAGCGCAGCCTTCAAACCAAAGAAACAGTTTTGGAG
TGGAGTGACAAGATTAAAGGGCAGTTGTCTACTTTCCTTGATTTTGAAAATGGTGATAATAAAGCAGAGCTTGTCAACAACTACGACTGGTTCTCG
CAAATCAGCTTTATTGACTTCCTCCGTGATGTCGGTAAATACTTCACCGTTAACTACATGATGAGTAAAGACTCTGTTAAAAAACGCATTGAAACA
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ACTTAC

SEQ ID 372

MNIFEELKARGLVFQTTDEQALVKALTEGQVSYYTGYDPTADSLHLGHLVAILTSRRLQLAGHKPYALVGGATGLIGDPSFKDAERSLQTKETVLE
WSDKIKGQLSTFLDFENGDNKAELVNNYDWFSQISFIDFLRDVGKYFTVNYMMSKDSVKKRIETGISYTEFAYQIMQGYDFYELNDKHNVTLQIGG
SDQWGNMTAGTELLRKKADKTGHVMTVPLITDSTGKKFGKSEGNAVWLDADKTSPYEMYQFWLNVMDDDAVRFLKIFTFLSLDEIAEIETQFNAAR
HERLAQKTLAREVVTLVHGEEAYKQALNITEQLFAGNIKNLSANELKQGLSNVPNYHVQSIDNHNIVEILVAAKISPSKRQAREDVQNGAIYINGD
RVQDLDYQLSNDDKIDDQLTVIRRGKKKYAVLTY

SEQ ID 373

ATGTTTAAAGGTAATAAGAAGTTGAATAGTTCTAAATTAGGTGATTACACACCACTTGAATTTGGTTCTATTTTTTTAAGAATTGTAAAGCTTTTA
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CGCGCTATTGAAGAGATTCAACAGGGAGGGTATACTATTAAAACTACTATCAATAAATCTGTTTATCAAGCCATGCAGGATGCTGCAGCTCAATAC
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GGACCTGGAACGATGACCTATCGTTTTGCTATTGGGGGAACTGATAGTGATTATCAAAAAGCTTGGTCTACTTTGGGTGGAAAACGA

SEQ ID 374

MFKGNKKLNSSKLGDYTPLEFGSIFLRIVKLLSDFIYVIILLFVMLGVGLAVGYLASQVDSVKVPSKNSLVTQVNTLTRVSRLTYSDKSQISEIAT
DLQRTPVAKDAISDNIKKAIIATEDENFNDHKGVVPKAVLRAAAGSVLGFGESSGGSTLTQQLLKQQILGDDPSFKRKSKEIIYALALERYMDKDS
ILSDYLNVSPFGRNNKGQNIAGIEEAAQGIFGVSAKDLTIPQAAFLAGLPQSPIVYSPYTADAQLKSDKDLSFGIKRQKNVLYNMYRTRALTKDEY
KSYKDYDIKKDFIKPAVATTNHHDYLYYSALSEAQKVMYNYLIKKDNVSEHDLKNDETRATYRHRAIEEIQQGGYTIKTTINKSVYQAMQDAAAQY
GGLLDDGTGKVQMGNVLTDNSSGAIIGFIGGRNYSENQNNHAFDTARSPGSSIKPILPYGIAIDQGMLGSGSVLSNYPTTYSSGEKIMHADEEGTA
MVNLQESLDISWNIPAFWTYKMLRDRGVDVKNYMEKLDYPIENFGIESLPLGGGIDTSVAQQTNLYQMIANGGVYHKQYMIESIEDSNGKVIYNHE
SKPVRVFSKATATILQQLLHGPINSGKTTTFKNRLQGLNSGLAGVDWIGKTGTTNSTSDVWLMLSTPKVTLGGWAGHDNNASLAKLTGYNNNANYM
AHLVNAINNADGNTFGKSERFRLDDSVIKAKVLKSTGLQPGVVTVNGRRITVGGESTTSYWAKNGPGTMTYRFAIGGTDSDYQKAWSTLGGKR

SEQ ID 375

ATGAGGTATTTTATGGTGAAATGGAACACGAAACAAAAGCGTATAAGTCATCAAAGATTAGGTCTCTTGGATTTGGGGCCGGTGCTATTACGTACG
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CAGCAATTAGTCAAGCAACAAGTTTTGGGAGACGATCCCACATTTAAGCGCAAGTCTAAGGAGATCGTTTACGCTCTTGCCTTAGAGCGTTATATG
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AAAAAT

SEQ ID 376

MRYFMVKWNTKQKRISHQRLGLLDLGPVLLRTLRLLSNFFYIVIFLFGMMGFGMAFGYLASQIESVKVPSKESLVKQVESLTMISQMNYSDNSLIS
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SKDNILCDYLNVSPFGRNNKGQNIAGVEEAARGIFGVSAKDLTVPQAAFLAGLPQSPIVYSPYLSTGQLKSEKDMAYGIKRQQNVLFNMYRTGVLS
KKEYEDYKAYPIQKDFIQPGSAIVNNHDYLYYTVLADAKKAMYSYLIKRDKVSSRDLKNDETKAAYEERALTELQQGGYTITTTINKPIYNAMQTA
AAQFGGLLDDGTGTVQMGNVLTDNATGAVLGFVGGRDYALNQNNHAFNTVRSPGSSIKPIIAYGPAIDQGLMGSASVLSNYPTTYSSGQKIMHADS
EGTAMMPLQEALNTSWNIPAFWTQKLLRKKGVDVENYMTKMGYKIADYSIESLPLGGGIEVSVAQQTNAYQMLSNNGLYQKQYIVDKITASDGTVV
YKHENKPIRIFSAATATILQELLRGPITSGATTTFKNRLAAINPWLANADWIGKTGTTENYTDVWLVLSTPKVTLGGWAGHDDNTSLAPLTGYNNN
SNYLAYLANAINQADPNVIGVGQRFNLDPGVIKANVLKSTGLQPGTVNVNGHTFSVGGEMTTSLWSQKGPGAMTYRFAIGGTDADYQKAWGNFGFR
KN

SEQ ID 377

TTGGCAGGACATGAAGTTCAGTACGGAAAACACCGTACACGTCGTAGCTTTTCAAGAATTAAGGAAGTTCTTGATTTACCAAACTTAATTGAAATT
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ACAACACTAGTCCGTGCACTTGGTTTCTCTGGAGACGATGAAATTGTTGACATCTTTGGTGACAGTGAACTTGTTCGCAATACTATTGAAAAAGAC
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CGTAGTCTTTTAGTTGCACGTTTCTTTGATCCACGTCGTTATGACTTAGCGGCTGTTGGTCGTTATAAGATTAATAAAAAACTGAATCTTAAAACA
CGCCTATTGAACCAAACAATCGCTGAAAATTTAGTTGATGGTGAAACAGGAGAGATTCTTGTTGAAGCTGGAACCGTTATGACACGAGATGTCATT
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CCTCAACAAATCATTAACATTCGTCCAGTGACTGCCGCCGTTAAAGAATTCTTTGGTTCATCACAGCTGTCACAATTCATGGACCAACACAACCCT
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TCTGAAGTCGTTCAAGAAGAT

SEQ ID 378

MAGHEVQYGKHRTRRSFSRIKEVLDLPNLIEIQTDSFQDFLDAGLKEVFEDVLPISNFTDTMDLEFVGYELKEPKYTLEEARIHDASYSAPIFVTF
RLVNKETGEIKTQEVFFGDFPIMTEMGTFIINGGERIIVSQLVRSPGVYFNDKVDKNGKVGYGSTVIPNRGAWLELETDAKDIAYTRIDRTRKIPF
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DAVIMSERLVKEDVYTSVHLEEFESETRDTKLGPEEITREIPNVGEDSLRDLDEMGIIRIGAEVKEGDILVGKVTPKGEKDLSAEERLLHAIFGDK
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RMNIGQVMELHLGMAARNLGIHIATPVFDGASSEDLWETVQEAGMDSDAKTVLYDGRTGEPFDNRVSVGVMYMIKLHHMVDDKLHARSVGPYSLVT
QQPLGGKAQFGGQRFGEMEVWALEAYGASNVLQEILTYKSDDVTGRLKAYEAITKGKPIPKPGVPESFRVLVKELQSLGLDMRVLDEDDNEVELRD
LDEGEDDDVMHVDDLEKARVKQEAEEKQAEQVSEVVQED

SEQ ID 379

TTGGCAGGACATGAAGTTCGATACGGAAAACACCGTACACGTCGTAGCTTTTCAAGAATCAAAGAAGTTCTTGATTTACCAAATTTGATTGAAATT
CAAACTGACTCATTCCAAGATTTCCTCGATTCAGGTTTGAAAGAAGTATTTGAAGATGTACTTCCTATTTCAAACTTTACGGATACTATGGAACTT
GAATTTGTTGGTTACGAATTTAAAGAACCTAAATATACCCTTGAAGAAGCTCGTATCCACGATGCAAGTTATTCTGCACCAATCTTTGTTACCTTC
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CGTCTTTTGAACCAAATCATTGCTGAAAACCTTGTGGATGCTGAAACTGGCGAAATTTTGGTAGAAGCTGGAACTGAGATGACTCGTAGCGTCATC
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CGGATGAATATTGGTCAGGTTATGGAACTTCACCTTGGTATGGCTGCTCGTAATCTTGGTATTCACATTGCAACACCTGTCTTTGACGGGGCTTCA
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CGTGTATCCGTTGGTGTCATGTATATGATCAAACTTCACCACATGGTTGATGATAAACTTCATGCCCGTTCTGTAGGACCATACTCACTTGTTACC
CAACAGCCACTTGGTGGTAAAGCTCAATTTGGTGGACAACGTTTTGGTGAGATGGAGGTTTGGGCCCTTGAAGCTTATGGTGCATCAAATGTTCTT
CAAGAAATCTTGACCTACAAGTCAGATGACGTCACAGGACGTTTGAAAGCCTATGAAGCGATTACTAAAGGTAAACCAATTCCAAAACCAGGTGTA
CCAGAATCCTTCCGTGTTCTTGTAAAAGAATTGCAATCGCTTGGTCTTGATATGCGTGTGCTTGACGAGGATGATAATGAAGTGGAACTTCGTGAT
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ACTGACGAAAAA

SEQ ID 380

LAGHEVRYGKHRTRRSFSRIKEVLDLPNLIEIQTDSFQDFLDSGLKEVFEDVLPISNFTDTMELEFVGYEFKEPKYTLEEARIHDASYSAPIFVTF
RLVNKETGEIKTQEVFFGDFPIMTEMGTFIINGGERIIVSQLVRSPGVYFNDKVDKNGKVGYGSTVIPNRGAWLELETDSKDIAYTRIDRTRKIPF
TTLVRALGFSGDDEIVDIFGESDLVRNTIEKDIHKNPSDSRTDEALKEIYERLRPGEPKTADSSRSLLIARFFDARRYDLAAVGRYKVNKKLNIKT

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ILAEMSYFLNLAEGLGKVDDIDHLGNRRIRAVGELLANQFRIGLARMERNVRERMSVQDNDVLTPQQIINIRPVTAAVKEFFGSSQLSQFMDQHNP
LSELSHKRRLSALGPGGLTRDRAGYEVRDVHYTHYGRMCPIETPEGPNIGLINNLSSFGHLNKYGFIQTPYRKVDRATGTVTNEIVWLTADEEDEY
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DSGAAVIAQQNGKVVFSDAEKVEIRRQDGSLDVYHITKFRRSNSGTAYNQRTLVKVGDIVEKGDFIADGPSMENGEMALGQNPVVAYMTWEGYNFE
DAVIMSERLVKEDVYTSVHLEEFESETRDTKLGPEEITREIPNVGEEALKDLDEMGIIRIGAEVKEGDILVGKVTPKGEKDLSAEERLLHAIFGDK
SREVRDTSLRVPHGGDGIVRDVKIFTRANGDELQSGVNMLVRVYIAQKRKIKVGDKMAGRHGNKGVVSRIVPVEDMPYLPDGTPVDIMLNPLGVPS
RMNIGQVMELHLGMAARNLGIHIATPVFDGASSEDLWDTVREAGMDSDAKTVLYDGRTGEPFDNRVSVGVMYMIKLHHMVDDKLHARSVGPYSLVT
QQPLGGKAQFGGQRFGEMEVWALEAYGASNVLQEILTYKSDDVTGRLKAYEAITKGKPIPKPGVPESFRVLVKELQSLGLDMRVLDEDDNEVELRD
LDEGEDDDIMHVDDLEKARSKQAQETQEVSETTDEK

SEQ ID 381

ATGATGATAAATCGAAGAAAGGTAAAACTAGTGGTTGACGTAAATCGTTTTAAAAGTATGCAAATCACATTAGCATCACCAAGTAAGGTCCGTTCA
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CCAGCGGGTACTGGTATGGCTCGTTACCGTAATATTGAACCACTTGCTGTTAATGAAGTTGAGATTATTGAAGGAACTCCTGTTGATGCAGAAGTT
ACGGAAGTATCAACACCTACAACAGAAGAT

SEQ ID 382

MMINRRKVKLVVDVNRFKSMQITLASPSKVRSWSYGEVKKPETINYRTLKPEREGLFDEVIFGPTKDWECACGKYKRIRYKGIICDRCGVEVTRAK
VRRERMGHIELKAPVSHIWYFKGIPSRMGLTLDMSPRALEEVIYFAAYVVIDPMDTPLEPKSLLTEREYREKLQEYGYGSFVAKMGAEAIQDLLKR
VDLDAEIAVLKEELKSATGQKRVKAVRRLDVLDAFKKSGNKPEWMVLNILPVIPPDLRPMVQLDGGRFAASDLNDLYRRVINRNNRLARLLELNAP
GIIVQNEKRMLQEAVDALIDNGRRGRPITGPGSRPLKSLSHMLKGKQGRFRQNLLGKRVDFSGRSVIAVGPTLKMYQCGVPREMAIELFKPFVMRE
IVARDLAGNVKAAKRMVERGDERIWDILEEVIKEHPVLLNRAPTLHRLGIQAFEPVLIDGKALRLHPLVCEAYNADFDGDQMAIHVPLSEEAQAEA
RLLMLAAEHILNPKDGKPVVTPSQDMVLGNYYLTMEDAGREGEGMIFKDHDEAVMAYQNGYVHLHTRVGIAVDSMPNKPWTEEQKHKIMVTTVGKI
LFNDIMPEDLPYLIEPNNANLTEKTPDKYFLEPGQDIQAVIDNLEINIPFKKKNLGNIIAETFKRFRTTETSAFLDRLKDLGYYHSTLAGLTVGIA
DIPVIDNKAEIIDAAHHRVEDINKAFRRGLMTEEDRYVAVTTTWREAKEALEKRLIETQDPKNPIVMMMDSGARGNISNFSQLACMRGLMAAPNGR
IMELPILSNFREGLSVLEMFFSTHGARKGMTDTALKTADSGYLTRRLVDVAQDVIIREDDCGTDRGLTITAITDGKEVTETLEERLIGRYTKKSIK
HPETGEILVGADTLITEDMAAKVVKAGVEEVTIRSVFTCNTRHGVCRHCYGINLATGDAVEVGEAVGTIAAQSIGEPGTQLTMRTFHTGGVASNTD
ITQGLPRIQEIFEARNPKGEAVITEVKGEVVAIEEDSSTRTKKVFVKGQTGEGEYVVPFTARMKVEVGDEVARGAALTEGSIQPKRLLEVRDTLSV
ETYLLAEVQKVYRSQGVEIGDKHVEVMVRQMLRKVRVMDPGDTDLLPGTLMDISDFTDANKDIVISGGIPATSRPVLMGITKASLETNSFLSAASF
QETTRVLTDAAIRGKKDHLLGLKENVIIGKIIPAGTGMARYRNIEPLAVNEVEIIEGTPVDAEVTEVSTPTTED

SEQ ID 383

GTGGTTGACGTAAATCGTTTTAAAAGTATGCAAATCACATTAGCCTCACCAAGTAAGGTCCGTTCATGGTCTTATGGTGAAGTTAAAAAACCTGAA
ACAATCAACTACCGTACATTAAAACCAGAACGTGAAGGACTCTTTGACGAAGTCATCTTTGGTCCAACAAAAGACTGGGAATGTGCGTGTGGTAAG
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CGTGAAGGTTTGAGCGTTTTGGAAATGTTCTTCTCAACCCACGGTGCACGTAAAGGGATGACCGATACGGCCCTTAAAACAGCCGACTCAGGTTAC
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GGTGAGCCTGGTACTCAGCTTACCATGCGTACCTTCCACACGGGTGGTGTAGCCTCAAATACCGATATCACCCAGGGTCTTCCTCGTATTCAAGAG
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AACATTGAACCACAAGCGATGAATGAGATTGAAGTGATTGATCATACAGAAGTCTCAGCAGAAGCCGTTTTTACAGCAGAAGCAGAA

SEQ ID 384

VVDVNRFKSMQITLASPSKVRSWSYGEVKKPETINYRTLKPEREGLFDEVIFGPTKDWECACGKYKRIRYKGIVCDRCGVEVTRAKVRRERMGHIE
LKAPVSHIWYFKGIPSRMGLTLDMSPRALEEVIYFAAYVVIDPKDTPLEPKSLLTEREYREKLQEYGHGSFVAKMGAEAIQDLLKRVDLAAEIAEL
KEELKSASGQKRIKAVRRLDVLDAFNKSGNKPEWMVLNILPVIPPDLRPMVQLDGGRFAASDLNDLYRRVINRNNRLARLLELNAPGIIVQNEKRM
LQEAVDALIDNGRRGRPITGPGSRPLKSLSHMLKGKQGRFRQNLLGKRVDFSGRSVIAVGPTLKMYQCGVPREMAIELFKPFVMREIVAKEYAGNV
KAAKRMVERGDERIWDILEEVIKEHPVLLNRAPTLHRLGIQAFEPVLIDGKALRLHPLVCEAYNADFDGDQMAIHVPLSEEAQAEARLLMLAAEHI
LNPKDGKPVVTPSQDMVLGNYYLTMEDAGREGEGMIFKDKDEAVMAYRNGYAHLHSRVGIAVDSMPNKPWKDNQRHKIMVTTVGKILFNDIMPEDL
PYLQEPNNANLTEGTPDKYFLEPGQDIQEVIDRLDINVPFKKKNLGNIIAETFKRFRTTETSAFLDRLKDLGYYHSTLAGLTVGIADIPVIDNKAE
IIDAAHHRVEEINKAFRRGLMTDDDRYVAVTTTWREAKEALEKRLIETQDPKNPIVMMMDSGARGNISNFSQLAGMRGLMAAPNGRIMELPILSNF
REGLSVLEMFFSTHGARKGMTDTALKTADSGYLTRRLVDVAQDVIIREDDCGTDRGLLIRAITDGKEVTETLEERLQGRYTRKSVKHPETGEVLIG
ADQLITEDMARKIVDAGVEEVTIRSVFTCATRHGVCRHCYGINLATGDAVEVGEAVGTIAAQSIGEPGTQLTMRTFHTGGVASNTDITQGLPRIQE
IFEARNPKGEAVITEVKGNVVEIEEDASTRTKKVYVQGKTGMGEYVIPFTARMKVEVGDEVNRGAALTEGSIQPKRLLEVRDTLSVETYLLAEVQK
VYRSQGVEIGDKHVEVMVRQMLRKVRVMDPGDTDLLPGTLMDISDFTDANKDIVISGGIPATSRPVLMGITKASLETNSFLSAASFQETTRVLTDA
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SEQ ID 385

ATGTATCAAGTTGTAAAAATGTTTGGTGATTGGGAACCATGGTGGTTTATTGAAGGTTGGGAGGAAGATATTACTGAAATTGCTGAGTATGATACC
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TGGAGTATAAAAGAAAAACGTTGGTGTGAAGAATGTGATGAGTACCTCCAACAGTATCATTCCTTAATGTTATTGAAAGAATGGCAAGAAATTCCT
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SEQ ID 386

MYQVVKMFGDWEPWWFIEGWEEDITEIAEYDTLSEALLYFQEEWDRGQEKWPYFQSKSSLLATFWSIKEKRWCEECDEYLQQYHSLMLLKEWQEIP
KEESIERFEVFNKIAELPSACSLNL

SEQ ID 387

ATGTATCAAGTAATTAAAATGTATGGTGATTGGGAGCCTTGGTGGTTCATCGATGGATGGCAAGACGATATTATAGATGAGCAACAATTTAGTGAC
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AGCAATAATTATATCCCTGAATTTGAACAACGAAATGATTCACCACAGGTAGCTTATCTTTGCAAGTTAAACCTT

SEQ ID 388

MYQVIKMYGDWEPWWFIDGWQDDIIDEQQFSDWQEALDYFNQEWQRMKAIFPSYHSQKNLLATFWEKEDKRWCEDCDEDLQQFHSLLLLKNKDIVP
SNNYIPEFEQRNDSPQVAYLCKLNL

SEQ ID 389

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CCAACTTTT

SEQ ID 390

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YRGQESLVIRILYSGHQDLKYWFDNIKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDAL
IKLSLRHRPDILIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVYDRLIELGVNYQELENSLKLIAYQRLIGGGSLIDFETGNFKKHSSDKW
NRQVDILAEEGHISKKQAQVEKIIPQETTESSPTF

SEQ ID 391

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TGCTTAGCATTAATTGCTTACCAAAGGTTACTTAATGGAGGAGCATTGATTGACTCTACTCAAAACGAATTTGAATATTATTCCTCATCGAACTGG
AATCAACAAATTGATCAGCTTCTTGAGGCAGGACATCTCAATCCCAAGCAAGCTAAGCTTGAAAAAATTATC

SEQ ID 392

MVQALAKAILAKAEQVHAQDIYILPRADQYDLFLRIGDERRLVDVYQSDRMAPLISHFKFVAGMIVGEKRRCQVGSCDYKLSKDKQLSLRLSSVGD
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IKLSLRHRPDILVIGEIRDSQTARAVIRASLTGAMVFSTVHAKSISGVYARLLELGVTKAELSNCLALIAYQRLLNGGALIDSTQNEFEYYSSSNW
NQQIDQLLEAGHLNPKQAKLEKII

SEQ ID 393

ATGGTCACCTTCTTAAAGAGGAGTAAGTTATTGTCTGATTGTTATACAGATAGTATGAATAAGGCATTATTAGAGGGAAAAGATTTATCAAAAATG
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TATTTAGCTAATCTTTTGTTAGTTAGAAAAAAAGTAATAGAAGTAGCTACTTACCCATTGATATTATTGTCTTTTCTGGTGCTAATTATGATTGGC
CTTAGGAATTATTTAATGCCCCAATTAGGAGAAAATAATTTTGCAACTAGACTGATTACAAATGTGCCGAATATTTTCTTATTACTTTTAGCAGTT
GTACTTATTTTTAGTTTAATATTTTATATTATTCAAAAGCGATTGTCGCGCATTAAAGTAGCTTGTTTTTTAACAACAATTCCCTTAGTTGGATCA
TATGTTAAGCTTTATTTAACTGCTTACTATGCCCGTGAGTGGGGAAATTTATTAAGTCAAGGTATTGAATTGGACCAAATTGTTAAAGTAATGCAA
AATCAGAAATCCAAACTTTTTAGGGAAATAGGATATGACATGGAAGAAGGTTTTCTATCAGGTAAAGCATTTCACCAAAAAGTATTAGACTATCCG
TTTTTCTTAACTGAGCTTAGTTTAATGATTGAATATGGCCAAGTTAAGGCGAAATTAGGAACAGAGTTAGATATATATGCTGATGAGAAGTGGGAG
GATTTTTTTACAAAATTAGCTAGAGCGACCCAGTTAATCCAACCCGTTATTTTATTTTTGTAGCTCTTATCATTGTTATGATTTATGCAGCAATG
CTGTTACCAATGTATCAAAATATGGAGATATTATCA

SEQ ID 394

MVTFLKRSKLLSDCYTDSMNKALLEGKDLSKMLGELGFSDTVITQVALADLHGNISRSLLKIESYLANLLLVRKKVIEVATYPLILLSFLVLIMIG
LRNYLMPQLGENNFATRLITNVPNIFLLLLAVVLIFSLIFYIIQKRLSRIKVACFLTTIPLVGSYVKLYLTAYYAREWGNLLSQGIELDQIVKVMQ
NQKSKLFREIGYDMEEGFLSGKAFHQKVLDYPFFLTELSLMIEYGQVKAKLGTELDIYADEKWEDFFTKLARATQLIQPVIFIFVALIIVMIYAAM
LLPMYQNMEILS

SEQ ID 395

TTGATCAGCTTCTTGAGGCAGGACATCTCAATCCCAAGCAAGCTAAGCTTGAAAAAATTATCTAGTAAACATCAGCATAAATTCATTCAATTACTA
GCTAATCTTTTATCTACAGGATTTAGCTTCGCAGAGGTTATTGCTTTTTTAAAAAGAAGCCAGTTGCTTCAGCTAGATTATGTTCTTAAAATGGAA
GAGTCTTTATTAAAAGGACAAGGCTTAGCAGATATGTTGTCGGGTTTAGGTTTTTCAGATGCTATTCTTACTCAAATTAGTTTAGCTGATAGACAC
GGTAATATTGAAACAACATTAGTAGCGATTCAACATTACTTGAACCAAATGGCAAGGATCAGACGAAAAACTGTTGAAGTTATCACCTATCCTCTT
ATTCTTTTACTTTTTCTTTTTGTGATGATGCTAGGGTTGAGACGCTATTTAGTCCCTCAATTAGAAACTCAAAATCAGATAACTTACTTTCTTAAC
CATTTTCCTGCCTTCTTTATAGGTTTTTGCTCAGGTCTTATTTTGTTGTTCGGGATGGTATGGCTACGATGGCGATCTCAAAGCCGCTTGAAACTC
TATAGTCGGCTAAGCCGTTATCCTTTTTTAGGTAAACTGTTAAAACAATACTTAACTAGTTATTATGCTAGAGAATGGGGTACGTTAATAGGTCAA
GGTCTTGATTTGATGACTATTTTAGACATTATGGCCATTGAGAAATCCTCACTAATGAAAGAATTAGCTGAGGACATCAGAATGAGTCTGCTTGAA
GGGCAAGCCTTTCACATTAAAGTAGCTACCTACCCTTTTTTTAAAAAAGAATTAAGTTTAATGATTGAATACGGTGAAATCAAATCGAAACTGGGG
GCTGAGTTGGAAATCTATGCCCAGGAAAGCTGGGAACAATTTTTTAGTCAGCTTTATCAAGTGACACAACTTATTCAACCAGCTATTTTTTTAGTA
GTTGCTGTGACAATCGTCATGATTTATGCGGCAATCCTATTACCAATTTACCAAAATATGGGAGGTATTTTT

SEQ ID 396

LISFLRQDISIPSKLSLKKLSSKHQHKFIQLLANLLSTGFSFAEVIAFLKRSQLLQLDYVLKMEESLLKGQGLADMLSGLGFSDAILTQISLADRH
GNIETTLVAIQHYLNQMARIRRKTVEVITYPLILLLFLFVMMLGLRRYLVPQLETQNQITYFLNHFPAFFIGFCSGLILLFGMVWLRWRSQSRLKL
YSRLSRYPFLGKLLKQYLTSYYAREWGTLIGQGLDLMTILDIMAIEKSSLMKELAEDIRMSLLEGQAFHIKVATYPFFKKELSLMIEYGEIKSKLG
AELEIYAQESWEQFFSQLYQVTQLIQPAIFLVVAVTIVMIYAAILLPIYQNMGGIF

SEQ ID 397

ATGAAAAATTTATTGTTAAAATGTAAGGATAAGAAGGTTAAAGCATTTACACTTTTAGAATGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTA
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AATGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAACTTTATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAAT
AAAGATGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGTCAAATGAGTCAGACCAAAAGTATG
GTAAAACTTGTTTTTTATTTTAAGGACGGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAACT

SEQ ID 398

MKNLLLKCKDKKVKAFTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLLTQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSN
KDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSMVKLVFYFKDGLKRTFYYDFKEET

SEQ ID 399

TTGAGTAAACAATTAAGTAACATAAAAGCTTTTACCCTTCTAGAGGCGTTAATAGCCTTACTCGTGATATCAGGGTCTTTATTGGTTTATCAAGGT
TTGACCCGAACCCTCCTTAAACATAGCCATTATCTAGCCCGTCATGATCAAGATAATTGGCTCTTATTTTCTCATCAATTGCGAGAGGAGTTAAGT
GGAGCAAGGTTTTACAAAGTAGCTGATAATAAACTATACGTTGAAAAAGGAAAGAAAGTACTAGCTTTTGGCCAATTTAAAAGTCATGATTTTCGA
AAATCAGCTAGTAATGGAAAAGGGTATCAACCCATGTTATTTGGAATATCACGTAGTCATATTCACATAGAGCAGTCACAGATTTGCATTACTTTA
AAGTGGAAAAGTGGGTTAGAAAGGACTTTTTATTATGCCTTTCAAGAC

SEQ ID 400

LSKQLSNIKAFTLLEALIALLVISGSLLVYQGLTRTLLKHSHYLARHDQDNWLLFSHQLREELSGARFYKVADNKLYVEKGKKVLAFGQFKSHDFR
KSASNGKGYQPMLFGISRSHIHIEQSQICITLKWKSGLERTFYYAFQD

SEQ ID 401

ATGAATTTTGAAAAAATTGAGACAGCCTATGAGCTGATTTTAGAAAATATCCAAACGATTGAGAACCAATTAAAAACTCATATTTATGATGCCTTA
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GAATGGCGTCGCACTTTCCAGTTCATTTTTATCAAATCTGCGCAAACAGAGCAATTACAAGCTAATCATCAGTTTACGCCAGATAGTATTGGTTTT
ATCTTGTTATTTCTTTTGGAAGAATTAACGAGTCAAGAGACAGTGGATGTCTTGGAAATTGGAAGTGGAACTGGGAATTTAGCTCAGACTCTCCTC
AATAACAGCTCGAAAGAGTTAAATTATATGGGCATTGAAGTTGATGATCTTTTGATTGATCTATCAGCAAGCATTGCTGAAATTATAGGTTCTAGT
GCCCAATTTATCCAAGAGGATGCTGTTAGACCACAAATTTTGAAAGAAAGCGATGTAATCATTAGTGATTTACCAGTTGGCTATTATCCTAATGAT
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GTTTTAACTCTACCAGAAACTATTTTTGGAAGTCGTCAAAATGCGAAATCTATATTTGTTCTCAAGAAGCAAGCAGAACAAAAACCAGAAACCTTT
GTATATCCGCTGACAGATTTGCAAAATCGTGAGAATATGGCAAACTTCATTGAAAATTTTCAAAAATGGAGCAGAGAAAATAGTCATTACTCAAAA
AATATGATAAAA

SEQ ID 402

MNFEKIETAYELILENIQTIENQLKTHIYDALIEQNSYYLGSSCDLDMVVVNNQKLRQLDLSQEEWRRTFQFIFIKSAQTEQLQANHQFTPDSIGF
ILLFLLEELTSQETVDVLEIGSGTGNLAQTLLNNSSKELNYMGIEVDDLLIDLSASIAEIIGSSAQFIQEDAVRPQILKESDVIISDLPVGYYPND
GIAKRYAVSSSKEHTYAHHLLMEQSLKYLKKDGIAIFLAPENLLTSPQSDLLKEWLKGYADVIAVLTLPETIFGSRQNAKSIFVLKKQAEQKPETF
VYPLTDLQNRENMANFIENFQKWSRENSHYSKNMIK

SEQ ID 403

GTGACACTTCTTTTCATTTCAAGTGTAATTTGGTATGATAAGGTTATGACTTTTGAAAAAATTGAAGAAGCTTATCAGCTGCTCTTAGAGAACTGT
CAACTAATTGAAAATGATCTAAAAACACATATATACGATGCCATTGTTGAACAAAACTCCTTTTATTTAGGGGCTGAGGGAGCTAGTCCTCAAGTT
GCTCAAAATAGTGATAAACTGAAAGCCTTGTGCCTGACAAAAGAAGAATGGCGTAAGGCCTACCAGTTTCTTTTTATTAAGGCAGCTCAGACTGAG
CAACTCCAAGCCAACCATCAGTTCACACCAGATGCTATTGGCTTCATTCTGCTGTATCTTTTGGAACAATTGAGTGATAAAGATAGCTTAGAGGTA
CTTGAGATTGGAAGTGGAACAGGGAACCTAGCCCAAACCCTTCTCAACAACACGAGCAAGAGCCTTGATTATGTAGGGATTGAACTTGATGATCTC
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GACATTGTCATCAGTGACTTACCAGTTGGTTATTATCCTAACGATGATATTGCCAAACGGTACAAGGTGGCTAGTTCAGATAAGCATACCTATGCC
CATCATTTATTAATGGAACAGTCTTTAAAATACTTGAAAAAAGACGGTTTTGCGATTTTTCTGGCACCAGTCAATTTATTGACGAGCCCTCAGAGC
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GAAAATTTCAAAAAATGGAAACTGAGTAATGTCAAT

SEQ ID 404

VTLLFISSVIWYDKVMTFEKIEEAYQLLLENCQLIENDLKTHIYDAIVEQNSFYLGAEGASPQVAQNSDKLKALCLTKEEWRKAYQFLFIKAAQTE
QLQANHQFTPDAIGFILLYLLEQLSDKDSLEVLEIGSGTGNLAQTLLNNTSKSLDYVGIELDDLLIDLSASIAEIMDSSAHFIQEDAVRPQLLKES
DIVISDLPVGYYPNDDIAKRYKVASSDKHTYAHHLLMEQSLKYLKKDGFAIFLAPVNLLTSPQSQLLKQWLKDYAQVVTLITLPDSIFGHPSNAKS
IIVLQKQTDHPMETFVYPIRDLKLAENIHDFMENFKKWKLSNVN

SEQ ID 405

ATGTCAAAAACAATAGCAATTAATGCTGGAAGTTCAAGTTTGAAATGGCAATTATATGAAATGCCAGAGGAGAAAGTAGTTGCCAAAGGGATTATC
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AAAATTCTTTTAGAAGATCTAACAAAACATGGTATTATCAAAGACTTTAATGAAATTACAGGTGTTGGTCATCGTGTCGTTGCTGGTGGTGAATAT
TTTAAAGAGTCTGCTTTAGTAGATGATAAAGTTGTAGAACAGGTTGAAGAATTATCAGCTTTAGCTCCACTCCACAACCCAGCAGCTGCAGCAGGG
ATTCGTGCGTTTAGAGAAATCTTACCAGATATCACGAGTGTATGTGTATTTGATACAGCCTTCCATACAACAATGCAACCTCATACCTACTTATAT
CCAATCCCACAAAAGTACTATACTGATTATAAAGTACGTAAATACGGTGCACACGGGACAAGCCACCAATACGTTGCACAAGAAGCAGCTAAGCAA
TTAGGACGTCCTTTAGAAGAATTAAAATTAATCACAGCACATGTGGGTAATGGTGTTTCTATTACAGCAAATTATCATGGACAGTCTATTGATACA
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GAATTGGAAGATGCAGCAGCTGTTGTTAATATGCTTAACAAACAATCAGGATTGCTTGGAGTATCAGGAACTTCAAGTGATATGCGAGATATTGAA
GCAGGTCTTCAAAGTAAAGATCCAAATGCAGTGTTAGCCTATAATGTCTTTATTGACCGTATTAAGAAATTTATTGGACAATACTTGGCAGTATTA
AATGGCGCGGATGCTATTATTTTTACTGCAGGTATGGGAGAAAATGCGCCATTAATGCGTCAAGATGTTATCGCAGGATTATCATGGTTTGGCATT
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SEQ ID 406

MSKTIAINAGSSSLKWQLYEMPEEKVVAKGIIERIGLKDSISTVKFDDKKDEQILDIVDHTQAVKILLEDLTKHGIIKDFNEITGVGHRVVAGGEY
FKESALVDDKVVEQVEELSALAPLHNPAAAAGIRAFREILPDITSVCVFDTAFHTTMQPHTYLYPIPQKYYTDYKVRKYGAHGTSHQYVAQEAAKQ
LGRPLEELKLITAHVGNGVSITANYHGQSIDTSMGFTPLAGPMMGTRSGDIDPAIIPYLVANDPELEDAAAVVNMLNKQSGLLGVSGTSSDMRDIE
AGLQSKDPNAVLAYNVFIDRIKKFIGQYLAVLNGADAIIFTAGMGENAPLMRQDVIAGLSWFGIELDPEKNVFGYFGDITKPDSKVKVLVIPTDEE
LMIARDVERLKAK

SEQ ID 407

ATGTCAAAGACAATTGCAATTAATGCAGGTAGTTCTAGTTTAAAATGGCAACTTTATCAGATGCCAGAAGAAGCAGTGTTAGCACAAGGAATTATT
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TTCAAAGAATCCGTTGTGGTTAATGACAAAGTTCTTGAACAGATTGAAGAATTATCCGTTTTAGCTCCACTTCACAATCCTGGAGCGGCGGCAGGG
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CCAATTCCTCAAAAATATTATACGGACTACAAGGTTCGTAAATATGGGGCGCATGGGACAAGTCATAAATATGTAGCGCAAGAAGCTGCTAAAATG
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GAGTTAAAAGACGCTGCTGACGTTGTTAATATGTTAAACAAAAAATCAGGTCTTAGTGGGGTGTCAGGCATTTCTAGTGATATGCGTGATATCGAG
GCTGGTTTACAAGAAGATAATCCAGATGCTGTTTTAGCTTACAATATCTTTATTGATCGCATTAAAAAATGCATTGGTCAATATTTTGCTGTTTTG
AATGGAGCAGATGCTTTGGTCTTTACAGCTGGTATGGGTGAAAATGCACCATTGATGCGTCAAGATGTTATTGGTGGCTTAACATGGTTCGGAATG
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TTGTGCATCGCGCGTGACGTTGAACGTTTAAAAAATACAAAA

SEQ ID 408

MSKTIAINAGSSSLKWQLYQMPEEAVLAQGIIERIGLKDSISTVKYDGKKEEQILDIHDHTEAVKILLNDLIHFGIIAAYDEITGVGHRVVAGGEL
FKESVVVNDKVLEQIEELSVLAPLHNPGAAAGIRAFRDILPDITSVCVFDTSFHTSMAKHTYLYPIPQKYYTDYKVRKYGAHGTSHKYVAQEAAKM
LGRPLEELKLITAHIGNGVSITANYHGKSVDTSMGFTPLAGPMMGTRSGDIDPAIIPYLIEQDPELKDAADVVNMLNKKSGLSGVSGISSDMRDIE
AGLQEDNPDAVLAYNIFIDRIKKCIGQYFAVLNGADALVFTAGMGENAPLMRQDVIGGLTWFGMDIDPEKNVFGYRGDISTPESKVKVLVISTDEE
LCIARDVERLKNTK

SEQ ID 409

ATGAAAAATTCTCTACAAAAGTTACGAAAATCTAGGAAATTAAGTCAAGCAGAACTTGCAGTTGCACTTGGAGTTACTAGGCAAACTATTATTTCT
CTAGAAAAAGAGAAATACACGGCATCTTTGGAGCTAGCATTTAAGATAGCGCGTTATTTTGATAAACAAATTGAGGAAGTTTTTATTTATACAGAA
AGTGAAGGAGGA

SEQ ID 410

MKNSLQKLRKSRKLSQAELAVALGVTRQTIISLEKEKYTASLELAFKIARYFDKQIEEVFIYTESEGG

SEQ ID 411

ATGAAGGAGATGGCAATGGAGGTTATTCTTAAAAATCGGCTCAAAGAATTACGAGCTAGAGATGGAATTAATCAAACGGAAATGGCTAAACTGGCA
GGAGTATCGAGGCAGACCATCAGTCTCATTGAGCGTAACGAGTACACCCCATCAGTTATAATTGCCATGAAAATTGCAAAGGTATTTCAGGAACCA
GTTGAAGAGGTGTTTCGTCTAGTGGAGGTCGAGGAA

SEQ ID 412
MKEMAMEVILKNRLKELRARDGINQTEMAKLAGVSRQTISLIERNEYTPSVIIAMKIAKVFQEPVEEVFRLVEVEE

SEQ ID 413
TTGGAGGTTTTTGTGTCATTTATTATTAGAAAAGGCAAAATTTTAGCTTTGCTAATAGCATTTTTAGTTATTAATCAACTTGTTCCTATATTGGCT
GTGTGGCTCCTAAAGAATCACTATCAAACGCCTTTTACTAGTATATTGTTGATTGGCTTAGAATTACTTATTATTGCTCTTTTCCTTTATTATGCC
AAGGTTAAACAAATAATCAGATGGAAAGCATTATTGACAAGGAAAGCATTAGTTACTATTCTCTTAGGTTGGTTATCATTGAGGGTTCCACAAATT
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TTAATTTTTGCCATAATTGGTGCCCCTATTATGGAAGAAATTATATTTCGCTATATTATCCCTAAAGAACTTTTTGCGAAACATCAAAAATGGGGT
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GTTTATTATAAAACTGAGCACTTAGAATATAGTATAATGATTCATTTTATTAACAATGCTCTTGCTTATAGCGTGTTAATCAGTACAATGATGAAT
AAC

SEQ ID 414
MEVFVSFIIRKGKILALLIAFLVINQLVPILAVWLLKNHYQTPFTSILLIGLELLIIALFLYYAKVKQIIRWKALLTRKALVTILLGWLSLRVPQI
IGYLIMTMQGVKDTANQTVIMELTKQLPLALMLIFAIIGAPIMEEIIFRYIIPKELFAKHQKWGFVIGTLAFALIHSPSDIGSFIIYAGMGAILSF
VYYKTEHLEYSIMIHFINNALAYSVLISTMMNN

SEQ ID 415
ATGAAAGGATTCATTAATTATTTAAAAATAGCAGTGCTCATTATTCTGGCTATGGTTTTCAATGTCCTTCCGATGATTTTATTGCAAAAGCAACAC
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CAAGACACTTTTATTAAACAGCAAAAAATGAGATTGGTTGACTGGGGTTATTTAGCATTATTTTGGTTAATCATCCGTGTGATAGCTATTGTAGGT
ACCCTTGTTAACCAGCTATGGTCTGGTCAACAAGTGAGTGCTAATGATGCTGCAATACATACCTTAGCTAGACTTATCAAAGGTGGTTTCCCGCTT
TATACTGCCCTATTTGTACTTGTGATAGCTTTTATCGCTCCTATTATGGAAGAACTAGTCTTTAGAGGATTTCCTATGATTGATCTCTTCAAAGGA
AAATCACTTAAGGTGGCAGGTTTAGTGACCTCTCTTGTTTTTGCTTTACCACATGCCACCAATAGTGTTGAATTTATCATGTACAGCTGTATGGGC
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TCAATAGGCTTAGGAGTCATA

SEQ ID 416
MKGFINYLKIAVLIILAMVFNVLPMILLQKQHDIPMVLNWGIGIFYLVIVGSVLIVLWGLYQAKQDTFIKQQKMRLVDWGYLALFWLIIRVIAIVG
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IFLFVAYQRRGNLKDAILLHIFNNLIEVILLMSIGLGVI

SEQ ID 417
ATGAAAATTGGAATTATCGGCGTCGGAAAAATGGCCAGTGCAATTATTCAAGGCCTCAAACAAACCCAACATGACATTATCATATCCGGATCTTGC
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GTATCAGATGAGTTACGACAATTAGCCAAAGAAATTACGGATAGTTTTGGAAGTAGCTTTGATATAGCAGAAACCAATTTTGATACCTTCACTGCT
CTAGCAGGTTCTAGCCCTGCCTATATCTATCTATTTATAGAAGCCTTAGCTAAAGCAGGTGTAAAATATGGATTTCCAAAAGAACAAGCACTCTCT
ATTGTAGGACAGACTGTCTTAGCTTCTAGTCAAAACCTATTACAAGGACAAAATAGCACCTCTGACTTAATCGACAACATTTGTAGCCCAGGCGGA
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SEQ ID 418
MKIGIIGVGKMASAIIQGLKQTQHDIIISGSCLERSKEIAERLDVTYAESHQSLINQADIIMLGIKPQLFEKVLLPLDITKPIISMAAGISLARLS
QLTRSDLPLIRIMPNINAQILQSCTAICYNNHVSDELRQLAKEITDSFGSSFDIAETNFDTFTALAGSSPAYIYLFIEALAKAGVKYGFPKEQALS
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SEQ ID 419
ATGAAAATTGGCATTATTGGTGTTGGCAAAATGGCTAGCGCTATCATCAAAGGCCTTAAACAAACACCCCATGAACTTATCATTTCAGGATCATCT
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ACATTCGTAGGACAAGACCTTCCGCTGCTACGTATCATGCCAAACATGAATGCACAAATTCTCCAAAGCAGTACCGCTTTAACGGGAAATGCTTTG
GTGTCCCAGGAATTACAAGCACGTGTTCGAGACTTAACAGATAGCTTTGGTAGCACATTTGATATTAGTGAAAAGGATTTTGACACCTTTACCGCT
TTAGCAGGGTCAAGTCCTGCCTATATTTATCTCTTTATTGAGGCTTTGGCTAAGGCTGGCGTCAAGAATGGCATACCTAAAGCAAAGGCGCTGGAG
ATTGTTACTCAAACAGTATTGGCTAGCGCCAGCAATCTCAAGACCAGTTCTCAAAGTCCGCACGATTTCATTGACGCTATTTGTAGCCCCGGTGGC
ACAACTATTGCTGGTCTGATGGAGTTAGAACGCCTTGGCCTCACAGCTACTGTCAGCTCTGCCATTGACAAAACCATCGATAAAGCTAAAAGCTTG

SEQ ID 420
MKIGIIGVGKMASAIIKGLKQTPHELIISGSSLERSKEIAEQLALPYAMSHQDLIDQVDLVILGIKPQLFETVLKPLHFKQPIISMAAGISLQRLA
TFVGQDLPLLRIMPNMNAQILQSSTALTGNALVSQELQARVRDLTDSFGSTFDISEKDFDTFTALAGSSPAYIYLFIEALAKAGVKNGIPKAKALE
IVTQTVLASASNLKTSSQSPHDFIDAICSPGGTTIAGLMELERLGLTATVSSAIDKTIDKAKSL

SEQ ID 421
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GCTGCAAATGGTGGTACCGATGCTGGGGCTGCTCACCTAAAAAATAGTGGTATTCCTTCTACAACTATCGGTGTCTGTGCACGCTACATTCATTCT
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AAAGGTTAT

SEQ ID 422
MSDLFNKIKTVTELDGIAGYEHNIRNFLRQEITPLVDQVETDGLGGIFGVKNTHETNAPKVMVAAHMDEVGFMVSHIQPDGTFRVLEVGGWNPLVV
SSQRFTLYTRSGDAIPVISGSVPPHFLRGQSGGTTLPKISDIVFDGGFTDKNEAESFGIAPGDIIVPKSETILTANQKHIMSKAWDNRYGVLMVTE
LLKSLKDQSLSNTLIAGANVQEEVGLRGAHVSTTKFNPDIFLAVDCSPAGDIYGEQGKIGEGTLIRFYDPGHIMLKDMRDFLLTTAEEAGIKYQYY
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SEQ ID 423
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GCGCACATGGACGAAGTCGGTTTTATGGTCAGTGATATCAAAGTTGACGGAACGCTACGCGTGGTTGGTATCGGTGGTTGGAACCCACTTGTTGTC
AGTTCACAACGGTTTACCCTTTACACACGCACTGGCCAAGTTATTCCCCTTATTTCAGGATCGGTACCTCCCCATTTTTTACGTGGGGCAAATGGC
TCTGCTAGTCTACCACATATCGAAGATATTGTGTTTGATGGTGGCTTTACGGATAAGGCAGAAGCTGAAAGATTTGGTATTACACCGGGTGATATT
ATTATCCCTCAATCTGAAACGATCCTAACAGCCAATCAAAAAAATATTATTTCAAAAGCTTGGGACAATCGCTATGGCGTTCTCATGATAACAGAA
ATGCTTGAAGCGTTAAAAGGACAAGACCTTAACAACACCCTAATTGCAGGTGCTAACGTTCAAGAAGAAGTTGGTCTGCGCGGAGCCCACGTCTCA
ACCACCAAGTTCGACCCTGAACTCTTTTTCGCAGTAGATTGTTCGCCTGCTGGTGATATTTATGGCAATCCTGGAACAATCGGAGATGGTACCTTG
TTGCGTTTCTACGACCCAGGCCATGTCATGCTCAAAGATATGCGCGACTTCTTACTGACTACTGCTGAGGAAGCTGGTGTCAATTTCCAATACTAT
TGTGGCAAGGGAGGCACAGATGCAGGTGCTGCACACCTTCAAAATGGTGGTGTCCCATCAACAACCATCGGAGTCTGTGCACGCTACATTCACTCT
CATCAAACCCTCTACGCTATGGATGATTTCGTAGAAGCCCAAGCCTTCTTACAAGCCATTATCAAAAAACTGGATCGCTCAACCGTTGACTTGATT
AAATGTTAC

SEQ ID 424

MTDLFSKIKEVTELDGIAGYEHSVRDYLRTKITPLVDRVETDGLGGIFGIRDSKAEKAPRILVAAHMDEVGFMVSDIKVDGTLRVVGIGGWNPLVV
SSQRFTLYTRTGQVIPLISGSVPPHFLRGANGSASLPHIEDIVFDGGFTDKAEAERFGITPGDIIIPQSETILTANQKNIISKAWDNRYGVLMITE
MLEALKGQDLNNTLIAGANVQEEVGLRGAHVSTTKFDPELFFAVDCSPAGDIYGNPGTIGDGTLLRFYDPGHVMLKDMRDFLLTTAEEAGVNFQYY
CGKGGTDAGAAHLQNGGVPSTTIGVCARYIHSHQTLYAMDDFVEAQAFLQAIIKKLDRSTVDLIKCY

SEQ ID 425

ATGGTTAATCATTCAAACAGAAAGAAAAAACATGAAAGAAAAATTATTAGTACCTGCTTTAAATTGTTTGCTAGGTCTACTCTTCCTAGG

SEQ ID 426

MVNHSNRKKKHERKIISTCFKLFARSTLPR

SEQ ID 427

GTGTCTAATTCCGGGGGGGTATGGTATAATAACAGTTATGAAAAATAAAAAAATCTTATTTGGGACTGGCCTTGCTGGTGTGGGTTTACTGGCAGCT
GCTGGTTATACCCTAACTAAAAAAGTAACAGATTATAAACGTCAGCAAATCACTCAGACCTTAAGAGAATTTTTTAGTCAGATGGGTGATATTCAG
GTATTTTATTTTAATGAATTTGAATCTGATATTAAAATGACCAGTGGTGGTCTTGTCTTGGAAGATGGCAGAATTTTCGAATTCATTTATCGTCAA
GGTGTTCTTGATTATGTGGAGGTGAGCAAA

SEQ ID 428

MSNSGGYGIITVMKNKKILFGTGLAGVGLLAAAGYTLTKKVTDYKRQQITQTLREFFSQMGDIQVFYFNEFESDIKMTSGGLVLEDGRIFEFIYRQ
GVLDYVEVSK

SEQ ID 429

ATGAGGGATATGAGTAAAAAGAAAATAGGTATGATTTCAGGTATCTTTGGATTTAGTTTAGCTATTGGCCTAGGAATAGTTATCAAAGATTATTGC
CAAGACAGGCAGCGTCGACAAATGACAAGGGATTTACGCACCTTTTTTTCACCTTTAGGACAAATCGAAGTTTTATATATCAATCCTTGTCAGGTC
AAACAAGATTATATTTCAGGTGGGGTTGTTATGTCAAACGGCAAACAGTACCAATTCACCTATCACAGTCGACAAATTAGTTTTGAGGAGGACAAG
GGA

SEQ ID 430

MRDMSKKKIGMISGIFGFSLAIGLGIVIKDYCQDRQRRQMTRDLRTFFSPLGQIEVLYINPCQVKQDYISGGVVMSNGKQYQFTYHSRQISFEEDK
G

SEQ ID 431

ATGATTTTACCAGAATCTTATGAAGAAATAGCAGCCTATATTGATAGCACTAAGAAAGTTGTTTTCTTTTTTACAGCAGATTGGTGTCCAGATTGT
CAATTTATATATCCAGTAATGCCATCAATTGAAAAAGATTTCTCAGATTTTGTCTTTGTACGTGTTAATCGTGATGACTATATAGAATTAGCTCAG
CAGTGGAATATTTTTGGGATTCCGAGTTTCGTTGTTGTGGAAAATGGTCAGGAACTGGGTCGTTTGGTTAATAAGAATCGCAAAACAAAGGCTGAA
ATTACTAAATTTCTCGCTGAAATTAACTATAAA

SEQ ID 432

MILPESYEEIAAYIDSTKKVVFFFTADWCPDCQFIYPVMPSIEKDFSDFVFVRVNRDDYIELAQQWNIFGIPSFVVVENGQELGRLVNKNRKTKAE
ITKFLAEINYK

SEQ ID 433

ATGATCAGACCGACTTCTTATGAGTCATTAGCGACTCTTATTGAAAAAGAAGATAAGCTGGTGTTATTTTTTACGGCAGACTGGTGTCCAGACTGT
CAATTTATTTATCCTATTATGCCAGAAATTGAAGCAGAACTTACAGATATGACTTTTGTTTGTGTTAATCGTGATCAGTTTATAGAGGTAGCACAA
AAGTGGAATATTTTTGGTATTCCTAGTTTTGTCGTGATTGAAAAAGGTCAGGAAGTAGGGCGTCTGGTTAACAAAATGAGAAAGACAAAAACTGAG
ATTATGCATTTTTTAGCTGCTTATCAA

SEQ ID 434

MIRPTSYESLATLIEKEDKLVLFFTADWCPDCQFIYPIMPEIEAELTDMTFVCVNRDQFIEVAQKWNIFGIPSFVVIEKGQEVGRLVNKMRKTKTE
IMHFLAAYQ

SEQ ID 435

ATGATTTTTACTTATAATAGAGAGCATGTTGGTGATACCTTAATGGTTATTGTTAAGGATAGTCAAGGAGCTAAGCTAGATGTTGATCGTCGCGGA
CAAGTAGCACGCGTCTATCTGCAAGATAGTAAAGAAACAGTTGCTTGGAATATCTTTGAAGTGTCAAGTTTAATTGTTATTGAGGGAGCAGGTCAA
ATAACTTTATCTGATCAAGATATTAAAATCCTTAATGCAGAACTACTGAAAGAAGGATTCGAAGACTCTCTTGTTAATAATATTGAACCTACATTT
GTTGTGGCGCAAATTAAAGAAATAATTGATCATCCAGATAGTGACCATTTACATATCTGTCAAGCAGAAATCAACGATGGGAAGACGGTCCAAATC
GTTTGTGGGGCACCTAATGCTTCAGTAGGTCTTAAAACAGTTGCAGCTCTTCCAGGAGCTATGATGCCAAATGGTAGCCTTATTTTCCCAGGAAAA
CTTCGTGGAGAAGATAGCTTTGGAATGTTATGTAGTGCTCGCGAGTTAGCTCTTCCAAATGCTCCTCAAGTCAGAGGTATCATTGAATTATCTGAT
CAGGTAATTGTTGGAGAGTCTTTCGACGCCAATAAACATTGGAAAAAT

SEQ ID 436

MIFTYNREHVGDTLMVIVKDSQGAKLDVDRRGQVARVYLQDSKETVAWNIFEVSSLIVIEGAGQITLSDQDIKILNAELLKEGFEDSLVNNIEPTF
VVAQIKEIIDHPDSDHLHICQAEINDGKTVQIVCGAPNASVGLKTVAALPGAMMPNGSLIFPGKLRGEDSFGMLCSARELALPNAPQVRGIIELSD
QVIVGESFDANKHWKN

SEQ ID 437

ATGATTTTTGCATACAATAAAGAACAAGTTGGCGATGTCTTGATGGTTATCTTACAAGACACCAAAGATATCAAACGTCAAGTAGAACGAAAAGGC
AAAGTAGCCCGTGTTTTTTGCAGAAGAAAGCGGCAAAACCCTTGCTTGGAATATCTTTGAAGCGTCAAGCTTGATTACTATTGAAGGCAATGGACAG
ATTTTTTTGACAGACGAGAACCTTGCAAGATTAAATGCAGAGCTTGCTAAGGAAGGATTTTCAGAAAGGCTTGAACCGATTGTGGGACCTGTTTTT
GTGGTTGGTCAAATTGTTGAGATGGTGGCTCATCCAGATAGCGACCATCTTAATATCTGCCAAGTGGCTATTGGTGAAGATCAAACGGTTCAAATC
GTAGCGGGCGCACCAAATGCTGCGCTTGGTTTAAAAACGATTGTTGCCTTACCAGGTGCTATAATGCCAAATGGTAGTCTGATTTTCCCAGGAAAA
TTGCGTGGTGAAGAAAGTTATGGTATGATGTGCTCTCCTCGTGAGTTAGCCTTGCCAAATGCACCGCAAAAACGTGGCATTATTGAATTTGATGAG
TCAGCTGTGGTAGGAGAAGCTTTTGACCCAGCCAAACATTGGAAAGGT

SEQ ID 438

MIFAYNKEQVGDVLMVILQDTKDIKRQVERKGKVARVFAEESGKTLAWNIFEASSLITIEGNGQIFLTDENLARLNAELAKEGFSERLEPIVGPVF
VVGQIVEMVAHPDSDHLNICQVAIGEDQTVQIVAGAPNAALGLKTIVALPGAIMPNGSLIFPGKLRGEESYGMMCSPRELALPNAPQKRGIIEFDE
SAVVGEAFDPAKHWKG

SEQ ID 439
ATGACAAATGTAACTAGTTATAAAGAAATGCTGGCTAAACCTTGGGGAAAAATACAATATGAAATAACTTTTGCTCAATTAAGCCATATCAAAAAT
CAGAACGTTTTAGATTTTGGAGCTGGTTTTTGTCTCACCGAACAACATCTAGCAAAAGAAAACAATGTAACTGCTATTGAACCCAATCCTAAACTG
CTTTACGATAATCAAAGTGACAATATTTATAAAATCCTAGGTTCCTACGAAGCATTAAGAGATTTGCCTGATCAAAGCTTTGATACTATTATTTGT
CATAATGTTCTTGAATATATAGACAAACATAATCATCCTGCTTATTTTGACGAATTTTCTCGACTTCTAAAACCCAATGGAGAACTATCTCTCATC
AAACATAATATAACCGGTAAAATATTACAATCAGTTATTTTTAGCAATGATACCTCCACTGCGATGGAACTCTTAACAGGAGAAGCAAACTTTAAA
AGTGCCAGTTTTGACCAGGGAAATATTTATACCTTAGAAGAACTAAAACAAAATACAAATTTATTAGTTGAACGTTATCAGGGTATTCGTACCTTC
TATTCATTACAACCAAACCATTTTAAAACTGAAACTGGTTGGCTAAACAAAATGCTTGCTATCGAGCTAAGTGTTGCTGACAAAGCTCCTTATAAA
GATATTGCTTTTTTGCAACACATCACACTTAAAAAGTCATTG

SEQ ID 440
MTNVTSYKEMLAKPWGKIQYEITFAQLSHIKNQNVLDFGAGFCLTEQHLAKENNVTAIEPNPKLLYDNQSDNIYKILGSYEALRDLPDQSFDTIIC
HNVLEYIDKHNHPAYFDEFSRLLKPNGELSLIKHNITGKILQSVIFSNDTSTAMELLTGEANFKSASFDQGNIYTLEELKQNTNLLVERYQGIRTF
YSLQPNHFKTETGWLNKMLAIELSVADKAPYKDIAFLQHITLKKSL

SEQ ID 441
ATGTATAATAAAGTTATTATGATTGGGCGTCTAACAGCAAAGCCTGAGATGGTAAAAACACCAACTGACAAGTCAGTGACGCGTGCAACTGTTGCT
GTTAATAGACGCTTTAAAGGAAGTAATGGTGAGCGTGAAGCAGATTTTATTAATGTGGTTATGTGGGGTCGTCTAGCGGAAACCCTTGCGAGCTAT
GGGACAAAGGGCTCTTTAATTTCAATAGATGGTGAATTGCGTACGCGCAAGTACGAAAAGGATGGTCAAACGCACTATATCACTGAAGTATTAGCA
TCATCATTTCAGTTGCTAGAAAGCCGTGCCCAACGTGCTATGCGTGAAAATAACGTTTCTGGTGATTTGTCAGATTTAGTATTGGAAGAAGAGGAG
CTCCCCTTT

SEQ ID 442
MYNKVIMIGRLTAKPEMVKTPTDKSVTRATVAVNRRFKGSNGEREADFINVVMWGRLAETLASYGTKGSLISIDGELRTRKYEKDGQTHYITEVLA
SSFQLLESRAQRAMRENNVSGDLSDLVLEEEELPF

SEQ ID 443
ATGTATAATAAAGTGATAGCAATCGGTCGTTTGGTAGCTAAACCAGAATTGGTAAAAACAGCTACGGATAAGCATGTAGCACGTCTCTCTTTAGCT
GTTAATCGAAGATTTAAAAATGCTTCTGGAGAGCGAGAAGCTGATTTTATTTCAGTTGTTGTTTGGGGAAAGTTAGCAGAAACTCTGGTTTCTTAT
GCTAGCAAAGGTAGTTTGATGTCTATTGATGGCGAACTTAGGACCCGCAAGTATGATAAAGATGGGCAAGTGCATTATGTGACAGAAGTTCTCTGC
CAATCATTTCAACTGCTTGAAAGTCGTGCTCAGCGCGCTATGAGAGAAAATAATGTTACTAATGATCTAGTTGATTTAGTCTTAGAAGAAGATACT
CTTCCCTTT

SEQ ID 444
MYNKVIAIGRLVAKPELVKTATDKHVARLSLAVNRRFKNASGEREADFISVVVWGKLAETLVSYASKGSLMSIDGELRTRKYDKDGQVHYVTEVLC
QSFQLLESRAQRAMRENNVTNDLVDLVLEEDTLPF

SEQ ID 445
TTGCTTTTCACAGAAAGCAACCTTTTTTTATTGAAAATAGAAAGGCAAACGATTACAATAAAGGGGATAGAAAGCAGGTTTAAGATGGAAAAAGTC
ATTATTTTTGATATGGACGGCGTTATTGTTGATTCCGAGTACACGTTTTTAGATAATAAGACAGAAATGTTACGTGAGGAGGGTATTGATACGGAC
GTCTCGTATCAATACCAGTACATGGGGACTACTTTTGAATTCATGTGGCAAGCTATGAAAGAGGAGTTTGGCTTACCGAAAACAGTAAAAGAGTAT
ATTGCTGAGATGAACAGACGTCGACAAGCGATTGTGGCGCGTGATGGTGTTAGGCCCATCAAAGGAGCTCAGCGACTGATTCATTGGTTACACCAA
CATGGCTATCGCTTAGCAGTTGCGTCCTCATCTCCAATGGTAGATATTAAGCGTAATCTAAAAGAGTTGGGTGTGACAGAATGCTTTGAATACATG
GTTACAGGAGAAGATGTATCGTCTTCTAAACCAGCACCAGATGTTTTTCTTAGAGCTGCAGAGCTTTTAGATGTAGACCCTAAAGTTTGTATAGTT
ATAGAAGATACAAGAAATGGGAGTTTAGCTGCTAAGGCAGCAGGAATGTATTGCTTTGGCTTTGCTAATCCTGATTATCCACCGCAAGATTTATCA
ATGGCAGACAAGGTTATTTCAGATTATCAAGATATCTATATTTATCTTCCGGAG

SEQ ID 446
MLFTESNLFLLKIERQTITIKGIESRFKMEKVIIFDMDGVIVDSEYTFLDNKTEMLREEGIDTDVSYQYQYMGTTFEFMWQAMKEEFGLPKTVKEY
IAEMNRRRQAIVARDGVRPIKGAQRLIHWLHQHGYRLAVASSSPMVDIKRNLKELGVTECFEYMVTGEDVSSSKPAPDVFLRAAELLDVDPKVCIV
IEDTRNGSLAAKAAGMYCFGFANPDYPPQDLSMADKVISDYQDIYIYLPE

SEQ ID 447
ATGTTGATGATTAAAGGAATTATTTTTGATATGGACGGTGTTTTATTTGATACAGAACCTTTTTATCTGAGGCGACGAGAAGATTTTTTTAAGACA
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GCTATCGTTAAGGCAATTACAACTGACTATGACGCTTACAAACAAGCGCATAAGCCTCCTTATCAAAAACTGTTGATTACAGAAGTGAACTCTTGT
CTTGAACAGTTGGAAAAACAAGGTATTAAACTGGCTGTGGCATCAAACTCGAAGCGTCAGGATGTTTTGTTGGCGTTGGAGACAACGCAAATAAAA
GATTATTTTGAAATAATCCTAGCGCGTGAAGATGTTTCTAGAGGCAAACCTTATCCAGATATTTATAATAAAGCAGTACAAAAACTAGGATTACAA
AAAAAACAACTGCTTGTAGTAGAGGACAGCCAAAAAGGCATTGCTGCCGCCAAAGCAGCCAATCTGACAGTTTTTGCCATTACCGACTACCGATAT
GGCATTGATCAGAGTCAAGCTGATCACAAGATAGATCATTTAGGACAACTGTGTGTAAAAATCGGTTGTTTTGGATCG

SEQ ID 448
MLMIKGIIFDMDGVLFDTEPFYLRRREDFFKTKGIPIDHLNSKDFIGGNLQELWKELLGKNRDDAIVKAITTDYDAYKQAHKPPYQKLLITEVNSC
LEQLEKQGIKLAVASNSKRQDVLLALETTQIKDYFEIILARED VSRGKPYPDIYNKAVQKLGLQKKQLLVVEDSQKGIAAAKAANLTVFAITDYRY
GIDQSQADHKIDHLGQLCVKIGCFGS

SEQ ID 449
TTGGTGGACCTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTT
CAGTTC

SEQ ID 450
MVDLWLDQLLVLLEEFIAFFKEAFQVLSILSVQF

SEQ ID 451
GTGGAACCTAAACTATTTAAAATCATCATTGGAATGACAATCATTTTGACAAGTTCCCATCCTGTAAAAATGCCAACAAATAGCATCTGGATACTT
TCGGCAATAATACTAATTAAAATAACTTGGCTTGTTGAAGGG

SEQ ID 452
MEPKLFKIIIGMTIILTSSHPVKMPTNSIWILSAIILIKITWLVEG

SEQ ID 453
ATGTTGATGGTGTTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCTTTTTATTGGTAAATAATAGTTATTTTAGACAGTTAATTGAAGAG
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TTGGTCGAGCGCCCTTTTCTAACAACGATTTCTCATTCTGACTCACTTGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGA
CCTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTCATCGCTTTTTTCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTCAGTTCAGTTCTA
GTCGGCATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAA
AGTATCCAGATGCTATTTGTTGGCATTTTTACAGGATGGGAACTTGTCAAAATGATTGTCATTCCAATGATGATTTTAAATAGTTTAGGTTCCACA
CTTTTCCTTGCGATTTTGAAAACTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTTGAATTGACTCGACAGACTCTG
CCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCATACTAACTTTGATGCTGTGGGATTAACAGAT